



#5

SEQUENCE LISTING

<110> Kleanthous, Harold
Al-Garawi, Amal
Miller, Charles
Tomb, Jean-Francois
Ooomen, Raymond P.

<120> Identification of Polynucleotides
Encoding Novel Helicobacter Polypeptides in the Helicobacter
Genome

<130> 06132/047002

<140> US 09/882,227

<141> 2001-06-15

<150> US 08/902,615

<151> 1997-07-29

<160> 638

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1613

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (64)...(1551)

<400> 1

```
taagaaaaac cgctagagtg caatacaatt cttgaaagat atgaaattaa aaaaggagac 60
ttt atg tta aaa atc aaa tta gaa aaa acc act ttt gaa aac gca aaa 108
    Met Leu Lys Ile Lys Leu Glu Lys Thr Thr Phe Glu Asn Ala Lys
      1             5             10             15

gct gaa tgc agt tta gtt ttt att atc aat aag gat ttt agc cac gct 156
Ala Glu Cys Ser Leu Val Phe Ile Ile Asn Lys Asp Phe Ser His Ala
      20             25             30

tgg gtc aaa aat aaa gag ttg cta gaa acc ttt aaa tac gaa ggc gaa 204
Trp Val Lys Asn Lys Glu Leu Leu Glu Thr Phe Lys Tyr Glu Gly Glu
      35             40             45

ggc gta ttt tta gac caa gaa aat aaa atc ctg tat gcg ggc gtt aaa 252
Gly Val Phe Leu Asp Gln Glu Asn Lys Ile Leu Tyr Ala Gly Val Lys
      50             55             60

gaa gat gat gtg cat tta ttg aga gag agc gcg tgt tta gcc gtt cgc 300
Glu Asp Asp Val His Leu Leu Arg Glu Ser Ala Cys Leu Ala Val Arg
      65             70             75

acc ctt aaa aaa ctc gct ttt aaa agc gtt aaa gtg ggc gtt tat act 348
Thr Leu Lys Lys Leu Ala Phe Lys Ser Val Lys Val Gly Val Tyr Thr
      80             85             90             95
```

tgt ggt gca cat tct aaa gat aac gcg ctt tta gaa aac ttg aaa gcg	396
Cys Gly Ala His Ser Lys Asp Asn Ala Leu Leu Glu Asn Leu Lys Ala	
100 105 110	
ctg ttt ttg ggc ttg aaa tta ggt ttg tat gaa tac gac act ttt aaa	444
Leu Phe Leu Gly Leu Lys Leu Gly Leu Tyr Glu Tyr Asp Thr Phe Lys	
115 120 125	
tcc aac aaa aaa gaa agc gtt tta aaa gaa gcc att gtc gct tta gaa	492
Ser Asn Lys Lys Glu Ser Val Leu Lys Glu Ala Ile Val Ala Leu Glu	
130 135 140	
ttg cac aaa cct tgc gaa aaa act tgc gca aat tct tta gaa aag agt	540
Leu His Lys Pro Cys Glu Lys Thr Cys Ala Asn Ser Leu Glu Lys Ser	
145 150 155	
gct aaa gaa gcg tta aaa tac gct gaa atc atg aca gaa agc ttg aat	588
Ala Lys Glu Ala Leu Lys Tyr Ala Glu Ile Met Thr Glu Ser Leu Asn	
160 165 170 175	
atc gtt aaa gat cta gtc aat acc ccc cct atg att ggc act ccg gtt	636
Ile Val Lys Asp Leu Val Asn Thr Pro Pro Met Ile Gly Thr Pro Val	
180 185 190	
tat atg gct gaa gtg gcg caa aaa gtg gct aaa gaa aac cat tta gaa	684
Tyr Met Ala Glu Val Ala Gln Lys Val Ala Lys Glu Asn His Leu Glu	
195 200 205	
atc cat gtt cat gat gaa aaa ttt tta gaa gaa aag aaa atg aac gcc	732
Ile His Val His Asp Glu Lys Phe Leu Glu Glu Lys Lys Met Asn Ala	
210 215 220	
ttt tta gcg gtc aat aaa gcc tct ctt agc gtc aat cct cct cgc ttg	780
Phe Leu Ala Val Asn Lys Ala Ser Leu Ser Val Asn Pro Pro Arg Leu	
225 230 235	
atc cat tta gtc tat aag cct aaa aaa gcg aag aaa aaa atc gct tta	828
Ile His Leu Val Tyr Lys Pro Lys Lys Ala Lys Lys Lys Ile Ala Leu	
240 245 250 255	
gtg ggt aag ggc ttg act tat gat tgt ggg ggt ttg agc ttg aaa ccg	876
Val Gly Lys Gly Leu Thr Tyr Asp Cys Gly Gly Leu Ser Leu Lys Pro	
260 265 270	
gcc gat tac atg gtt act atg aaa gcg gat aaa ggc ggt ggc tct gcg	924
Ala Asp Tyr Met Val Thr Met Lys Ala Asp Lys Gly Gly Gly Ser Ala	
275 280 285	
gtg att ggg ctt tta aac gca tta gcc aaa cta ggc gtg gag gct gaa	972
Val Ile Gly Leu Leu Asn Ala Leu Ala Lys Leu Gly Val Glu Ala Glu	
290 295 300	
gtg cat ggc att att ggg gct aca gaa aac atg ata ggc cca gcc gct	1020
Val His Gly Ile Ile Gly Ala Thr Glu Asn Met Ile Gly Pro Ala Ala	
305 310 315	
tat aaa cca gat gat att ttg atc tcc aaa gaa ggc aag agc ata gag	1068
Tyr Lys Pro Asp Asp Ile Leu Ile Ser Lys Glu Gly Lys Ser Ile Glu	

320	325	330	335	
gtc cgt aat acc gac gct gag ggg cgt ttg gtt tta gcg gat tgt ttg				1116
Val Arg Asn Thr Asp Ala Glu Gly Arg Leu Val Leu Ala Asp Cys Leu	340	345	350	
agc tac gct caa gat tta aac cct gat gtg atc gtg gat ttt gcg acc				1164
Ser Tyr Ala Gln Asp Leu Asn Pro Asp Val Ile Val Asp Phe Ala Thr	355	360	365	
ctt act ggg gca tgc gtt gta ggc tta ggc gaa ttc act tca gcg atc				1212
Leu Thr Gly Ala Cys Val Val Gly Leu Gly Glu Phe Thr Ser Ala Ile	370	375	380	
atg ggg cat aat gaa gag tta aaa aac ctc ttt gaa act tca ggg tta				1260
Met Gly His Asn Glu Glu Leu Lys Asn Leu Phe Glu Thr Ser Gly Leu	385	390	395	
gaa tcc ggc gaa tta tta gcc aaa ctc ccc ttt aac cgc cat tta aag				1308
Glu Ser Gly Glu Leu Leu Ala Lys Leu Pro Phe Asn Arg His Leu Lys	400	405	410	415
aaa ttg att gaa tct aaa atc gct gat gtg tgc aat att tct tct tca				1356
Lys Leu Ile Glu Ser Lys Ile Ala Asp Val Cys Asn Ile Ser Ser Ser	420	425	430	
cgc tat ggc ggt gcg atc aca gcg ggc ttg ttt tta aat gaa ttt att				1404
Arg Tyr Gly Gly Ala Ile Thr Ala Gly Leu Phe Leu Asn Glu Phe Ile	435	440	445	
aga gat gag ttt aag gat aag tgg cta cac att gac att gca ggc cct				1452
Arg Asp Glu Phe Lys Asp Lys Trp Leu His Ile Asp Ile Ala Gly Pro	450	455	460	
gct tat gtg gaa aaa gaa tgg gat gtg aat agc ttt gga gcg agt ggg				1500
Ala Tyr Val Glu Lys Glu Trp Asp Val Asn Ser Phe Gly Ala Ser Gly	465	470	475	
gct ggc gtg aga gct tgc aca gct ttt gtg gaa gag ctt ttg aaa aag				1548
Ala Gly Val Arg Ala Cys Thr Ala Phe Val Glu Glu Leu Leu Lys Lys	480	485	490	495
gct tgaaatgggc ttgtctgtag gcattgtggg ttgcctaata gtgggcaaat				1601
Ala				
ccagcacctt ta				1613
<210> 2				
<211> 496				
<212> PRT				
<213> Helicobacter pylori				
<400> 2				
Met Leu Lys Ile Lys Leu Glu Lys Thr Thr Phe Glu Asn Ala Lys Ala				
1 5 10 15				
Glu Cys Ser Leu Val Phe Ile Ile Asn Lys Asp Phe Ser His Ala Trp				
20 25 30				
Val Lys Asn Lys Glu Leu Leu Glu Thr Phe Lys Tyr Glu Gly Glu Gly				

BEST AVAILABLE COPY -4-

-5-

<213> Helicobacter pylori

<400> 4

```
Met His Leu Gly Leu Ala Ile Leu Val Ala Gly Ile Gly Gly Phe Val
 1          5          10          15
Gly Asp Gln Ile Tyr Phe Tyr Ile Gly Arg Thr Asn Lys Ala Tyr Ile
 20          25          30
Gln Lys Lys Leu Glu Lys Gln Arg Arg Lys Leu Ala Leu Ala His Leu
 35          40          45
Leu Leu Gln Lys His Gly Trp Phe Ile Ile Phe Ile Gln Arg Tyr Met
 50          55          60
Tyr Gly Met Arg Thr Ile Ile Pro Ile Ser Ile Gly Leu Thr Arg Tyr
 65          70          75          80
Ser Ala Leu Lys Phe Ala Ile Ile Asn Leu Ile Ser Ala Met Val Trp
 85          90          95
Ala Ser Ile Thr Ile Ile Leu Ala Trp Tyr Leu Gly Glu Glu Leu Leu
100          105          110
His Ala Leu Gly Trp Leu Lys Lys His Pro Tyr Ala Leu Ile Leu Leu
115          120          125
Leu Val Ser Phe Leu Ala Leu Val Leu Trp Tyr Phe Gln Tyr Tyr Ser
130          135          140
Lys Lys Asn Arg
145
```

<210> 5

<211> 609

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (61)...(600)

<400> 5

```
taaaaacgct ataataaattc aaaattctac aaccaatccg ttatatataaa ggaaatcaaa 60
atg aat gaa acg ctc aaa gaa gaa ctt tta caa agc atc aga gaa gtg 108
Met Asn Glu Thr Leu Lys Glu Glu Leu Leu Gln Ser Ile Arg Glu Val
 1          5          10          15

aaa gac tac cct aaa aaa ggg att tta ttc aaa gac att acc acg cta 156
Lys Asp Tyr Pro Lys Lys Gly Ile Leu Phe Lys Asp Ile Thr Thr Leu
 20          25          30

ctc aac tac cct aaa ctc ttt aac aaa ctc att gac acg ctc aaa aaa 204
Leu Asn Tyr Pro Lys Leu Phe Asn Lys Leu Ile Asp Thr Leu Lys Lys
 35          40          45

cgc tat ctc gct ctc aat ata gac ttt atc gtg ggc att gaa gcg aga 252
Arg Tyr Leu Ala Leu Asn Ile Asp Phe Ile Val Gly Ile Glu Ala Arg
 50          55          60

ggg ttt att tta ggc tct gct ctc gct tat gcg ctt ggg gtg ggt ttt 300
Gly Phe Ile Leu Gly Ser Ala Leu Ala Tyr Ala Leu Gly Val Gly Phe
 65          70          75          80

gtg cct gtg agg aaa aag ggc aaa ctc ccc gca cac acc cta tct caa 348
Val Pro Val Arg Lys Lys Gly Lys Leu Pro Ala His Thr Leu Ser Gln
 85          90          95
```

agc tac agc cta gaa tac ggg agc gac agc ata gaa atc cac tcc gac	396
Ser Tyr Ser Leu Glu Tyr Gly Ser Asp Ser Ile Glu Ile His Ser Asp	
100 105 110	
gct ttt agg gga att aag ggg gta agg gtg gtg ttg att gat gat tta	444
Ala Phe Arg Gly Ile Lys Gly Val Arg Val Val Leu Ile Asp Asp Leu	
115 120 125	
tta gcc act gga ggc aca gct tta gcg agc ctt gag ctt atc aaa gcc	492
Leu Ala Thr Gly Gly Thr Ala Leu Ala Ser Leu Glu Leu Ile Lys Ala	
130 135 140	
cta caa gcc gaa tgc ata gaa gca tgc ttt ttg ata ggg tta aaa gaa	540
Leu Gln Ala Glu Cys Ile Glu Ala Cys Phe Leu Ile Gly Leu Lys Glu	
145 150 155 160	
tta ccg ggt atc caa ctt tta gaa gaa cgc gtg aaa acc ttt tgt ttg	588
Leu Pro Gly Ile Gln Leu Leu Glu Glu Arg Val Lys Thr Phe Cys Leu	
165 170 175	
tta gag tta gaa taagggtga	609
Leu Glu Leu Glu	
180	

<210> 6
 <211> 180
 <212> PRT
 <213> Helicobacter pylori

<400> 6	
Met Asn Glu Thr Leu Lys Glu Glu Leu Leu Gln Ser Ile Arg Glu Val	
1 5 10 15	
Lys Asp Tyr Pro Lys Lys Gly Ile Leu Phe Lys Asp Ile Thr Thr Leu	
20 25 30	
Leu Asn Tyr Pro Lys Leu Phe Asn Lys Leu Ile Asp Thr Leu Lys Lys	
35 40 45	
Arg Tyr Leu Ala Leu Asn Ile Asp Phe Ile Val Gly Ile Glu Ala Arg	
50 55 60	
Gly Phe Ile Leu Gly Ser Ala Leu Ala Tyr Ala Leu Gly Val Gly Phe	
65 70 75 80	
Val Pro Val Arg Lys Lys Gly Lys Leu Pro Ala His Thr Leu Ser Gln	
85 90 95	
Ser Tyr Ser Leu Glu Tyr Gly Ser Asp Ser Ile Glu Ile His Ser Asp	
100 105 110	
Ala Phe Arg Gly Ile Lys Gly Val Arg Val Val Leu Ile Asp Asp Leu	
115 120 125	
Leu Ala Thr Gly Gly Thr Ala Leu Ala Ser Leu Glu Leu Ile Lys Ala	
130 135 140	
Leu Gln Ala Glu Cys Ile Glu Ala Cys Phe Leu Ile Gly Leu Lys Glu	
145 150 155 160	
Leu Pro Gly Ile Gln Leu Leu Glu Glu Arg Val Lys Thr Phe Cys Leu	
165 170 175	
Leu Glu Leu Glu	
180	

<210> 7

				85					90					95
Asn	Arg	Ile	Lys	Glu	Leu	Glu	Gln	Lys	Ile	Glu	Ala	Leu	Leu	
			100					105					110	

<210> 9
 <211> 778
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (78)...(728)

<400> 9
 aaaaaagaaa acgcaacgca ttaagggtttt ttgtgcaatt ttttgatttc tcttttagaaa 60
 gttttattac cacctta atg aaa atc cta gcc ctt tta atc gct atc ata 110
 Met Lys Ile Leu Ala Leu Leu Ile Ala Ile Ile
 1 5 10

ggg cat gag atc atg cat ggc ttg agc gcg ttt tta ttt ggg gat agg 158
 Gly His Glu Ile Met His Gly Leu Ser Ala Phe Leu Phe Gly Asp Arg
 15 20 25

agc act aaa gac gct agg cgt ttg agt tta aac cct atc agg cat tta 206
 Ser Thr Lys Asp Ala Arg Arg Leu Ser Leu Asn Pro Ile Arg His Leu
 30 35 40

gac atg atg ggt tcg gtg ctt tta ccg gct tta tta ctc att ttt caa 254
 Asp Met Met Gly Ser Val Leu Leu Pro Ala Leu Leu Leu Ile Phe Gln
 45 50 55

gcc cct ttt ttg ttt ggg tgg gcc aaa ccc gtg cct gtt gat atg cgc 302
 Ala Pro Phe Leu Phe Gly Trp Ala Lys Pro Val Pro Val Asp Met Arg
 60 65 70 75

tac att gtc tct caa aaa ggc tct cta gca tgc gta gtg gtg agt tta 350
 Tyr Ile Val Ser Gln Lys Gly Ser Leu Ala Cys Val Val Val Ser Leu
 80 85 90

gcc ggg gtg gct tat aat ttc act ctg gcc gtt ctg ctc gct ttc atc 398
 Ala Gly Val Ala Tyr Asn Phe Thr Leu Ala Val Leu Leu Ala Phe Ile
 95 100 105

acg cat tgg agc ttc caa caa cta ggg atc aac gct tta agc att gat 446
 Thr His Trp Ser Phe Gln Gln Leu Gly Ile Asn Ala Leu Ser Ile Asp
 110 115 120

gaa ttg aat ctt tat cag ctc gct tta gta acc ttt ctc att caa ggc 494
 Glu Leu Asn Leu Tyr Gln Leu Ala Leu Val Thr Phe Leu Ile Gln Gly
 125 130 135

att ctt tat aat ctt gtc tta ggc gtt ttc aat agc ctc cct atc ccg 542
 Ile Leu Tyr Asn Leu Val Leu Gly Val Phe Asn Ser Leu Pro Ile Pro
 140 145 150 155

ccc tta gac ggc tcc aaa gcg tta ggc ttt tta gcg ttg cat ttt aaa 590
 Pro Leu Asp Gly Ser Lys Ala Leu Gly Phe Leu Ala Leu His Phe Lys
 160 165 170

agt gcg ttt tta ttg gaa tgg ttt tct aaa atg gaa cgc tac ggc ttg 638
 Ser Ala Phe Leu Leu Glu Trp Phe Ser Lys Met Glu Arg Tyr Gly Leu
 175 180 185

ttg gta gtg ttt att ttt ttg ttt atc ccc cct tta tcg gag ttt ttt 686
 Leu Val Val Phe Ile Phe Leu Phe Ile Pro Pro Leu Ser Glu Phe Phe
 190 195 200

atc cat gcg ccc aca aga ttt tta ttt tct tta ctc ctc tct 728
 Ile His Ala Pro Thr Arg Phe Leu Phe Ser Leu Leu Leu Ser
 205 210 215

taatctttta tcaaggagag tttatgaata agctcttaaa gttttctcaa 778

<210> 10
 <211> 217
 <212> PRT
 <213> Helicobacter pylori

<400> 10
 Met Lys Ile Leu Ala Leu Leu Ile Ala Ile Ile Gly His Glu Ile Met
 1 5 10 15
 His Gly Leu Ser Ala Phe Leu Phe Gly Asp Arg Ser Thr Lys Asp Ala
 20 25 30
 Arg Arg Leu Ser Leu Asn Pro Ile Arg His Leu Asp Met Met Gly Ser
 35 40 45
 Val Leu Leu Pro Ala Leu Leu Leu Ile Phe Gln Ala Pro Phe Leu Phe
 50 55 60
 Gly Trp Ala Lys Pro Val Pro Val Asp Met Arg Tyr Ile Val Ser Gln
 65 70 75 80
 Lys Gly Ser Leu Ala Cys Val Val Val Ser Leu Ala Gly Val Ala Tyr
 85 90 95
 Asn Phe Thr Leu Ala Val Leu Leu Ala Phe Ile Thr His Trp Ser Phe
 100 105 110
 Gln Gln Leu Gly Ile Asn Ala Leu Ser Ile Asp Glu Leu Asn Leu Tyr
 115 120 125
 Gln Leu Ala Leu Val Thr Phe Leu Ile Gln Gly Ile Leu Tyr Asn Leu
 130 135 140
 Val Leu Gly Val Phe Asn Ser Leu Pro Ile Pro Pro Leu Asp Gly Ser
 145 150 155 160
 Lys Ala Leu Gly Phe Leu Ala Leu His Phe Lys Ser Ala Phe Leu Leu
 165 170 175
 Glu Trp Phe Ser Lys Met Glu Arg Tyr Gly Leu Leu Val Val Phe Ile
 180 185 190
 Phe Leu Phe Ile Pro Pro Leu Ser Glu Phe Phe Ile His Ala Pro Thr
 195 200 205
 Arg Phe Leu Phe Ser Leu Leu Leu Ser
 210 215

<210> 11
 <211> 373
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (70)...(336)

<400> 11
catcagatat tatccaagcg ccttttaaaaa tcttgcgccg tattttcaca cctattgaca 60
tcacgtgg atg aag tca aaa aaa aca ttg att caa aaa gga agt aaa atg 111
Met Lys Ser Lys Lys Thr Leu Ile Gln Lys Gly Ser Lys Met
1 5 10

acg ctc aat gaa gcc att aaa gac aaa gtt tat gaa atc gta gaa atc 159
Thr Leu Asn Glu Ala Ile Lys Asp Lys Val Tyr Glu Ile Val Glu Ile
15 20 25 30

gct aac tgc gat gaa gcc ctt aaa aaa cgc ttt ctc tct ttt ggt atc 207
Ala Asn Cys Asp Glu Ala Leu Lys Lys Arg Phe Leu Ser Phe Gly Ile
35 40 45

cat gaa ggg gtt caa tgc att ctt ttg cat tat tcc atg aaa aaa gcc 255
His Glu Gly Val Gln Cys Ile Leu Leu His Tyr Ser Met Lys Lys Ala
50 55 60

acg ctt tgc gtt aaa atc aac cgc att caa gtg gct tta aga tcc cat 303
Thr Leu Ser Val Lys Ile Asn Arg Ile Gln Val Ala Leu Arg Ser His
65 70 75

gaa gca caa tac ctt gtc atc aaa gaa agc gtg tgaaaatggg tttaaaacgc 356
Glu Ala Gln Tyr Leu Val Ile Lys Glu Ser Val
80 85

gctaaacgct ataataa 373

<210> 12
<211> 89
<212> PRT
<213> Helicobacter pylori

<400> 12
Met Lys Ser Lys Lys Thr Leu Ile Gln Lys Gly Ser Lys Met Thr Leu
1 5 10 15
Asn Glu Ala Ile Lys Asp Lys Val Tyr Glu Ile Val Glu Ile Ala Asn
20 25 30
Cys Asp Glu Ala Leu Lys Lys Arg Phe Leu Ser Phe Gly Ile His Glu
35 40 45
Gly Val Gln Cys Ile Leu Leu His Tyr Ser Met Lys Lys Ala Thr Leu
50 55 60
Ser Val Lys Ile Asn Arg Ile Gln Val Ala Leu Arg Ser His Glu Ala
65 70 75 80
Gln Tyr Leu Val Ile Lys Glu Ser Val
85

<210> 13
<211> 450
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (46)...(375)

<400> 13
gagccagtta attccatggg ttcataagtg attttttggg gctgt atg agg agc tgt 57

	Met	Arg	Ser	Cys	
	1				
ttg ttt ttg aaa act aat tcg gtt tta tcc att tta atg ggc gat aag	105				
Leu Phe Leu Lys Thr Asn Ser Val Leu Ser Ile Leu Met Gly Asp Lys					
5 10 15 20					
cca tca tta aaa acg act gaa ggc ttc atc aaa gtg gct tta att aca	153				
Pro Ser Leu Lys Thr Thr Glu Gly Phe Ile Lys Val Ala Leu Ile Thr					
25 30 35					
gaa ttt ttt aaa agc gat ggg aca aac tcg cta gga gtg aaa ttg gct	201				
Glu Phe Phe Lys Ser Asp Gly Thr Asn Ser Leu Gly Val Lys Leu Ala					
40 45 50					
ttg att gaa gcg tta tca atc tta aag cta gcg aat tgg atc tta tca	249				
Leu Ile Glu Ala Leu Ser Ile Leu Lys Leu Ala Asn Trp Ile Leu Ser					
55 60 65					
aaa atc cat gtt ttt aaa ttt ttt tgc gat tgg cgt tgg aaa aga ggc	297				
Lys Ile His Val Phe Lys Phe Phe Cys Asp Trp Arg Trp Lys Arg Gly					
70 75 80					
ttt aaa aac gcc agg ctt ttc att aca gaa gtg tta att ttt aat tct	345				
Phe Lys Asn Ala Arg Leu Phe Ile Thr Glu Val Leu Ile Phe Asn Ser					
85 90 95 100					
atg gtt ttt aaa tcg gtt agc cct tgc aaa taaattgcag cgctgggttc	395				
Met Val Phe Lys Ser Val Ser Pro Cys Lys					
105 110					
gattaagggc ttgacaatca aattaaacgc cattttccta gctttgggtg aatag	450				
<210> 14					
<211> 110					
<212> PRT					
<213> Helicobacter pylori					
<400> 14					
Met Arg Ser Cys Leu Phe Leu Lys Thr Asn Ser Val Leu Ser Ile Leu					
1 5 10 15					
Met Gly Asp Lys Pro Ser Leu Lys Thr Thr Glu Gly Phe Ile Lys Val					
20 25 30					
Ala Leu Ile Thr Glu Phe Phe Lys Ser Asp Gly Thr Asn Ser Leu Gly					
35 40 45					
Val Lys Leu Ala Leu Ile Glu Ala Leu Ser Ile Leu Lys Leu Ala Asn					
50 55 60					
Trp Ile Leu Ser Lys Ile His Val Phe Lys Phe Phe Cys Asp Trp Arg					
65 70 75 80					
Trp Lys Arg Gly Phe Lys Asn Ala Arg Leu Phe Ile Thr Glu Val Leu					
85 90 95					
Ile Phe Asn Ser Met Val Phe Lys Ser Val Ser Pro Cys Lys					
100 105 110					
<210> 15					
<211> 450					
<212> DNA					
<213> Helicobacter pylori					

<222> (56) ... (394)

1

taatgcgtga gattatttct gatgggaatg aattagtcgc taaagcggcg attgaa 450

<213> Helicobacter pylori

Ala Asn Lys Tyr Met Leu Leu Glu Glu Thr Ile Leu Glu Gly Arg Asp
100 105 110

Lys

<210> 17
 <211> 1350
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (127)...(1251)

<400> 17
 tgtggctgac aggaaggatt tcaaattcgc taaagtttct aaagaagccc aagaaagaag 60
 cgaaaagggt aaggccaata aatacatgct cttagaagag actatttttag aagggagaga 120
 caaata atg cgt gag att att tct gat ggg aat gaa tta gtc gct aaa 168
 Met Arg Glu Ile Ile Ser Asp Gly Asn Glu Leu Val Ala Lys
 1 5 10

gcg gcg att gaa gtg ggg tgt cgg ttt ttt ggg ggc tat cct atc acg 216
 Ala Ala Ile Glu Val Gly Cys Arg Phe Phe Gly Gly Tyr Pro Ile Thr
 15 20 25 30

cca agt tcg gat att atg cat gcg atg agc gtg gct tta ccc aaa tgc 264
 Pro Ser Ser Asp Ile Met His Ala Met Ser Val Ala Leu Pro Lys Cys
 35 40 45

ggc ggt cat ttt atc caa atg gaa gat gaa atc agc ggg att agc gtg 312
 Gly Gly His Phe Ile Gln Met Glu Asp Glu Ile Ser Gly Ile Ser Val
 50 55 60

tct tta gga gcg agc atg agc ggg acg aag tct atg aca gca agc tct 360
 Ser Leu Gly Ala Ser Met Ser Gly Thr Lys Ser Met Thr Ala Ser Ser
 65 70 75

ggg cct ggt att tca ttg aaa gtg gag caa atc ggt tat tct ttc atg 408
 Gly Pro Gly Ile Ser Leu Lys Val Glu Gln Ile Gly Tyr Ser Phe Met
 80 85 90

gcg gaa atc cct tta gtg atc gct gat gtg atg cgt tca ggc cca tca 456
 Ala Glu Ile Pro Leu Val Ile Ala Asp Val Met Arg Ser Gly Pro Ser
 95 100 105 110

acc gga atg ccc act cgt gtg gct caa ggc gat gtg aat ttc tta aga 504
 Thr Gly Met Pro Thr Arg Val Ala Gln Gly Asp Val Asn Phe Leu Arg
 115 120 125

cac ccc ata cat ggg gat ttt aaa gcc gtc gcg ctc gct cct gcg aat 552
 His Pro Ile His Gly Asp Phe Lys Ala Val Ala Leu Ala Pro Ala Asn
 130 135 140

tta gaa gaa gct tac acc gaa acc gtt cgc gcg ttc aat ttg gct gaa 600
 Leu Glu Glu Ala Tyr Thr Glu Thr Val Arg Ala Phe Asn Leu Ala Glu
 145 150 155

atg ctc atg act cct gta ttc ttg ctc atg gat gaa acc gtg ggg cat 648
 Met Leu Met Thr Pro Val Phe Leu Leu Met Asp Glu Thr Val Gly His
 160 165 170

atg tat ggc aag gtg caa atc cca gat tta gaa gaa gtg caa aag atg	696
Met Tyr Gly Lys Val Gln Ile Pro Asp Leu Glu Glu Val Gln Lys Met	
175 180 185 190	
act att aat cgt aag gaa ttt ctg ggc gat aaa aaa gac tac aag cct	744
Thr Ile Asn Arg Lys Glu Phe Leu Gly Asp Lys Lys Asp Tyr Lys Pro	
195 200 205	
tat ggg gtc gca caa gac gag ccg gct gtt ttg aac cct ttc ttt aaa	792
Tyr Gly Val Ala Gln Asp Glu Pro Ala Val Leu Asn Pro Phe Phe Lys	
210 215 220	
ggg tat cgc tac cat gtt tca ggc ttg cac cat ggg cct att ggc ttt	840
Gly Tyr Arg Tyr His Val Ser Gly Leu His His Gly Pro Ile Gly Phe	
225 230 235	
cct act gaa gac gct aaa att ggt ggg gat ttg att gac aga tta ttt	888
Pro Thr Glu Asp Ala Lys Ile Gly Gly Asp Leu Ile Asp Arg Leu Phe	
240 245 250	
aat aag att gaa tcc aag caa gac att atc aac gaa aat gag gaa atg	936
Asn Lys Ile Glu Ser Lys Gln Asp Ile Ile Asn Glu Asn Glu Glu Met	
255 260 265 270	
gat tta gag ggt gct gaa atc gtt gtt atc gct tac ggt tcg gtt tct	984
Asp Leu Glu Gly Ala Glu Ile Val Val Ile Ala Tyr Gly Ser Val Ser	
275 280 285	
ttg gcg gtt aaa gag gcc ttg aaa gat tac cat aaa gaa agc aag caa	1032
Leu Ala Val Lys Glu Ala Leu Lys Asp Tyr His Lys Glu Ser Lys Gln	
290 295 300	
aaa gtc ggc ttt ttc agg cct aaa acc tta tgg cca agc ccg gct aaa	1080
Lys Val Gly Phe Phe Arg Pro Lys Thr Leu Trp Pro Ser Pro Ala Lys	
305 310 315	
cgc ttg aaa gaa ata ggg gat aaa tac gaa aaa atc ctt gtg att gaa	1128
Arg Leu Lys Glu Ile Gly Asp Lys Tyr Glu Lys Ile Leu Val Ile Glu	
320 325 330	
ttg aat aaa ggg cag tat tta gaa gaa att gaa agg gct atg caa aga	1176
Leu Asn Lys Gly Gln Tyr Leu Glu Glu Ile Glu Arg Ala Met Gln Arg	
335 340 345 350	
aag gtg cat ttc ttg ggg caa gcc aat ggg cgc acg att tcg cct aaa	1224
Lys Val His Phe Leu Gly Gln Ala Asn Gly Arg Thr Ile Ser Pro Lys	
355 360 365	
caa atc atc gca aaa ttg aag gag ctt taaaatggcg tttaattatg	1271
Gln Ile Ile Ala Lys Leu Lys Glu Leu	
370 375	
atgaatatatt gcgtgtggat aaaataccca ctttgtggtg ttggggctgt ggcgatggcg	1331
tgattttgaa atccattat	1350

<210> 18
 <211> 375
 <212> PRT

<213> Helicobacter pylori

<400> 18

Met	Arg	Glu	Ile	Ile	Ser	Asp	Gly	Asn	Glu	Leu	Val	Ala	Lys	Ala	Ala		
1				5				10						15			
Ile	Glu	Val	Gly	Cys	Arg	Phe	Phe	Gly	Gly	Tyr	Pro	Ile	Thr	Pro	Ser		
		20						25					30				
Ser	Asp	Ile	Met	His	Ala	Met	Ser	Val	Ala	Leu	Pro	Lys	Cys	Gly	Gly		
	35						40					45					
His	Phe	Ile	Gln	Met	Glu	Asp	Glu	Ile	Ser	Gly	Ile	Ser	Val	Ser	Leu		
	50				55						60						
Gly	Ala	Ser	Met	Ser	Gly	Thr	Lys	Ser	Met	Thr	Ala	Ser	Ser	Gly	Pro		
65					70					75					80		
Gly	Ile	Ser	Leu	Lys	Val	Glu	Gln	Ile	Gly	Tyr	Ser	Phe	Met	Ala	Glu		
			85						90					95			
Ile	Pro	Leu	Val	Ile	Ala	Asp	Val	Met	Arg	Ser	Gly	Pro	Ser	Thr	Gly		
		100						105						110			
Met	Pro	Thr	Arg	Val	Ala	Gln	Gly	Asp	Val	Asn	Phe	Leu	Arg	His	Pro		
		115					120					125					
Ile	His	Gly	Asp	Phe	Lys	Ala	Val	Ala	Leu	Ala	Pro	Ala	Asn	Leu	Glu		
	130					135					140						
Glu	Ala	Tyr	Thr	Glu	Thr	Val	Arg	Ala	Phe	Asn	Leu	Ala	Glu	Met	Leu		
145					150					155					160		
Met	Thr	Pro	Val	Phe	Leu	Leu	Met	Asp	Glu	Thr	Val	Gly	His	Met	Tyr		
			165					170						175			
Gly	Lys	Val	Gln	Ile	Pro	Asp	Leu	Glu	Val	Gln	Lys	Met	Thr	Ile			
		180					185					190					
Asn	Arg	Lys	Glu	Phe	Leu	Gly	Asp	Lys	Lys	Asp	Tyr	Lys	Pro	Tyr	Gly		
		195					200					205					
Val	Ala	Gln	Asp	Glu	Pro	Ala	Val	Leu	Asn	Pro	Phe	Phe	Lys	Gly	Tyr		
	210					215					220						
Arg	Tyr	His	Val	Ser	Gly	Leu	His	His	Gly	Pro	Ile	Gly	Phe	Pro	Thr		
225					230					235					240		
Glu	Asp	Ala	Lys	Ile	Gly	Gly	Asp	Leu	Ile	Asp	Arg	Leu	Phe	Asn	Lys		
			245						250					255			
Ile	Glu	Ser	Lys	Gln	Asp	Ile	Ile	Asn	Glu	Asn	Glu	Glu	Met	Asp	Leu		
		260						265					270				
Glu	Gly	Ala	Glu	Ile	Val	Val	Ile	Ala	Tyr	Gly	Ser	Val	Ser	Leu	Ala		
		275					280					285					
Val	Lys	Glu	Ala	Leu	Lys	Asp	Tyr	His	Lys	Glu	Ser	Lys	Gln	Lys	Val		
	290					295					300						
Gly	Phe	Phe	Arg	Pro	Lys	Thr	Leu	Trp	Pro	Ser	Pro	Ala	Lys	Arg	Leu		
305					310					315					320		
Lys	Glu	Ile	Gly	Asp	Lys	Tyr	Glu	Lys	Ile	Leu	Val	Ile	Glu	Leu	Asn		
			325						330					335			
Lys	Gly	Gln	Tyr	Leu	Glu	Glu	Ile	Glu	Arg	Ala	Met	Gln	Arg	Lys	Val		
		340						345					350				
His	Phe	Leu	Gly	Gln	Ala	Asn	Gly	Arg	Thr	Ile	Ser	Pro	Lys	Gln	Ile		
		355					360					365					
Ile	Ala	Lys	Leu	Lys	Glu	Leu											
	370					375											

<210> 19

<211> 192

<212> DNA

<213> Helicobacter pylori

<220>

```
<400> 19  
tatgataaaa gctctcatat aaccgcgtac tagccataag caacagcaag gca atg      56  
                                         Met  
                                         1  
  
tat tta ggc tta aac cca aaa cgc acc acc aaa agc gcc aca gcc cct      104  
Tyr Leu Gly Leu Asn Pro Lys Arg Thr Thr Lys Ser Ala Thr Ala Pro  
          5                      10                      15  
  
att aaa atc atg ttg atg cgt tgc gcc cag caa aaa ata caa ggc gaa      152  
Ile Lys Ile Met Leu Met Arg Cys Ala Gln Gln Lys Ile Gln Gly Glu  
          20                  25                      30  
  
tct ttc aaa aca tagccaaaat aaccttaaaa aacgcttt      192  
Ser Phe Lys Thr  
        35
```

```
<210> 20
<211> 37
<212> PRT
<213> Helicobacter pylori
```

```

<400> 20
Met Tyr Leu Gly Leu Asn Pro Lys Arg Thr Thr Lys Ser Ala Thr Ala
 1           5           10           15
Pro Ile Lys Ile Met Leu Met Arg Cys Ala Gln Gln Lys Ile Gln Gly
      20           25           30
Glu Ser Phe Lys Thr
      35

```

```
<210> 21
<211> 1080
<212> DNA
<213> Helicobacter pylori
```

```
<220>  
<221> CDS  
<222> (30) ... (1049)
```

<400> 21																	
accataatta gacaaacctt taaggattt atg atg att ttc att gat gca tgt																	53
Met Met Ile Phe Ile Asp Ala Cys																	
1 5																	
ttt aga aag gaa acg cct tac acg ccc att tgg atg atg agg caa gcg																	101
Phe Arg Lys Glu Thr Pro Tyr Thr Pro Ile Trp Met Met Arg Gln Ala																	
10 15 20																	
ggg cgt tac ctt agc gaa tac caa gag agc cgt aaa aaa gcg ggg agt																	149
Gly Arg Tyr Leu Ser Glu Tyr Gln Glu Ser Arg Lys Lys Ala Gly Ser																	
25 30 35 40																	
ttc ttg gaa ttg tgt aaa aat agc gat cta gcc aca gaa gtt acc tta																	197
Phe Leu Glu Leu Cys Lys Asn Ser Asp Leu Ala Thr Glu Val Thr Leu																	

45						50						55						
cag	ccg	gta	gag	att	tta	ggc	gtg	gat	gcg	gct	att	ttg	ttt	agc	gat	245		
Gln	Pro	Val	Glu	Ile	Leu	Gly	Val	Asp	Ala	Ala	Ile	Leu	Phe	Ser	Asp			
		60						65					70					
att	tta	gta	gtg	cct	ttg	gaa	atg	ggc	ttg	aat	ttg	gag	ttt	atc	ccc	293		
Ile	Leu	Val	Val	Pro	Leu	Glu	Met	Gly	Leu	Asn	Leu	Glu	Phe	Ile	Pro			
		75					80					85						
aaa	aag	ggg	ccg	cat	ttt	tta	gag	acg	att	acg	gat	tta	aaa	agc	gtg	341		
Lys	Lys	Gly	Pro	His	Phe	Leu	Glu	Thr	Ile	Thr	Asp	Leu	Lys	Ser	Val			
	90					95					100							
gaa	agc	cta	aaa	gta	ggg	gct	tat	aaa	caa	cta	aac	tat	gtc	tat	gat	389		
Glu	Ser	Leu	Lys	Val	Gly	Ala	Tyr	Lys	Gln	Leu	Asn	Tyr	Val	Tyr	Asp			
105					110					115					120			
acg	att	tct	caa	acg	cgc	caa	aag	ctt	tct	aga	gag	aaa	gcg	tta	atc	437		
Thr	Ile	Ser	Gln	Thr	Arg	Gln	Lys	Leu	Ser	Arg	Glu	Lys	Ala	Leu	Ile			
			125					130						135				
ggt	ttt	tgc	gga	tcg	cct	tgg	act	tta	gcg	act	tac	atg	ata	gaa	ggc	485		
Gly	Phe	Cys	Gly	Ser	Pro	Trp	Thr	Leu	Ala	Thr	Tyr	Met	Ile	Glu	Gly			
		140					145					150						
gag	ggg	agc	aaa	tcg	tat	gcc	aaa	agc	aag	aaa	atg	ctt	tat	agc	gag	533		
Glu	Gly	Ser	Lys	Ser	Tyr	Ala	Lys	Ser	Lys	Lys	Met	Leu	Tyr	Ser	Glu			
		155					160					165						
cct	gaa	gtt	tta	aaa	gcg	ctt	tta	gaa	aaa	tta	agc	ctt	gaa	ttg	ata	581		
Pro	Glu	Val	Leu	Lys	Ala	Leu	Leu	Glu	Lys	Leu	Ser	Leu	Glu	Leu	Ile			
	170					175					180							
gag	tat	ttg	agc	ctt	caa	atc	caa	gca	ggg	gtc	aat	gca	gtg	atg	atc	629		
Glu	Tyr	Leu	Ser	Leu	Gln	Ile	Gln	Ala	Gly	Val	Asn	Ala	Val	Met	Ile			
185					190				195						200			
ttt	gac	tca	tgg	gct	agc	gct	tta	gaa	aaa	gaa	gcg	tat	ttg	aaa	ttc	677		
Phe	Asp	Ser	Trp	Ala	Ser	Ala	Leu	Glu	Lys	Glu	Ala	Tyr	Leu	Lys	Phe			
			205					210					215					
agt	tgg	gat	tat	ttg	aaa	aaa	atc	tct	aaa	gag	ctt	aaa	aaa	cgc	tat	725		
Ser	Trp	Asp	Tyr	Leu	Lys	Lys	Ile	Ser	Lys	Glu	Leu	Lys	Lys	Arg	Tyr			
		220					225					230						
gcg	cat	atc	cca	gtt	atc	ctt	ttc	cct	aaa	ggg	att	ggc	gct	tat	ttg	773		
Ala	His	Ile	Pro	Val	Ile	Leu	Phe	Pro	Lys	Gly	Ile	Gly	Ala	Tyr	Leu			
		235				240						245						
gat	agc	ata	gat	ggg	gaa	ttt	gat	gtg	ttt	ggc	gtg	gat	tgg	ggc	acg	821		
Asp	Ser	Ile	Asp	Gly	Glu	Phe	Asp	Val	Phe	Gly	Val	Asp	Trp	Gly	Thr			
	250				255					260								
cct	tta	act	gcg	gca	aaa	aag	att	tta	ggc	ggt	aag	tat	gtt	ttg	caa	869		
Pro	Leu	Thr	Ala	Ala	Lys	Lys	Ile	Leu	Gly	Gly	Lys	Tyr	Val	Leu	Gln			
265					270				275						280			
ggg	aat	tta	gaa	ccc	acc	cgc	ctt	tat	gat	aaa	aac	gct	tta	gaa	gaa	917		

Gly	Asn	Leu	Glu	Pro	Thr	Arg	Leu	Tyr	Asp	Lys	Asn	Ala	Leu	Glu	Glu	
				285					290					295		
ggg	gtt	gaa	acg	att	cta	aaa	gtc	atg	ggc	aat	caa	ggg	cat	att	ttt	965
Gly	Val	Glu	Thr	Ile	Leu	Lys	Val	Met	Gly	Asn	Gln	Gly	His	Ile	Phe	
			300					305					310			
aat	tta	ggg	cat	ggg	atg	ttg	ccg	gat	tta	ccc	aga	gaa	aac	gcc	aaa	1013
Asn	Leu	Gly	His	Gly	Met	Leu	Pro	Asp	Leu	Pro	Arg	Glu	Asn	Ala	Lys	
		315					320					325				
tat	tta	gtg	caa	tta	gtg	cat	gct	aaa	acc	aga	cga	taggggggatt				1059
Tyr	Leu	Val	Gln	Leu	Val	His	Ala	Lys	Thr	Arg	Arg					
	330					335					340					
gatgaataact atcataagat a																1080
<210> 22																
<211> 340																
<212> PRT																
<213> Helicobacter pylori																
<400> 22																
Met	Met	Ile	Phe	Ile	Asp	Ala	Cys	Phe	Arg	Lys	Glu	Thr	Pro	Tyr	Thr	
1				5					10					15		
Pro	Ile	Trp	Met	Met	Arg	Gln	Ala	Gly	Arg	Tyr	Leu	Ser	Glu	Tyr	Gln	
			20					25					30			
Glu	Ser	Arg	Lys	Lys	Ala	Gly	Ser	Phe	Leu	Glu	Leu	Cys	Lys	Asn	Ser	
		35				40						45				
Asp	Leu	Ala	Thr	Glu	Val	Thr	Leu	Gln	Pro	Val	Glu	Ile	Leu	Gly	Val	
	50					55					60					
Asp	Ala	Ala	Ile	Leu	Phe	Ser	Asp	Ile	Leu	Val	Val	Pro	Leu	Glu	Met	
65				70					75					80		
Gly	Leu	Asn	Leu	Glu	Phe	Ile	Pro	Lys	Lys	Gly	Pro	His	Phe	Leu	Glu	
			85					90						95		
Thr	Ile	Thr	Asp	Leu	Lys	Ser	Val	Glu	Ser	Leu	Lys	Val	Gly	Ala	Tyr	
		100						105					110			
Lys	Gln	Leu	Asn	Tyr	Val	Tyr	Asp	Thr	Ile	Ser	Gln	Thr	Arg	Gln	Lys	
		115					120					125				
Leu	Ser	Arg	Glu	Lys	Ala	Leu	Ile	Gly	Phe	Cys	Gly	Ser	Pro	Trp	Thr	
	130					135					140					
Leu	Ala	Thr	Tyr	Met	Ile	Glu	Gly	Glu	Gly	Ser	Lys	Ser	Tyr	Ala	Lys	
145					150					155					160	
Ser	Lys	Lys	Met	Leu	Tyr	Ser	Glu	Pro	Glu	Val	Leu	Lys	Ala	Leu	Leu	
			165					170						175		
Glu	Lys	Leu	Ser	Leu	Glu	Leu	Ile	Glu	Tyr	Leu	Ser	Leu	Gln	Ile	Gln	
			180					185					190			
Ala	Gly	Val	Asn	Ala	Val	Met	Ile	Phe	Asp	Ser	Trp	Ala	Ser	Ala	Leu	
	195					200						205				
Glu	Lys	Glu	Ala	Tyr	Leu	Lys	Phe	Ser	Trp	Asp	Tyr	Leu	Lys	Lys	Ile	
	210					215					220					
Ser	Lys	Glu	Leu	Lys	Lys	Arg	Tyr	Ala	His	Ile	Pro	Val	Ile	Leu	Phe	
225					230					235					240	
Pro	Lys	Gly	Ile	Gly	Ala	Tyr	Leu	Asp	Ser	Ile	Asp	Gly	Glu	Phe	Asp	
			245					250						255		
Val	Phe	Gly	Val	Asp	Trp	Gly	Thr	Pro	Leu	Thr	Ala	Ala	Lys	Lys	Ile	
			260					265					270			
Leu	Gly	Gly	Lys	Tyr	Val	Leu	Gln	Gly	Asn	Leu	Glu	Pro	Thr	Arg	Leu	
		275					280					285				

Tyr Asp Lys Asn Ala Leu Glu Glu Gly Val Glu Thr Ile Leu Lys Val
 290 295 300
 Met Gly Asn Gln Gly His Ile Phe Asn Leu Gly His Gly Met Leu Pro
 305 310 315 320
 Asp Leu Pro Arg Glu Asn Ala Lys Tyr Leu Val Gln Leu Val His Ala
 325 330 335
 Lys Thr Arg Arg
 340

<210> 23
 <211> 766
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (31)...(732)

<400> 23
 tagacgacta tgtgcattaa gggaatgaaa atg ata cga aaa att tta ata gga 54
 Met Ile Arg Lys Ile Leu Ile Gly
 1 5

ctt ttt ttg agt ttt ttg agc atg gaa gct ggc gaa aaa gtg tat gcg 102
 Leu Phe Leu Ser Phe Leu Ser Met Glu Ala Gly Glu Lys Val Tyr Ala
 10 15 20

att ttc aat gtg aaa gcg aca caa gat tcc aaa ctc acc tta gac agc 150
 Ile Phe Asn Val Lys Ala Thr Gln Asp Ser Lys Leu Thr Leu Asp Ser
 25 30 35 40

aca gga att gtg gat agc att aag gtt act gag ggg agc gtg gtc aaa 198
 Thr Gly Ile Val Asp Ser Ile Lys Val Thr Glu Gly Ser Val Val Lys
 45 50 55

aag ggc gat gtt ttg ttg ctt tta tat aat caa gac aaa cag gct caa 246
 Lys Gly Asp Val Leu Leu Leu Leu Tyr Asn Gln Asp Lys Gln Ala Gln
 60 65 70

agc gat tcc acc gaa caa caa ctc att ttc gct aaa aag caa tac caa 294
 Ser Asp Ser Thr Glu Gln Gln Leu Ile Phe Ala Lys Lys Gln Tyr Gln
 75 80 85

cga tac agc aaa att ggg ggc gct gtg gat aaa aac act cta gag ggt 342
 Arg Tyr Ser Lys Ile Gly Gly Ala Val Asp Lys Asn Thr Leu Glu Gly
 90 95 100

tat gag ttc act tac agg cgc ttg gag tct gat tac gct tat tct att 390
 Tyr Glu Phe Thr Tyr Arg Arg Leu Glu Ser Asp Tyr Ala Tyr Ser Ile
 105 110 115 120

gcg gta ttg aat aaa acc att tta aga gcc cct ttt gat ggc gtg ata 438
 Ala Val Leu Asn Lys Thr Ile Leu Arg Ala Pro Phe Asp Gly Val Ile
 125 130 135

gcg agt aaa aac att caa gtg ggc gaa ggg gtg agc gcg aat aac acg 486
 Ala Ser Lys Asn Ile Gln Val Gly Glu Gly Val Ser Ala Asn Asn Thr
 140 145 150

gtg tta ttg aga tta gtc agc cat gct agg aaa tta gtt att gaa ttt	534
Val Leu Leu Arg Leu Val Ser His Ala Arg Lys Leu Val Ile Glu Phe	
155 160 165	
gat tct aaa tat att aat gcg gtc aaa gta ggg gac act tac acc tat	582
Asp Ser Lys Tyr Ile Asn Ala Val Lys Val Gly Asp Thr Tyr Thr Tyr	
170 175 180	
tct ata gac ggg gat tct aat cag cat gaa gct aaa atc act aag att	630
Ser Ile Asp Gly Asp Ser Asn Gln His Glu Ala Lys Ile Thr Lys Ile	
185 190 195 200	
tac ccc acg gtt gat gaa aac acc agg aaa gtg agc gct gaa gcc ctt	678
Tyr Pro Thr Val Asp Glu Asn Thr Arg Lys Val Ser Ala Glu Ala Leu	
205 210 215	
tta tct aag cct atg gca gtg ggg ctt ttt ggc gat ggg ttt atc caa	726
Leu Ser Lys Pro Met Ala Val Gly Leu Phe Gly Asp Gly Phe Ile Gln	
220 225 230	
acg aaa taataggata ttttgatgta taaaacagcg atta	766
Thr Lys	

<210> 24
 <211> 234
 <212> PRT
 <213> Helicobacter pylori

<400> 24

Met Ile Arg Lys Ile Leu Ile Gly Leu Phe Leu Ser Phe Leu Ser Met	
1 5 10 15	
Glu Ala Gly Glu Lys Val Tyr Ala Ile Phe Asn Val Lys Ala Thr Gln	
20 25 30	
Asp Ser Lys Leu Thr Leu Asp Ser Thr Gly Ile Val Asp Ser Ile Lys	
35 40 45	
Val Thr Glu Gly Ser Val Val Lys Lys Gly Asp Val Leu Leu Leu Leu	
50 55 60	
Tyr Asn Gln Asp Lys Gln Ala Gln Ser Asp Ser Thr Glu Gln Gln Leu	
65 70 75 80	
Ile Phe Ala Lys Lys Gln Tyr Gln Arg Tyr Ser Lys Ile Gly Gly Ala	
85 90 95	
Val Asp Lys Asn Thr Leu Glu Gly Tyr Glu Phe Thr Tyr Arg Arg Leu	
100 105 110	
Glu Ser Asp Tyr Ala Tyr Ser Ile Ala Val Leu Asn Lys Thr Ile Leu	
115 120 125	
Arg Ala Pro Phe Asp Gly Val Ile Ala Ser Lys Asn Ile Gln Val Gly	
130 135 140	
Glu Gly Val Ser Ala Asn Asn Thr Val Leu Leu Arg Leu Val Ser His	
145 150 155 160	
Ala Arg Lys Leu Val Ile Glu Phe Asp Ser Lys Tyr Ile Asn Ala Val	
165 170 175	
Lys Val Gly Asp Thr Tyr Thr Tyr Ser Ile Asp Gly Asp Ser Asn Gln	
180 185 190	
His Glu Ala Lys Ile Thr Lys Ile Tyr Pro Thr Val Asp Glu Asn Thr	
195 200 205	
Arg Lys Val Ser Ala Glu Ala Leu Leu Ser Lys Pro Met Ala Val Gly	

210 215 220
 Leu Phe Gly Asp Gly Phe Ile Gln Thr Lys
 225 230

<210> 25
 <211> 630
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (62)...(544)

<221> misc_feature
 <222> 42, 47
 <223> n = A,T,C or G

<400> 25
 acgccaaaga gagcaacggg gagtttttag tcgcttttagc gnagcgnnttg tgctgattta 60
 t atg att tta gcg gcg ttg tat gag tcc att tta gag cct ttt atc atc 109
 Met Ile Leu Ala Ala Leu Tyr Glu Ser Ile Leu Glu Pro Phe Ile Ile
 1 5 10 15

 atg gtt acc atg cct tta agt ttt tca ggg gcg ttt ttt gct cta ggt 157
 Met Val Thr Met Pro Leu Ser Phe Ser Gly Ala Phe Phe Ala Leu Gly
 20 25 30

 tta gtc cat cag cct ttg agc atg ttc tct atg ata ggc ttg att ttg 205
 Leu Val His Gln Pro Leu Ser Met Phe Ser Met Ile Gly Leu Ile Leu
 35 40 45

 ctc att ggt atg gtg ggt aaa aac gcc acg ctt tta att gat gtg gcg 253
 Leu Ile Gly Met Val Gly Lys Asn Ala Thr Leu Leu Ile Asp Val Ala
 50 55 60

 aat gaa gag cgt aaa aaa ggt ttg aat atc caa gag gcc att tta ttt 301
 Asn Glu Glu Arg Lys Lys Gly Leu Asn Ile Gln Glu Ala Ile Leu Phe
 65 70 75 80

 gcc ggc aaa acc cgt cta aga ccg att tta atg acg acc att gcg atg 349
 Ala Gly Lys Thr Arg Leu Arg Pro Ile Leu Met Thr Thr Ile Ala Met
 85 90 95

 gtt tgc ggg atg ctg cct tta gcg ttg gcg agt ggg gat gga gcg gcg 397
 Val Cys Gly Met Leu Pro Leu Ala Leu Ala Ser Gly Asp Gly Ala Ala
 100 105 110

 atg aaa tcc cct ata ggg att gcg atg agt ggg ggc ttg atg att tct 445
 Met Lys Ser Pro Ile Gly Ile Ala Met Ser Gly Gly Leu Met Ile Ser
 115 120 125

 atg gtg tta agc tta ctc att gtg ccg gtg ttt tat cgt ttg ctc gct 493
 Met Val Leu Ser Leu Leu Ile Val Pro Val Phe Tyr Arg Leu Leu Ala
 130 135 140

 ccc ata gac gac aaa atc aag cgg ttt tat caa aac caa aaa act tta 541
 Pro Ile Asp Asp Lys Ile Lys Arg Phe Tyr Gln Asn Gln Lys Thr Leu
 145 150 155 160

gaa tgaaaaaaat tgctttcatt ttggctttat ggggtgggctt gttaggggcg 594
Glu

tttgagccta aaaaaagtca tatttatittt ggggct 630

<210> 26
<211> 161
<212> PRT
<213> Helicobacter pylori

<400> 26
Met Ile Leu Ala Ala Leu Tyr Glu Ser Ile Leu Glu Pro Phe Ile Ile
1 5 10 15
Met Val Thr Met Pro Leu Ser Phe Ser Gly Ala Phe Phe Ala Leu Gly
20 25 30
Leu Val His Gln Pro Leu Ser Met Phe Ser Met Ile Gly Leu Ile Leu
35 40 45
Leu Ile Gly Met Val Gly Lys Asn Ala Thr Leu Leu Ile Asp Val Ala
50 55 60
Asn Glu Glu Arg Lys Lys Gly Leu Asn Ile Gln Glu Ala Ile Leu Phe
65 70 75 80
Ala Gly Lys Thr Arg Leu Arg Pro Ile Leu Met Thr Thr Ile Ala Met
85 90 95
Val Cys Gly Met Leu Pro Leu Ala Leu Ala Ser Gly Asp Gly Ala Ala
100 105 110
Met Lys Ser Pro Ile Gly Ile Ala Met Ser Gly Gly Leu Met Ile Ser
115 120 125
Met Val Leu Ser Leu Leu Ile Val Pro Val Phe Tyr Arg Leu Leu Ala
130 135 140
Pro Ile Asp Asp Lys Ile Lys Arg Phe Tyr Gln Asn Gln Lys Thr Leu
145 150 155 160
Glu

<210> 27
<211> 1007
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (19)...(945)

<221> misc_feature
<222> 920
<223> n = A,T,C or G

<400> 27
taaaagggttt ttacaaac atg ata aaa agc caa aaa gaa tat tta gaa aga 51
Met Ile Lys Ser Gln Lys Glu Tyr Leu Glu Arg
1 5 10
att gca tat tta aac acc cta tcg cac cat tat tac aac ctt gat gaa 99
Ile Ala Tyr Leu Asn Thr Leu Ser His His Tyr Tyr Asn Leu Asp Glu
15 20 25

ccc atc gta agc gat gcg atc tat gat gaa ctt tac caa gaa ttg aaa	147
Pro Ile Val Ser Asp Ala Ile Tyr Asp Glu Leu Tyr Gln Glu Leu Lys	
30 35 40	
gct tat gaa gaa aaa aac cct aat ggc att caa gct aat tcc cct acc	195
Ala Tyr Glu Glu Lys Asn Pro Asn Gly Ile Gln Ala Asn Ser Pro Thr	
45 50 55	
caa aaa gtg ggg gct act acc acc aat tcg ttc aat aaa aac ccc cat	243
Gln Lys Val Gly Ala Thr Thr Thr Asn Ser Phe Asn Lys Asn Pro His	
60 65 70 75	
tta atg cgg atg tgg agc tta gat gat gtg ttc aat caa agc gaa ttg	291
Leu Met Arg Met Trp Ser Leu Asp Asp Val Phe Asn Gln Ser Glu Leu	
80 85 90	
caa gcg tgg ttg caa cgc att tta aaa gcc tat cct agt gct tcg ttc	339
Gln Ala Trp Leu Gln Arg Ile Leu Lys Ala Tyr Pro Ser Ala Ser Phe	
95 100 105	
gtg tgt tcg ccc aaa ctt gat ggg gtt tcg ctc aat ctt ttg tat caa	387
Val Cys Ser Pro Lys Leu Asp Gly Val Ser Leu Asn Leu Leu Tyr Gln	
110 115 120	
cat ggc aag cta gtg aag gcg acc act agg ggc aac ggc tta gaa gga	435
His Gly Lys Leu Val Lys Ala Thr Thr Arg Gly Asn Gly Leu Glu Gly	
125 130 135	
gaa tta gtt agc gca aac gct aaa cac atc gct aat atc ccc cac gct	483
Glu Leu Val Ser Ala Asn Ala Lys His Ile Ala Asn Ile Pro His Ala	
140 145 150 155	
atc gct tat aat gga gaa ata gaa atc agg ggc gaa gtg atc att tct	531
Ile Ala Tyr Asn Gly Glu Ile Glu Ile Arg Gly Glu Val Ile Ile Ser	
160 165 170	
aaa aag gat ttt gac gct ttg aat caa gag cgc tta aac gct aat gaa	579
Lys Lys Asp Phe Asp Ala Leu Asn Gln Glu Arg Leu Asn Ala Asn Glu	
175 180 185	
ccc cta ttc gct aac ccc aga aac gcc gca tca ggg agt ttg agg caa	627
Pro Leu Phe Ala Asn Pro Arg Asn Ala Ala Ser Gly Ser Leu Arg Gln	
190 195 200	
ctt gat agc gaa atc act aaa aag cgt aaa ttg caa ttc att cct tgg	675
Leu Asp Ser Glu Ile Thr Lys Lys Arg Lys Leu Gln Phe Ile Pro Trp	
205 210 215	
ggc gtg ggc aag cat tct tta aat ttt tta agc ttt aag gag tgt ttg	723
Gly Val Gly Lys His Ser Leu Asn Phe Leu Ser Phe Lys Glu Cys Leu	
220 225 230 235	
gat ttt atc gtc tcg tta ggt ttt agc gcc att caa tac tta agc cta	771
Asp Phe Ile Val Ser Leu Gly Phe Ser Ala Ile Gln Tyr Leu Ser Leu	
240 245 250	
aac aaa aac cac caa gaa ata gaa gac aat tac cac acc cta att aga	819
Asn Lys Asn His Gln Glu Ile Glu Asp Asn Tyr His Thr Leu Ile Arg	
255 260 265	

gaa agg gag ggc ttt ttt gcc ctt tta gac ggc atg gtg atc gtt gtg 867
 Glu Arg Glu Gly Phe Phe Ala Leu Leu Asp Gly Met Val Ile Val Val
 270 275 280

 aat gaa tta aat att caa aag gag cta ggc tac acg caa aaa tcc cct 915
 Asn Glu Leu Asn Ile Gln Lys Glu Leu Gly Tyr Thr Gln Lys Ser Pro
 285 290 295

 aaa tng ctt gcg ctt ata aat tcc cgg ctt tagaaaaaca caccaaaatt 965
 Lys Xaa Leu Ala Leu Ile Asn Ser Arg Leu
 300 305

 gtaggagtca ttaaccaagt ggggcgcass gggcgatcac ac 1007

<210> 28
 <211> 309
 <212> PRT
 <213> Helicobacter pylori

<220>
 <221> VARIANT
 <222> 301
 <223> Xaa = Any Amino Acid

<400> 28
 Met Ile Lys Ser Gln Lys Glu Tyr Leu Glu Arg Ile Ala Tyr Leu Asn
 1 5 10 15
 Thr Leu Ser His His Tyr Tyr Asn Leu Asp Glu Pro Ile Val Ser Asp
 20 25 30
 Ala Ile Tyr Asp Glu Leu Tyr Gln Glu Leu Lys Ala Tyr Glu Glu Lys
 35 40 45
 Asn Pro Asn Gly Ile Gln Ala Asn Ser Pro Thr Gln Lys Val Gly Ala
 50 55 60
 Thr Thr Thr Asn Ser Phe Asn Lys Asn Pro His Leu Met Arg Met Trp
 65 70 75 80
 Ser Leu Asp Asp Val Phe Asn Gln Ser Glu Leu Gln Ala Trp Leu Gln
 85 90 95
 Arg Ile Leu Lys Ala Tyr Pro Ser Ala Ser Phe Val Cys Ser Pro Lys
 100 105 110
 Leu Asp Gly Val Ser Leu Asn Leu Leu Tyr Gln His Gly Lys Leu Val
 115 120 125
 Lys Ala Thr Thr Arg Gly Asn Gly Leu Glu Gly Glu Leu Val Ser Ala
 130 135 140
 Asn Ala Lys His Ile Ala Asn Ile Pro His Ala Ile Ala Tyr Asn Gly
 145 150 155 160
 Glu Ile Glu Ile Arg Gly Glu Val Ile Ile Ser Lys Lys Asp Phe Asp
 165 170 175
 Ala Leu Asn Gln Glu Arg Leu Asn Ala Asn Glu Pro Leu Phe Ala Asn
 180 185 190
 Pro Arg Asn Ala Ala Ser Gly Ser Leu Arg Gln Leu Asp Ser Glu Ile
 195 200 205
 Thr Lys Lys Arg Lys Leu Gln Phe Ile Pro Trp Gly Val Gly Lys His
 210 215 220
 Ser Leu Asn Phe Leu Ser Phe Lys Glu Cys Leu Asp Phe Ile Val Ser
 225 230 235 240
 Leu Gly Phe Ser Ala Ile Gln Tyr Leu Ser Leu Asn Lys Asn His Gln
 245 250 255
 Glu Ile Glu Asp Asn Tyr His Thr Leu Ile Arg Glu Arg Glu Gly Phe

			260					265				270					
Phe	Ala	Leu	Leu	Asp	Gly	Met	Val	Ile	Val	Val	Asn	Glu	Leu	Asn	Ile		
		275					280					285					
Gln	Lys	Glu	Leu	Gly	Tyr	Thr	Gln	Lys	Ser	Pro	Lys	Xaa	Leu	Ala	Leu		
	290					295					300						
Ile	Asn	Ser	Arg	Leu													
305																	

<210> 29
 <211> 937
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (44)...(880)

<400> 29																
gtg	ctt	ttaga	ttagatgcag	aaaaagacgc	ccaactttat	ggc	atg	aat	att	ttt						55
							Met	Asn	Ile	Phe						
							1									
aag	atc	cga	gaa	att	atc	cat	tat	gac	ggg	gag	gtt	aca	gag	att	ctt	103
Lys	Ile	Arg	Glu	Ile	Ile	His	Tyr	Asp	Gly	Glu	Val	Thr	Glu	Ile	Leu	
5					10					15					20	
ggg	ggg	agc	gat	ggc	gtg	atg	ctc	ggg	ttt	ctt	agc	gtt	agg	ggc	gag	151
Gly	Gly	Ser	Asp	Gly	Val	Met	Leu	Gly	Phe	Leu	Ser	Val	Arg	Gly	Glu	
				25					30					35		
tct	atc	cct	tta	gtg	gat	gtg	aaa	agg	tgg	ttg	cat	tat	aac	gct	aat	199
Ser	Ile	Pro	Leu	Val	Asp	Val	Lys	Arg	Trp	Leu	His	Tyr	Asn	Ala	Asn	
			40				45						50			
gat	ccg	agc	cgt	gat	cta	aaa	gaa	tgc	agc	gtt	aaa	gat	gac	cat	aat	247
Asp	Pro	Ser	Arg	Asp	Leu	Lys	Glu	Cys	Ser	Val	Lys	Asp	Asp	His	Asn	
		55					60					65				
ttg	gtg	att	gtg	tgc	cat	ttt	tct	aac	cat	tcc	atc	gct	cta	aag	gtt	295
Leu	Val	Ile	Val	Cys	His	Phe	Ser	Asn	His	Ser	Ile	Ala	Leu	Lys	Val	
	70					75					80					
tta	aaa	att	gaa	agg	atc	atc	cat	aaa	aat	tgg	act	gag	att	agc	gct	343
Leu	Lys	Ile	Glu	Arg	Ile	Ile	His	Lys	Asn	Trp	Thr	Glu	Ile	Ser	Ala	
	85				90					95					100	
ggg	gac	aaa	caa	ggc	att	aat	gaa	gag	ggt	aag	ctt	agc	gct	atc	act	391
Gly	Asp	Lys	Gln	Gly	Ile	Asn	Glu	Glu	Gly	Lys	Leu	Ser	Ala	Ile	Thr	
				105					110					115		
cgt	ttt	gat	gaa	gaa	cga	gtg	gtg	cag	atc	tta	gat	gtg	gaa	aaa	atg	439
Arg	Phe	Asp	Glu	Glu	Arg	Val	Val	Gln	Ile	Leu	Asp	Val	Glu	Lys	Met	
			120					125					130			
att	agc	gat	gtt	ttc	cct	agc	ttg	aaa	gat	tta	gac	gat	ttg	act	ttg	487
Ile	Ser	Asp	Val	Phe	Pro	Ser	Leu	Lys	Asp	Leu	Asp	Asp	Leu	Thr	Leu	
		135					140					145				

cg	tgc	ata	gaa	gcc	att	caa	agc	caa	aaa	ctc	att	tta	atc	gct	gaa	535
Arg	Cys	Ile	Glu	Ala	Ile	Gln	Ser	Gln	Lys	Leu	Ile	Leu	Ile	Ala	Glu	
	150					155					160					
gac	tcc	cta	agc	gct	ctt	aaa	acc	tta	gaa	aag	atc	gtt	caa	act	tta	583
Asp	Ser	Leu	Ser	Ala	Leu	Lys	Thr	Leu	Glu	Lys	Ile	Val	Gln	Thr	Leu	
	165				170					175					180	
gaa	ttg	cg	tat	tta	gct	ttt	cca	aac	ggg	agg	gaa	ttg	ttg	gat	tat	631
Glu	Leu	Arg	Tyr	Leu	Ala	Phe	Pro	Asn	Gly	Arg	Glu	Leu	Leu	Asp	Tyr	
				185					190						195	
ttg	tat	gaa	aaa	gaa	cat	tac	caa	caa	gtt	ggc	gtg	gtc	att	acg	gat	679
Leu	Tyr	Glu	Lys	Glu	His	Tyr	Gln	Gln	Val	Gly	Val	Val	Ile	Thr	Asp	
			200					205					210			
tta	gaa	atg	cct	aac	att	tca	ggg	ttt	gaa	gtg	tta	aaa	acc	att	aaa	727
Leu	Glu	Met	Pro	Asn	Ile	Ser	Gly	Phe	Glu	Val	Leu	Lys	Thr	Ile	Lys	
		215					220					225				
gct	gat	cat	aga	act	gag	cat	ctt	cct	gtg	att	atc	aat	tcg	tcc	atg	775
Ala	Asp	His	Arg	Thr	Glu	His	Leu	Pro	Val	Ile	Ile	Asn	Ser	Ser	Met	
	230					235					240					
agc	agc	gat	tct	aac	cgc	cag	tta	gcc	caa	tct	tta	gaa	gcg	gat	ggt	823
Ser	Ser	Asp	Ser	Asn	Arg	Gln	Leu	Ala	Gln	Ser	Leu	Glu	Ala	Asp	Gly	
	245				250					255					260	
ttt	gtg	gta	aaa	tct	aac	att	ctt	gaa	atc	cat	gaa	atg	ctt	aaa	aaa	871
Phe	Val	Val	Lys	Ser	Asn	Ile	Leu	Glu	Ile	His	Glu	Met	Leu	Lys	Lys	
				265				270						275		
acg	ctt	tca	taa	att	ta	tt	gt	tt	tt	ta	aa	agg	g	g	g	920
Thr	Leu	Ser														
cg	aag	tc	att	tt	gc	ac										937
<210> 30																
<211> 279																
<212> PRT																
<213> Helicobacter pylori																
<400> 30																
Met	Asn	Ile	Phe	Lys	Ile	Arg	Glu	Ile	Ile	His	Tyr	Asp	Gly	Glu	Val	
1				5					10					15		
Thr	Glu	Ile	Leu	Gly	Gly	Ser	Asp	Gly	Val	Met	Leu	Gly	Phe	Leu	Ser	
			20					25					30			
Val	Arg	Gly	Glu	Ser	Ile	Pro	Leu	Val	Asp	Val	Lys	Arg	Trp	Leu	His	
		35					40					45				
Tyr	Asn	Ala	Asn	Asp	Pro	Ser	Arg	Asp	Leu	Lys	Glu	Cys	Ser	Val	Lys	
	50					55					60					
Asp	Asp	His	Asn	Leu	Val	Ile	Val	Cys	His	Phe	Ser	Asn	His	Ser	Ile	
65					70					75					80	
Ala	Leu	Lys	Val	Leu	Lys	Ile	Glu	Arg	Ile	Ile	His	Lys	Asn	Trp	Thr	
			85					90						95		
Glu	Ile	Ser	Ala	Gly	Asp	Lys	Gln	Gly	Ile	Asn	Glu	Glu	Gly	Lys	Leu	
			100					105					110			
Ser	Ala	Ile	Thr	Arg	Phe	Asp	Glu	Glu	Arg	Val	Val	Gln	Ile	Leu	Asp	

95						100						105						
gaa	gtg	atc	tta	aaa	agc	gtg	att	gaa	gta	gaa	gtg	agt	gaa	aac	act	389		
Glu	Val	Ile	Leu	Lys	Ser	Val	Ile	Glu	Val	Glu	Val	Ser	Glu	Asn	Thr			
		110					115					120						
gct	aaa	gaa	agg	gtt	tta	ggg	cgc	tct	agg	ggg	gct	gat	gat	aat	gaa	437		
Ala	Lys	Glu	Arg	Val	Leu	Gly	Arg	Ser	Arg	Gly	Ala	Asp	Asp	Asn	Glu			
	125					130					135							
aag	gtg	ttt	cat	aac	cgc	atg	cgg	gtg	ttt	ttg	gat	ccg	ttg	ggc	gag	485		
Lys	Val	Phe	His	Asn	Arg	Met	Arg	Val	Phe	Leu	Asp	Pro	Leu	Gly	Glu			
	140				145					150					155			
atc	caa	aat	ttt	tac	aag	aat	aag	aag	gtg	tat	aaa	gcg	atc	gat	ggg	533		
Ile	Gln	Asn	Phe	Tyr	Lys	Asn	Lys	Lys	Val	Tyr	Lys	Ala	Ile	Asp	Gly			
				160					165					170				
gag	agg	agc	att	gaa	gag	att	gtg	ggc	gaa	atg	caa	gag	tat	atc	ttg	581		
Glu	Arg	Ser	Ile	Glu	Glu	Ile	Val	Gly	Glu	Met	Gln	Glu	Tyr	Ile	Leu			
			175					180					185					
tct	ttc	ggt	aat	taaaatgcac	tctcaaggag	aatagctgtg	atttctg									630		
Ser	Phe	Gly	Asn															
			190															

<210> 32

<211> 191

<212> PRT

<213> Helicobacter pylori

<400> 32

Met	Lys	Gln	Leu	Phe	Leu	Ile	Ile	Gly	Ala	Pro	Gly	Ser	Gly	Lys	Thr	
1				5					10					15		
Thr	Asp	Ala	Glu	Leu	Ile	Ala	Lys	Asn	Asn	Ser	Glu	Thr	Ile	Ala	His	
			20					25					30			
Phe	Ser	Thr	Gly	Asp	Leu	Leu	Arg	Ala	Glu	Ser	Ala	Lys	Lys	Thr	Glu	
		35					40					45				
Arg	Gly	Leu	Leu	Ile	Glu	Lys	Phe	Thr	Ser	Gln	Gly	Glu	Leu	Val	Pro	
	50				55						60					
Leu	Glu	Ile	Val	Val	Glu	Thr	Ile	Leu	Ser	Ala	Ile	Lys	Ser	Ser	Gly	
	65				70					75					80	
Lys	Gly	Ile	Ile	Leu	Ile	Asp	Gly	Tyr	Pro	Arg	Ser	Val	Glu	Gln	Met	
			85						90					95		
Gln	Ala	Leu	Asp	Lys	Glu	Leu	Asn	Ala	Gln	Asn	Glu	Val	Ile	Leu	Lys	
			100					105					110			
Ser	Val	Ile	Glu	Val	Glu	Val	Ser	Glu	Asn	Thr	Ala	Lys	Glu	Arg	Val	
		115					120					125				
Leu	Gly	Arg	Ser	Arg	Gly	Ala	Asp	Asp	Asn	Glu	Lys	Val	Phe	His	Asn	
	130				135						140					
Arg	Met	Arg	Val	Phe	Leu	Asp	Pro	Leu	Gly	Glu	Ile	Gln	Asn	Phe	Tyr	
	145				150					155					160	
Lys	Asn	Lys	Lys	Val	Tyr	Lys	Ala	Ile	Asp	Gly	Glu	Arg	Ser	Ile	Glu	
			165						170					175		
Glu	Ile	Val	Gly	Glu	Met	Gln	Glu	Tyr	Ile	Leu	Ser	Phe	Gly	Asn		
			180					185						190		

<210> 33
 <211> 777
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (1)...(717)

```

<400> 33
agt tac ccc ccc ccc ccc aat ccc aca caa gaa acg caa caa gat ttt 48
Ser Tyr Pro Pro Pro Pro Asn Pro Thr Gln Glu Thr Gln Gln Asp Phe
1 5 10 15

att att gaa gca caa caa gat ttg att att gaa acg caa caa gac ccc 96
Ile Ile Glu Ala Gln Gln Asp Leu Ile Ile Glu Thr Gln Gln Asp Pro
20 25 30

aaa gaa cta cct gag tct tgc aaa ata acg ccc caa aaa atc tct ttt 144
Lys Glu Leu Pro Glu Ser Cys Lys Ile Thr Pro Gln Lys Ile Ser Phe
35 40 45

aac caa gtg gtt ttt aaa aaa att aaa aga aaa ctc aac cgc ttc att 192
Asn Gln Val Val Phe Lys Lys Ile Lys Arg Lys Leu Asn Arg Phe Ile
50 55 60

gga agc att tta gct cgg aca gaa gtg tat aag aat ctc gtg gca aaa 240
Gly Ser Ile Leu Ala Arg Thr Glu Val Tyr Lys Asn Leu Val Ala Lys
65 70 75 80

tac gat gaa ctc aca gga aaa tac gaa tca tta ttg gca aaa gag gca 288
Tyr Asp Glu Leu Thr Gly Lys Tyr Glu Ser Leu Leu Ala Lys Glu Ala
85 90 95

aac atc aaa gag acc ttt tgg gaa agg cgt gct gat agc gaa aaa gaa 336
Asn Ile Lys Glu Thr Phe Trp Glu Arg Arg Ala Asp Ser Glu Lys Glu
100 105 110

gcc ttt ttt tta gag cat ttt tac ctc act agc gtg tat gtg gct tct 384
Ala Phe Phe Leu Glu His Phe Tyr Leu Thr Ser Val Tyr Val Ala Ser
115 120 125

aca gca gga tac tat atc acg cct aag ggc gct aaa acc ttt ata gaa 432
Thr Ala Gly Tyr Tyr Ile Thr Pro Lys Gly Ala Lys Thr Phe Ile Glu
130 135 140

gcc acg gag cgt ttt aaa atc ata gag ccg gtg gat atg ttc ata aac 480
Ala Thr Glu Arg Phe Lys Ile Ile Glu Pro Val Asp Met Phe Ile Asn
145 150 155 160

aac ccc act tac cat gat gtg gct aat ttt acc tat ttg cct tgc cct 528
Asn Pro Thr Tyr His Asp Val Ala Asn Phe Thr Tyr Leu Pro Cys Pro
165 170 175

gtt tct tta aac aag cat gct ttc aat agc acc att caa aat gca aaa 576
Val Ser Leu Asn Lys His Ala Phe Asn Ser Thr Ile Gln Asn Ala Lys
180 185 190

aag cct gac att tca tta aaa ccc cct aga aaa tcc tat ttt gat aat 624

```

Lys Pro Asp Ile Ser Leu Lys Pro Pro Arg Lys Ser Tyr Phe Asp Asn
 195 200. 205
 ctt ttt tat gat caa tta aac act aga aag tgc tta aaa gcc ttt cac 672
 Leu Phe Tyr Asp Gln Leu Asn Thr Arg Lys Cys Leu Lys Ala Phe His
 210 215 220
 aaa tac agc aga cga tac gct cct tta aaa acc cct aaa gag gtt 717
 Lys Tyr Ser Arg Arg Tyr Ala Pro Leu Lys Thr Pro Lys Glu Val
 225 230 235
 taaaaagagc gggctttatg ttagaataag tctttttatt caaaggagat tgcaatgaat 777

<210> 34
 <211> 239
 <212> PRT
 <213> *Helicobacter pylori*

<400> 34
 Ser Tyr Pro Pro Pro Pro Asn Pro Thr Gln Glu Thr Gln Gln Asp Phe
 1 5 10 15
 Ile Ile Glu Ala Gln Gln Asp Leu Ile Ile Glu Thr Gln Gln Asp Pro
 20 25 30
 Lys Glu Leu Pro Glu Ser Cys Lys Ile Thr Pro Gln Lys Ile Ser Phe
 35 40 45
 Asn Gln Val Val Phe Lys Lys Ile Lys Arg Lys Leu Asn Arg Phe Ile
 50 55 60
 Gly Ser Ile Leu Ala Arg Thr Glu Val Tyr Lys Asn Leu Val Ala Lys
 65 70 75 80
 Tyr Asp Glu Leu Thr Gly Lys Tyr Glu Ser Leu Leu Ala Lys Glu Ala
 85 90 95
 Asn Ile Lys Glu Thr Phe Trp Glu Arg Ala Asp Ser Glu Lys Glu
 100 105 110
 Ala Phe Phe Leu Glu His Phe Tyr Leu Thr Ser Val Tyr Val Ala Ser
 115 120 125
 Thr Ala Gly Tyr Tyr Ile Thr Pro Lys Gly Ala Lys Thr Phe Ile Glu
 130 135 140
 Ala Thr Glu Arg Phe Lys Ile Ile Glu Pro Val Asp Met Phe Ile Asn
 145 150 155 160
 Asn Pro Thr Tyr His Asp Val Ala Asn Phe Thr Tyr Leu Pro Cys Pro
 165 170 175
 Val Ser Leu Asn Lys His Ala Phe Asn Ser Thr Ile Gln Asn Ala Lys
 180 185 190
 Lys Pro Asp Ile Ser Leu Lys Pro Pro Arg Lys Ser Tyr Phe Asp Asn
 195 200 205
 Leu Phe Tyr Asp Gln Leu Asn Thr Arg Lys Cys Leu Lys Ala Phe His
 210 215 220
 Lys Tyr Ser Arg Arg Tyr Ala Pro Leu Lys Thr Pro Lys Glu Val
 225 230 235

<210> 35
 <211> 1350
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS

<222> (50)...(1252)

<400> 35

```

aagtggaaaa tttagctaaa gaaagagaaa aaagtttaaa ggattaggc atg atc aat 58
                               Met Ile Asn
                               1

aag ttt aaa aat ttt gtg agc aac tac cag caa tct aac cac tat aaa 106
Lys Phe Lys Lys Asn Phe Val Ser Asn Tyr Gln Gln Ser Asn His Tyr Lys
      5                               10                               15

gag cct tta ggt ttt ggc att gcc aga gtg gat att gcc cct att tcc 154
Glu Pro Leu Gly Phe Gly Ile Ala Arg Val Asp Ile Ala Pro Ile Ser
      20                               25                               30                               35

aaa aag att tta tgc gcc act tac cct gtt ttg aat tgg aaa gat gaa 202
Lys Lys Ile Leu Cys Ala Thr Tyr Pro Val Leu Asn Trp Lys Asp Glu
                               40                               45                               50

aat tta ggc tct tat gcg gtg ttt tgc aac tcg ctt tca aaa gaa aaa 250
Asn Leu Gly Ser Tyr Ala Val Phe Cys Asn Ser Leu Ser Lys Glu Lys
                               55                               60                               65

atc cta aaa gag agc gcg agc gag cgc gtt att gag att gat gaa agt 298
Ile Leu Lys Glu Ser Ala Ser Glu Arg Val Ile Glu Ile Asp Glu Ser
      70                               75                               80

ttt gtg tta aaa gcg ttg gat ttt tat acg ccc ttt ttg aat gaa gcc 346
Phe Val Leu Lys Ala Leu Asp Phe Tyr Thr Pro Phe Leu Asn Glu Ala
      85                               90                               95

tat tct aat aaa atg gct cat aaa aac atc caa gtg gtt tta gag ctt 394
Tyr Ser Asn Lys Met Ala His Lys Asn Ile Gln Val Val Leu Glu Leu
     100                               105                               110                               115

tta aag gct tta gaa gaa aat cgt ttg aaa aat agc gat ggg gag tct 442
Leu Lys Ala Leu Glu Glu Asn Arg Leu Lys Asn Ser Asp Gly Glu Ser
      120                               125                               130

ctt tat cgc ttg gtg atc ttg tat gaa gat aag cct tgc gag agc gtg 490
Leu Tyr Arg Leu Val Ile Leu Tyr Glu Asp Lys Pro Cys Glu Ser Val
      135                               140                               145

gag agc gcg tat atg aaa ctt tta gcg ctc tct tta ggt aaa gcc cct 538
Glu Ser Ala Tyr Met Lys Leu Leu Ala Leu Ser Leu Gly Lys Ala Pro
      150                               155                               160

ttg agg agt ttg aat tta gag ggt att ttt aac cag ctt tct aat gcg 586
Leu Arg Ser Leu Asn Leu Glu Gly Ile Phe Asn Gln Leu Ser Asn Ala
      165                               170                               175

gcc tgg agc ggt aac aag ccc tat gaa tta gaa tgg ctt aga atg aac 634
Ala Trp Ser Gly Asn Lys Pro Tyr Glu Leu Glu Trp Leu Arg Met Asn
     180                               185                               190                               195

gaa gtg gct tta aaa atg cga gac cat ttc cct agc att gat ttc ata 682
Glu Val Ala Leu Lys Met Arg Asp His Phe Pro Ser Ile Asp Phe Ile
      200                               205                               210

```

gat aaa ttc cca cgc tat ttg atg caa tta atc cct gag ttt gat aat	730
Asp Lys Phe Pro Arg Tyr Leu Met Gln Leu Ile Pro Glu Phe Asp Asn	
215 220 225	
atc cgc tta ttg gat agc tca aaa acg cgc ttt ggg gcg tat tta ggg	778
Ile Arg Leu Leu Asp Ser Ser Lys Thr Arg Phe Gly Ala Tyr Leu Gly	
230 235 240	
act gga ggt tat acc caa atg cct ggg gct agt tat gtg aat ttt aac	826
Thr Gly Gly Tyr Thr Gln Met Pro Gly Ala Ser Tyr Val Asn Phe Asn	
245 250 255	
gca ggg gct atg gga gtg tgc atg aat gag ggg cgt att tct tca tcg	874
Ala Gly Ala Met Gly Val Cys Met Asn Glu Gly Arg Ile Ser Ser Ser	
260 265 270 275	
gtg gtg gtt gga gca ggc act gat att ggt ggg gga gcg agc gtg tta	922
Val Val Val Gly Ala Gly Thr Asp Ile Gly Gly Gly Ala Ser Val Leu	
280 285 290	
ggc gtt tta agt gga ggg aat aac aac ccc att agc atc ggg aaa aat	970
Gly Val Leu Ser Gly Gly Asn Asn Asn Pro Ile Ser Ile Gly Lys Asn	
295 300 305	
tgt ttg cta ggg gct aat agc gtt act gga att agt cta ggc gat ggc	1018
Cys Leu Leu Gly Ala Asn Ser Val Thr Gly Ile Ser Leu Gly Asp Gly	
310 315 320	
tgt atc gtg gat gca ggc gtt gcg ata cta gcc ggg agc gtg ata gaa	1066
Cys Ile Val Asp Ala Gly Val Ala Ile Leu Ala Gly Ser Val Ile Glu	
325 330 335	
att gaa gaa aat gag ttt aaa aag ctt tta gaa gtg aat agc gct tta	1114
Ile Glu Glu Asn Glu Phe Lys Lys Leu Leu Glu Val Asn Ser Ala Leu	
340 345 350 355	
gaa aaa cat gcc aac aac ctt tac aaa ggc aaa gaa ctt tcc gga aaa	1162
Glu Lys His Ala Asn Asn Leu Tyr Lys Gly Lys Glu Leu Ser Gly Lys	
360 365 370	
aat ggc gtg cat ttt cgt tcc aat agt cag aat ggc aag ctg att gct	1210
Asn Gly Val His Phe Arg Ser Asn Ser Gln Asn Gly Lys Leu Ile Ala	
375 380 385	
ttt agg agc gtg aaa aaa att gag ttg aat caa aac ctg cat	1252
Phe Arg Ser Val Lys Lys Ile Glu Leu Asn Gln Asn Leu His	
390 395 400	
taaggattaa aagaatgctc aaaaaaagtt tgttattgct tgttttttta gtcttacagc	1312
ttagcggcgc tgaagaaaac aatcaagccc caaaaaac	1350

<210> 36
 <211> 401
 <212> PRT
 <213> Helicobacter pylori

<400> 36
 Met Ile Asn Lys Phe Lys Asn Phe Val Ser Asn Tyr Gln Gln Ser Asn
 1 5 10 15

<222> (50)...(1201)

<400> 37

ttatttttat tatgttaaga taatgaaaat ttctaattaa ggagtggtc atg ttc tac 58
Met Phe Tyr
1

gat gaa aaa aag acc tat caa aag att gaa gaa cgc ctt gat ata gtc 106
Asp Glu Lys Lys Thr Tyr Gln Lys Ile Glu Glu Arg Leu Asp Ile Val
5 10 15

cgt tcg ttt aac gct cac aac gag cat aaa aac ttg caa gac gag ttt 154
Arg Ser Phe Asn Ala His Asn Glu His Lys Asn Leu Gln Asp Glu Phe
20 25 30 35

aaa ggg gcg ggc att tct agg cgc gat tta ttg aag tgg gcg ggc atg 202
Lys Gly Ala Gly Ile Ser Arg Arg Asp Leu Leu Lys Trp Ala Gly Met
40 45 50

atg agc aca gcg tta gcc ttg ccg gct agt ttt gct ccc ttg act ttg 250
Met Ser Thr Ala Leu Ala Leu Pro Ala Ser Phe Ala Pro Leu Thr Leu
55 60 65

aag gcg gtg gaa gtg gct aac aga ttg ccc gtg att tgg ttg cac atg 298
Lys Ala Val Glu Val Ala Asn Arg Leu Pro Val Ile Trp Leu His Met
70 75 80

gca gaa tgc acc ggt tgt agc gaa agt ttg tta agg agc gca gac ccc 346
Ala Glu Cys Thr Gly Cys Ser Glu Ser Leu Leu Arg Ser Ala Asp Pro
85 90 95

acc att gat agc att atc ttt gat tac atc aac cta gaa tac cat gag 394
Thr Ile Asp Ser Ile Ile Phe Asp Tyr Ile Asn Leu Glu Tyr His Glu
100 105 110 115

acc atc atg gta gcg agc ggt ttt caa gct gaa aaa agc ttg cat gac 442
Thr Ile Met Val Ala Ser Gly Phe Gln Ala Glu Lys Ser Leu His Asp
120 125 130

gcc ata gaa aag cat aaa aac aat tac att tta atg gta gaa ggg ggt 490
Ala Ile Glu Lys His Lys Asn Asn Tyr Ile Leu Met Val Glu Gly Gly
135 140 145

atc ccc caa ggc acg gaa tac ttc ctc act caa ggc cca aac gct gaa 538
Ile Pro Gln Gly Thr Glu Tyr Phe Leu Thr Gln Gly Pro Asn Ala Glu
150 155 160

acg gga gct gaa gag tgt agg aaa gcc gct caa tac gca gcc gct att 586
Thr Gly Ala Glu Glu Cys Arg Lys Ala Ala Gln Tyr Ala Ala Ala Ile
165 170 175

ttt gcc ata ggc aca tgc tca agt ttt ggg ggc gtt caa gcg gct tac 634
Phe Ala Ile Gly Thr Cys Ser Ser Phe Gly Gly Val Gln Ala Ala Tyr
180 185 190 195

cct aac ccc tct aac gcg caa ccc ttg cat aaa atc att gat aaa ccc 682
Pro Asn Pro Ser Asn Ala Gln Pro Leu His Lys Ile Ile Asp Lys Pro
200 205 210

gtg atc aat gtt cct ggt tgc ccg cct agt gaa aaa aat atc gtg ggt 730
 Val Ile Asn Val Pro Gly Cys Pro Pro Ser Glu Lys Asn Ile Val Gly 215 220 225

 aat gtg ctt tat tac ttg atg ttt ggg gct ctc cct aaa ttg gat gcg 778
 Asn Val Leu Tyr Tyr Leu Met Phe Gly Ala Leu Pro Lys Leu Asp Ala 230 235 240

 tat aac cgc ccc tct tgg gct tat ggg aac agg atc cat gat ttg tgc 826
 Tyr Asn Arg Pro Ser Trp Ala Tyr Gly Asn Arg Ile His Asp Leu Cys 245 250 255

 gaa agg aga ggg cat ttt gat gcg ggc gaa ttt gtg gag cat ttt ggc 874
 Glu Arg Arg Gly His Phe Asp Ala Gly Glu Phe Val Glu His Phe Gly 260 265 270 275

 gat gaa aac gct aaa agg ggc ttt tgt ttg tat aaa atg ggc tgt aaa 922
 Asp Glu Asn Ala Lys Arg Gly Phe Cys Leu Tyr Lys Met Gly Cys Lys 280 285 290

 ggg cct tac act ttc aac aat tgc tcc aaa ctc cgc ttc aat tca cac 970
 Gly Pro Tyr Thr Phe Asn Asn Cys Ser Lys Leu Arg Phe Asn Ser His 295 300 305

 acc tct tgg ccc ata ggt gca ggg cat ggg tgt ata ggg tgt tct gag 1018
 Thr Ser Trp Pro Ile Gly Ala Gly His Gly Cys Ile Gly Cys Ser Glu 310 315 320

 cct aat ttt tgg gat acg atg agt cct ttt gaa gag cct tta gcg aat 1066
 Pro Asn Phe Trp Asp Thr Met Ser Pro Phe Glu Glu Pro Leu Ala Asn 325 330 335

 cgt tcc att aaa acc gct ttt gac gga tta ggg gct gat aaa gta gcg 1114
 Arg Ser Ile Lys Thr Ala Phe Asp Gly Leu Gly Ala Asp Lys Val Ala 340 345 350 355

 gat aaa gta ggc acg act ttg ctg agc gca acc gct att ggc att gtt 1162
 Asp Lys Val Gly Thr Thr Leu Leu Ser Ala Thr Ala Ile Gly Ile Val 360 365 370

 gcg cat gcg ctc ctt tct aaa gcg atc aaa aac aaa gag taagggatta 1211
 Ala His Ala Leu Leu Ser Lys Ala Ile Lys Asn Lys Glu 375 380

 acatgtcaaa aaaaatcgta gtcgataccta tcactaggat tgagggggcat ttaaggattg 1271
 aagtgatcgt agatgatgat aacgtgatca ctg 1304

<210> 38
 <211> 384
 <212> PRT
 <213> Helicobacter pylori

<400> 38
 Met Phe Tyr Asp Glu Lys Lys Thr Tyr Gln Lys Ile Glu Glu Arg Leu
 1 5 10 15
 Asp Ile Val Arg Ser Phe Asn Ala His Asn Glu His Lys Asn Leu Gln
 20 25 30
 Asp Glu Phe Lys Gly Ala Gly Ile Ser Arg Arg Asp Leu Leu Lys Trp
 35 40 45

Ala	Gly	Met	Met	Ser	Thr	Ala	Leu	Ala	Leu	Pro	Ala	Ser	Phe	Ala	Pro
50						55				60					
Leu	Thr	Leu	Lys	Ala	Val	Glu	Val	Ala	Asn	Arg	Leu	Pro	Val	Ile	Trp
65					70				75						80
Leu	His	Met	Ala	Glu	Cys	Thr	Gly	Cys	Ser	Glu	Ser	Leu	Leu	Arg	Ser
				85					90					95	
Ala	Asp	Pro	Thr	Ile	Asp	Ser	Ile	Ile	Phe	Asp	Tyr	Ile	Asn	Leu	Glu
			100					105					110		
Tyr	His	Glu	Thr	Ile	Met	Val	Ala	Ser	Gly	Phe	Gln	Ala	Glu	Lys	Ser
		115					120					125			
Leu	His	Asp	Ala	Ile	Glu	Lys	His	Lys	Asn	Asn	Tyr	Ile	Leu	Met	Val
		130				135					140				
Glu	Gly	Gly	Ile	Pro	Gln	Gly	Thr	Glu	Tyr	Phe	Leu	Thr	Gln	Gly	Pro
145					150					155					160
Asn	Ala	Glu	Thr	Gly	Ala	Glu	Glu	Cys	Arg	Lys	Ala	Ala	Gln	Tyr	Ala
				165					170					175	
Ala	Ala	Ile	Phe	Ala	Ile	Gly	Thr	Cys	Ser	Ser	Phe	Gly	Gly	Val	Gln
			180					185					190		
Ala	Ala	Tyr	Pro	Asn	Pro	Ser	Asn	Ala	Gln	Pro	Leu	His	Lys	Ile	Ile
		195					200					205			
Asp	Lys	Pro	Val	Ile	Asn	Val	Pro	Gly	Cys	Pro	Pro	Ser	Glu	Lys	Asn
		210				215					220				
Ile	Val	Gly	Asn	Val	Leu	Tyr	Tyr	Leu	Met	Phe	Gly	Ala	Leu	Pro	Lys
225					230					235					240
Leu	Asp	Ala	Tyr	Asn	Arg	Pro	Ser	Trp	Ala	Tyr	Gly	Asn	Arg	Ile	His
				245					250					255	
Asp	Leu	Cys	Glu	Arg	Arg	Gly	His	Phe	Asp	Ala	Gly	Glu	Phe	Val	Glu
			260					265					270		
His	Phe	Gly	Asp	Glu	Asn	Ala	Lys	Arg	Gly	Phe	Cys	Leu	Tyr	Lys	Met
		275					280					285			
Gly	Cys	Lys	Gly	Pro	Tyr	Thr	Phe	Asn	Asn	Cys	Ser	Lys	Leu	Arg	Phe
		290				295					300				
Asn	Ser	His	Thr	Ser	Trp	Pro	Ile	Gly	Ala	Gly	His	Gly	Cys	Ile	Gly
305					310					315					320
Cys	Ser	Glu	Pro	Asn	Phe	Trp	Asp	Thr	Met	Ser	Pro	Phe	Glu	Glu	Pro
				325					330					335	
Leu	Ala	Asn	Arg	Ser	Ile	Lys	Thr	Ala	Phe	Asp	Gly	Leu	Gly	Ala	Asp
			340					345					350		
Lys	Val	Ala	Asp	Lys	Val	Gly	Thr	Thr	Leu	Leu	Ser	Ala	Thr	Ala	Ile
		355					360					365			
Gly	Ile	Val	Ala	His	Ala	Leu	Leu	Ser	Lys	Ala	Ile	Lys	Asn	Lys	Glu
		370				375					380				

<210> 39
 <211> 810
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (39)...(710)

<400> 39
 tagagcctaa ttctgctaaa ttctaaaaag gggttacgc atg gat aaa atg aat aag 56
 Met Asp Lys Met Asn Lys
 1 5

gtc gtt tta cac aaa gaa tat tcc ggt ttt gtg cgc ttt ttc cat tgg 104

Val	Val	Leu	His	Lys	Glu	Tyr	Ser	Gly	Phe	Val	Arg	Phe	Phe	His	Trp	
			10					15					20			
ggt	agg	gct	ttg	agt	att	ttc	gct	tta	atc	gct	aca	ggg	ttt	tac	atc	152
Val	Arg	Ala	Leu	Ser	Ile	Phe	Ala	Leu	Ile	Ala	Thr	Gly	Phe	Tyr	Ile	
		25					30					35				
gct	tac	cct	ttt	ttg	cag	cct	aat	tcc	agc	ttt	tat	aaa	ggg	gtg	tat	200
Ala	Tyr	Pro	Phe	Leu	Gln	Pro	Asn	Ser	Ser	Phe	Tyr	Lys	Gly	Val	Tyr	
		40				45					50					
ctt	tta	caa	gct	tat	gtg	cgt	tct	ttt	cat	gtc	atg	ttt	ggg	ttt	ttg	248
Leu	Leu	Gln	Ala	Tyr	Val	Arg	Ser	Phe	His	Val	Met	Phe	Gly	Phe	Leu	
		55			60					65					70	
ctc	att	agc	gca	tta	atc	ttt	aga	acc	tat	ctt	ttt	ttc	act	aaa	gaa	296
Leu	Ile	Ser	Ala	Leu	Ile	Phe	Arg	Thr	Tyr	Leu	Phe	Phe	Thr	Lys	Glu	
				75				80						85		
agc	ttg	atg	gaa	cgc	aag	agt	ttt	agc	caa	ctt	tta	agc	cca	aaa	gcc	344
Ser	Leu	Met	Glu	Arg	Lys	Ser	Phe	Ser	Gln	Leu	Leu	Ser	Pro	Lys	Ala	
			90					95					100			
tgg	att	gat	cag	atg	aaa	gcg	tat	ttt	ctt	atc	agc	ggc	aaa	ccc	cac	392
Trp	Ile	Asp	Gln	Met	Lys	Ala	Tyr	Phe	Leu	Ile	Ser	Gly	Lys	Pro	His	
		105				110						115				
act	aaa	gga	gcg	tat	aac	cct	atc	caa	ctc	gtg	gct	tat	tcc	act	ttg	440
Thr	Lys	Gly	Ala	Tyr	Asn	Pro	Ile	Gln	Leu	Val	Ala	Tyr	Ser	Thr	Leu	
		120				125					130					
att	gtt	ttg	atc	gtg	ttg	atg	agt	ttg	agc	ggg	atg	gtg	ctg	tat	tat	488
Ile	Val	Leu	Ile	Val	Leu	Met	Ser	Leu	Ser	Gly	Met	Val	Leu	Tyr	Tyr	
		135			140					145					150	
aat	gtc	tat	cat	gcg	ggg	ctt	gga	gcg	ttt	tta	gga	agc	gct	ttt	aag	536
Asn	Val	Tyr	His	Ala	Gly	Leu	Gly	Ala	Phe	Leu	Gly	Ser	Ala	Phe	Lys	
				155				160						165		
tgg	ttt	gaa	acg	ctt	tgt	gga	ggg	tta	gcg	aat	gtt	cgt	ttc	atc	cac	584
Trp	Phe	Glu	Thr	Leu	Cys	Gly	Gly	Leu	Ala	Asn	Val	Arg	Phe	Ile	His	
			170					175					180			
cac	tta	gcg	act	tgg	ggg	ttt	att	ttg	ttt	gtc	cct	gtg	cat	gtt	tat	632
His	Leu	Ala	Thr	Trp	Gly	Phe	Ile	Leu	Phe	Val	Pro	Val	His	Val	Tyr	
		185					190					195				
atg	gtg	ttt	ttc	cat	tct	atc	agg	tat	gaa	agt	tcg	ggg	gcg	gat	tct	680
Met	Val	Phe	Phe	His	Ser	Ile	Arg	Tyr	Glu	Ser	Ser	Gly	Ala	Asp	Ser	
		200				205					210					
atg	att	aat	ggc	tat	ggt	tat	acc	aaa	gaa	tgagtcaaaa	aatcctaatt					730
Met	Ile	Asn	Gly	Tyr	Gly	Tyr	Thr	Lys	Glu							
		215			220											
ctaggtattg	gcaatatacct	ttttggcgat	gaagggattg	gggtgcattt	agcccactac											790
ctcaaaaaaa	atTTTTcttt															810

<210> 40

<211> 224
 <212> PRT
 <213> Helicobacter pylori

<400> 40
 Met Asp Lys Met Asn Lys Val Val Leu His Lys Glu Tyr Ser Gly Phe
 1 5 10 15
 Val Arg Phe Phe His Trp Val Arg Ala Leu Ser Ile Phe Ala Leu Ile
 20 25 30
 Ala Thr Gly Phe Tyr Ile Ala Tyr Pro Phe Leu Gln Pro Asn Ser Ser
 35 40 45
 Phe Tyr Lys Gly Val Tyr Leu Leu Gln Ala Tyr Val Arg Ser Phe His
 50 55 60
 Val Met Phe Gly Phe Leu Leu Ile Ser Ala Leu Ile Phe Arg Thr Tyr
 65 70 75 80
 Leu Phe Phe Thr Lys Glu Ser Leu Met Glu Arg Lys Ser Phe Ser Gln
 85 90 95
 Leu Leu Ser Pro Lys Ala Trp Ile Asp Gln Met Lys Ala Tyr Phe Leu
 100 105 110
 Ile Ser Gly Lys Pro His Thr Lys Gly Ala Tyr Asn Pro Ile Gln Leu
 115 120 125
 Val Ala Tyr Ser Thr Leu Ile Val Leu Ile Val Leu Met Ser Leu Ser
 130 135 140
 Gly Met Val Leu Tyr Tyr Asn Val Tyr His Ala Gly Leu Gly Ala Phe
 145 150 155 160
 Leu Gly Ser Ala Phe Lys Trp Phe Glu Thr Leu Cys Gly Gly Leu Ala
 165 170 175
 Asn Val Arg Phe Ile His His Leu Ala Thr Trp Gly Phe Ile Leu Phe
 180 185 190
 Val Pro Val His Val Tyr Met Val Phe Phe His Ser Ile Arg Tyr Glu
 195 200 205
 Ser Ser Gly Ala Asp Ser Met Ile Asn Gly Tyr Gly Tyr Thr Lys Glu
 210 215 220

<210> 41
 <211> 1543
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (32)...(1495)

<400> 41
 aagcctgaat tttacgcccc ttttagagcg a atg gca tgc aat ttg caa gcg 52
 Met Ala Cys Asn Leu Gln Ala
 1 5
 cgt ttt tat agc gtt tat aag gat aat acc act tct ttc tac ctc caa 100
 Arg Phe Tyr Ser Val Tyr Lys Asp Asn Thr Thr Ser Phe Tyr Leu Gln
 10 15 20
 gcg agc gct gaa acc act tta gag ttc gcg caa aaa ctc agc gaa att 148
 Ala Ser Ala Glu Thr Thr Leu Glu Phe Ala Gln Lys Leu Ser Glu Ile
 25 30 35
 ctg ccc ttt tct tta gat ttt agc ttt ttg tct tta aag gaa atc aca 196
 Leu Pro Phe Ser Leu Asp Phe Ser Phe Leu Ser Leu Lys Glu Ile Thr

40	45	50	55	
gag cct tta gat gaa aat ctt ttc caa aca gca agc ctt tca aag ccc	244			
Glu Pro Leu Asp Glu Asn Leu Phe Gln Thr Ala Ser Leu Ser Lys Pro				
60 65 70				
ctt ttt atg aac gct aaa gag cat caa gat ttt tta gac aaa aat tca	292			
Leu Phe Met Asn Ala Lys Glu His Gln Asp Phe Leu Asp Lys Asn Ser				
75 80 85				
tct ttg tat gcc gat act ctg ggc ttg att aaa aac acc gct ttt aag	340			
Ser Leu Tyr Ala Asp Thr Leu Gly Leu Ile Lys Asn Thr Ala Phe Lys				
90 95 100				
ggg gat ata atc cat agc cct aaa gag ctt ata gat tgc tta acc caa	388			
Gly Asp Ile Ile His Ser Pro Lys Glu Leu Ile Asp Cys Leu Thr Gln				
105 110 115				
tta aaa ggc atg ctc aaa acg caa gat ttt atc cct att ttc act tct	436			
Leu Lys Gly Met Leu Lys Thr Gln Asp Phe Ile Pro Ile Phe Thr Ser				
120 125 130 135				
aga gag gcg tta tcc ctt tct tta aaa aat ccc tct cca agc gtt att	484			
Arg Glu Ala Leu Ser Leu Ser Leu Lys Asn Pro Ser Pro Ser Val Ile				
140 145 150				
ttt agc gat ctt tct agc gtt ttg agc tgc act aaa ttg cct tta gag	532			
Phe Ser Asp Leu Ser Ser Val Leu Ser Cys Thr Lys Leu Pro Leu Glu				
155 160 165				
gac gct aaa tat ttg gcc agt ttg gaa aaa ccc tcc atc aaa gcc cca	580			
Asp Ala Lys Tyr Leu Ala Ser Leu Glu Lys Pro Ser Ile Lys Ala Pro				
170 175 180				
tta aaa agc gtg ttt aaa gac act ttc aaa aac gat gaa atc atc gcc	628			
Leu Lys Ser Val Phe Lys Asp Thr Phe Lys Asn Asp Glu Ile Ile Ala				
185 190 195				
cag cta ccc tat gac ccc ata ttg aat tta ttg tgc cat att tta caa	676			
Gln Leu Pro Tyr Asp Pro Ile Leu Asn Leu Leu Cys His Ile Leu Gln				
200 205 210 215				
gat gag ggg ata gaa ttt gtt ttt atg cat gaa agc cgt tct tgt gaa	724			
Asp Glu Gly Ile Glu Phe Val Phe Met His Glu Ser Arg Ser Cys Glu				
220 225 230				
gcg ctt ttg tat tat gaa gcg ctt ttt aaa acc cct aaa cgc ttg atc	772			
Ala Leu Leu Tyr Tyr Glu Ala Leu Phe Lys Thr Pro Lys Arg Leu Ile				
235 240 245				
aca ccc act aaa aaa ttc gtg cta gaa aat aat ttt tct acc ttt ccc	820			
Thr Pro Thr Lys Lys Phe Val Leu Glu Asn Asn Phe Ser Thr Phe Pro				
250 255 260				
ttt aaa gat gaa tta gag ttt tta agc gca acc ccc aat tct atc gtt	868			
Phe Lys Asp Glu Leu Glu Phe Leu Ser Ala Thr Pro Asn Ser Ile Val				
265 270 275				
ttg tat ctc agt ttc aag cgc cct aca agg ttg tta ttg cat gct aat	916			

Leu	Tyr	Leu	Ser	Phe	Lys	Arg	Pro	Thr	Arg	Leu	Leu	Leu	His	Ala	Asn	
280					285					290					295	
ggt	tct	tta	aaa	acg	ctt	tta	agc	gtc	agt	ttt	gat	ttt	aac	aaa	atg	964
Gly	Ser	Leu	Lys	Thr	Leu	Leu	Ser	Val	Ser	Phe	Asp	Phe	Asn	Lys	Met	
				300					305					310		
ttt	aac	gcg	ctc	aaa	caa	gat	gaa	aaa	gcc	tcc	aga	atg	cta	caa	aac	1012
Phe	Asn	Ala	Leu	Lys	Gln	Asp	Glu	Lys	Ala	Ser	Arg	Met	Leu	Gln	Asn	
				315				320					325			
tac	gcc	act	aaa	ttc	cct	gat	ttt	tac	gcg	cgc	att	gta	gag	ctt	tct	1060
Tyr	Ala	Thr	Lys	Phe	Pro	Asp	Phe	Tyr	Ala	Arg	Ile	Val	Glu	Leu	Ser	
				330			335					340				
aaa	tac	gat	cta	ggg	ggc	gcg	aat	tta	ttg	gat	ttt	ttt	tgc	att	tta	1108
Lys	Tyr	Asp	Leu	Gly	Gly	Ala	Asn	Leu	Leu	Asp	Phe	Phe	Cys	Ile	Leu	
						350					355					
ggg	ttt	ggt	ttg	ggc	tat	agc	gag	gat	ttt	tgc	aca	cag	agc	gtt	att	1156
Gly	Phe	Val	Leu	Gly	Tyr	Ser	Glu	Asp	Phe	Cys	Thr	Gln	Ser	Val	Ile	
360					365					370					375	
cct	ttg	gct	aaa	gaa	tgc	tta	cgc	cct	aaa	ggc	cct	agg	att	gat	tat	1204
Pro	Leu	Ala	Lys	Glu	Cys	Leu	Arg	Pro	Lys	Gly	Pro	Arg	Ile	Asp	Tyr	
				380					385					390		
aaa	atc	ctt	aaa	gac	aat	tct	ttg	aaa	atg	gct	tta	aac	ttt	tca	aag	1252
Lys	Ile	Leu	Lys	Asp	Asn	Ser	Leu	Lys	Met	Ala	Leu	Asn	Phe	Ser	Lys	
				395				400					405			
atc	atg	cac	agt	gcg	atg	agt	ttc	agg	ctc	gca	ggc	gtg	gaa	aat	gaa	1300
Ile	Met	His	Ser	Ala	Met	Ser	Phe	Arg	Leu	Ala	Gly	Val	Glu	Asn	Glu	
				410			415					420				
att	ttg	agt	ttg	ggg	att	ttg	gat	tct	tta	gcg	gag	ttt	tta	ggg	aat	1348
Ile	Leu	Ser	Leu	Gly	Ile	Leu	Asp	Ser	Leu	Ala	Glu	Phe	Leu	Gly	Asn	
				425			430				435					
ttc	att	tggt	gat	aac	gcg	caa	aat	ttt	agc	gtt	caa	gaa	gta	acg	atc	1396
Phe	Ile	Trp	Asp	Asn	Ala	Gln	Asn	Phe	Ser	Val	Gln	Glu	Val	Thr	Ile	
440					445					450					455	
gct	ggg	gat	ttc	ttt	ggc	gaa	aaa	gtg	ttt	ttg	gat	ttg	ttt	gtg	cggt	1444
Ala	Gly	Asp	Phe	Phe	Gly	Glu	Lys	Val	Phe	Leu	Asp	Leu	Phe	Val	Arg	
				460				465						470		
tat	ttc	cct	aaa	acc	cta	gcc	ctt	aaa	acg	cat	gca	ttt	ttg	gat	tat	1492
Tyr	Phe	Pro	Lys	Thr	Leu	Ala	Leu	Lys	Thr	His	Ala	Phe	Leu	Asp	Tyr	
			475					480					485			
gaa	taagg	gctta	aaagc	ggatg	tgcat	catca	gccc	gccgtc	catgtatt							1543
Glu																

<210> 42
 <211> 488
 <212> PRT

<213> Helicobacter pylori

<400> 42

Met	Ala	Cys	Asn	Leu	Gln	Ala	Arg	Phe	Tyr	Ser	Val	Tyr	Lys	Asp	Asn
1				5					10					15	
Thr	Thr	Ser	Phe	Tyr	Leu	Gln	Ala	Ser	Ala	Glu	Thr	Thr	Leu	Glu	Phe
			20					25					30		
Ala	Gln	Lys	Leu	Ser	Glu	Ile	Leu	Pro	Phe	Ser	Leu	Asp	Phe	Ser	Phe
		35					40					45			
Leu	Ser	Leu	Lys	Glu	Ile	Thr	Glu	Pro	Leu	Asp	Glu	Asn	Leu	Phe	Gln
	50					55					60				
Thr	Ala	Ser	Leu	Ser	Lys	Pro	Leu	Phe	Met	Asn	Ala	Lys	Glu	His	Gln
65					70				75					80	
Asp	Phe	Leu	Asp	Lys	Asn	Ser	Ser	Leu	Tyr	Ala	Asp	Thr	Leu	Gly	Leu
				85					90					95	
Ile	Lys	Asn	Thr	Ala	Phe	Lys	Gly	Asp	Ile	Ile	His	Ser	Pro	Lys	Glu
			100					105					110		
Leu	Ile	Asp	Cys	Leu	Thr	Gln	Leu	Lys	Gly	Met	Leu	Lys	Thr	Gln	Asp
		115					120					125			
Phe	Ile	Pro	Ile	Phe	Thr	Ser	Arg	Glu	Ala	Leu	Ser	Leu	Ser	Leu	Lys
	130					135					140				
Asn	Pro	Ser	Pro	Ser	Val	Ile	Phe	Ser	Asp	Leu	Ser	Ser	Val	Leu	Ser
145					150					155				160	
Cys	Thr	Lys	Leu	Pro	Leu	Glu	Asp	Ala	Lys	Tyr	Leu	Ala	Ser	Leu	Glu
				165					170					175	
Lys	Pro	Ser	Ile	Lys	Ala	Pro	Leu	Lys	Ser	Val	Phe	Lys	Asp	Thr	Phe
			180					185					190		
Lys	Asn	Asp	Glu	Ile	Ile	Ala	Gln	Leu	Pro	Tyr	Asp	Pro	Ile	Leu	Asn
		195					200					205			
Leu	Leu	Cys	His	Ile	Leu	Gln	Asp	Glu	Gly	Ile	Glu	Phe	Val	Phe	Met
	210					215					220				
His	Glu	Ser	Arg	Ser	Cys	Glu	Ala	Leu	Leu	Tyr	Tyr	Glu	Ala	Leu	Phe
225					230					235				240	
Lys	Thr	Pro	Lys	Arg	Leu	Ile	Thr	Pro	Thr	Lys	Lys	Phe	Val	Leu	Glu
				245					250					255	
Asn	Asn	Phe	Ser	Thr	Phe	Pro	Phe	Lys	Asp	Glu	Leu	Glu	Phe	Leu	Ser
			260					265					270		
Ala	Thr	Pro	Asn	Ser	Ile	Val	Leu	Tyr	Leu	Ser	Phe	Lys	Arg	Pro	Thr
			275				280					285			
Arg	Leu	Leu	Leu	His	Ala	Asn	Gly	Ser	Leu	Lys	Thr	Leu	Leu	Ser	Val
	290					295					300				
Ser	Phe	Asp	Phe	Asn	Lys	Met	Phe	Asn	Ala	Leu	Lys	Gln	Asp	Glu	Lys
305					310					315				320	
Ala	Ser	Arg	Met	Leu	Gln	Asn	Tyr	Ala	Thr	Lys	Phe	Pro	Asp	Phe	Tyr
				325					330					335	
Ala	Arg	Ile	Val	Glu	Leu	Ser	Lys	Tyr	Asp	Leu	Gly	Gly	Ala	Asn	Leu
			340					345					350		
Leu	Asp	Phe	Phe	Cys	Ile	Leu	Gly	Phe	Val	Leu	Gly	Tyr	Ser	Glu	Asp
		355					360					365			
Phe	Cys	Thr	Gln	Ser	Val	Ile	Pro	Leu	Ala	Lys	Glu	Cys	Leu	Arg	Pro
	370					375					380				
Lys	Gly	Pro	Arg	Ile	Asp	Tyr	Lys	Ile	Leu	Lys	Asp	Asn	Ser	Leu	Lys
385					390					395				400	
Met	Ala	Leu	Asn	Phe	Ser	Lys	Ile	Met	His	Ser	Ala	Met	Ser	Phe	Arg
				405					410					415	
Leu	Ala	Gly	Val	Glu	Asn	Glu	Ile	Leu	Ser	Leu	Gly	Ile	Leu	Asp	Ser
			420					425					430		
Leu	Ala	Glu	Phe	Leu	Gly	Asn	Phe	Ile	Trp	Asp	Asn	Ala	Gln	Asn	Phe
		435					440					445			

Ser Val Gln Glu Val Thr Ile Ala Gly Asp Phe Phe Gly Glu Lys Val
450 455 460
Phe Leu Asp Leu Phe Val Arg Tyr Phe Pro Lys Thr Leu Ala Leu Lys
465 470 475 480
Thr His Ala Phe Leu Asp Tyr Glu
485

<210> 43
<211> 715
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (17)...(694)

<400> 43
ttttaagga attttg atg gaa caa aaa att tgc gtg atc ggt ttt agc ggc 52
Met Glu Gln Lys Ile Cys Val Ile Gly Phe Ser Gly
1 5 10
ggg caa gac agc acc act tta gcc gtg tgg gcg aaa aag cgt ttt aaa 100
Gly Gln Asp Ser Thr Thr Leu Ala Val Trp Ala Lys Lys Arg Phe Lys
15 20 25
aaa gtc tgt tta gtg ggg ttt gat tat gcg caa aaa cac tct gtg gaa 148
Lys Val Cys Leu Val Gly Phe Asp Tyr Ala Gln Lys His Ser Val Glu
30 35 40
tta gaa tgc gct caa aaa atc gct tct ctt tta caa ctc cct tat gaa 196
Leu Glu Cys Ala Gln Lys Ile Ala Ser Leu Leu Gln Leu Pro Tyr Glu
45 50 55 60
atc atc cca tta gat ttt tta gaa aat atc acc cgc tct gcg ctt ttt 244
Ile Ile Pro Leu Asp Phe Leu Glu Asn Ile Thr Arg Ser Ala Leu Phe
65 70 75
aaa aac tct aac gat tta ata ggg cat tcg cat gcg caa aat aaa gat 292
Lys Asn Ser Asn Asp Leu Ile Gly His Ser His Ala Gln Asn Lys Asp
80 85 90
tta ccc aat tct ttt gtg cct aat cgt aac gct att ttt atc acc ctt 340
Leu Pro Asn Ser Phe Val Pro Asn Arg Asn Ala Ile Phe Ile Thr Leu
95 100 105
ttg cat tct tac gcg caa aaa cta ggg gct agc aat atc gct tta gga 388
Leu His Ser Tyr Ala Gln Lys Leu Gly Ala Ser Asn Ile Ala Leu Gly
110 115 120
gtt tcg caa gcg gat ttt agc ggc tat ccg gat tgt aaa gaa gat ttt 436
Val Ser Gln Ala Asp Phe Ser Gly Tyr Pro Asp Cys Lys Glu Asp Phe
125 130 135 140
att aaa agc atc gag cat gcc tta aat tta gga tca aac acg gcg att 484
Ile Lys Ser Ile Glu His Ala Leu Asn Leu Gly Ser Asn Thr Ala Ile
145 150 155
aaa atc cta acg cct tta atg ttt ttg aat aaa gcg caa gaa ttt caa 532

Lys Ile Leu Thr Pro Leu Met Phe Leu Asn Lys Ala Gln Glu Phe Gln
 160 165 170
 atg gct aaa gat ttg ggc gtc ttg gat tta gtc atc aaa gaa acg cac 580
 Met Ala Lys Asp Leu Gly Val Leu Asp Leu Val Ile Lys Glu Thr His
 175 180 185
 acc tgc tat caa gga gag cga aag att ttg cat gct tat ggt tat ggt 628
 Thr Cys Tyr Gln Gly Glu Arg Lys Ile Leu His Ala Tyr Gly Tyr Gly
 190 195 200
 tgc gat aaa tgc ccg gca tgc caa ttg aga aaa aaa ggc ttt gaa gag 676
 Cys Asp Lys Cys Pro Ala Cys Gln Leu Arg Lys Lys Gly Phe Glu Glu
 205 210 215 220
 ttt caa gct aat aaa aaa taagggttttt taaaaaacca a 715
 Phe Gln Ala Asn Lys Lys
 225

<210> 44
 <211> 226
 <212> PRT
 <213> Helicobacter pylori

<400> 44
 Met Glu Gln Lys Ile Cys Val Ile Gly Phe Ser Gly Gly Gln Asp Ser
 1 5 10 15
 Thr Thr Leu Ala Val Trp Ala Lys Lys Arg Phe Lys Lys Val Cys Leu
 20 25 30
 Val Gly Phe Asp Tyr Ala Gln Lys His Ser Val Glu Leu Glu Cys Ala
 35 40 45
 Gln Lys Ile Ala Ser Leu Leu Gln Leu Pro Tyr Glu Ile Ile Pro Leu
 50 55 60
 Asp Phe Leu Glu Asn Ile Thr Arg Ser Ala Leu Phe Lys Asn Ser Asn
 65 70 75 80
 Asp Leu Ile Gly His Ser His Ala Gln Asn Lys Asp Leu Pro Asn Ser
 85 90 95
 Phe Val Pro Asn Arg Asn Ala Ile Phe Ile Thr Leu Leu His Ser Tyr
 100 105 110
 Ala Gln Lys Leu Gly Ala Ser Asn Ile Ala Leu Gly Val Ser Gln Ala
 115 120 125
 Asp Phe Ser Gly Tyr Pro Asp Cys Lys Glu Asp Phe Ile Lys Ser Ile
 130 135 140
 Glu His Ala Leu Asn Leu Gly Ser Asn Thr Ala Ile Lys Ile Leu Thr
 145 150 155 160
 Pro Leu Met Phe Leu Asn Lys Ala Gln Glu Phe Gln Met Ala Lys Asp
 165 170 175
 Leu Gly Val Leu Asp Leu Val Ile Lys Glu Thr His Thr Cys Tyr Gln
 180 185 190
 Gly Glu Arg Lys Ile Leu His Ala Tyr Gly Tyr Gly Cys Asp Lys Cys
 195 200 205
 Pro Ala Cys Gln Leu Arg Lys Lys Gly Phe Glu Glu Phe Gln Ala Asn
 210 215 220
 Lys Lys
 225

<210> 45

<211> 1201
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (49)...(1155)

<400> 45
 tcctctcatg agctttactt ggtagggggg tgcgtgcgcg attatttta atg ggc att 57
 Met Gly Ile
 1

acc cca aaa gat tac gat tta acc tca aac gct tta gtc aat gaa agc 105
 Thr Pro Lys Asp Tyr Asp Leu Thr Ser Asn Ala Leu Val Asn Glu Ser
 5 10 15

aaa gag ctt ctt tta aag cgc cat ttt agg gtg cta gaa acc ggt atc 153
 Lys Glu Leu Leu Leu Lys Arg His Phe Arg Val Leu Glu Thr Gly Ile
 20 25 30 35

aaa cat ggt acg atc acg gct ctt aaa aac cat caa agc tat gaa atc 201
 Lys His Gly Thr Ile Thr Ala Leu Lys Asn His Gln Ser Tyr Glu Ile
 40 45 50

aca act ttt aga att gaa aag ggg cat atc aaa cac cga aag cct aaa 249
 Thr Thr Phe Arg Ile Glu Lys Gly His Ile Lys His Arg Lys Pro Lys
 55 60 65

gaa ttg gtt ttt agc gtt cat tta aca gac gat tta aag cgg cgc gat 297
 Glu Leu Val Phe Ser Val His Leu Thr Asp Asp Leu Lys Arg Arg Asp
 70 75 80

ttt agc atg aat gcg atc gct tat agc cct aca aaa ggg ctg att gat 345
 Phe Ser Met Asn Ala Ile Ala Tyr Ser Pro Thr Lys Gly Leu Ile Asp
 85 90 95

cct ttt aaa ggg cag aat gcg att gaa aat caa atg att gaa tgc gtg 393
 Pro Phe Lys Gly Gln Asn Ala Ile Glu Asn Gln Met Ile Glu Cys Val
 100 105 110 115

ggg gaa gcg cga tta agg ttt ttt gaa gac gct tta agg att tta aga 441
 Gly Glu Ala Arg Leu Arg Phe Phe Glu Asp Ala Leu Arg Ile Leu Arg
 120 125 130

tcg ctg cga ttc agt gca act tta ggc ttt aag ata gcg cca aac acc 489
 Ser Leu Arg Phe Ser Ala Thr Leu Gly Phe Lys Ile Ala Pro Asn Thr
 135 140 145

aaa gaa gcg gtt ttt gcg tgt aag gat ttg tta aaa cac ctt tct aaa 537
 Lys Glu Ala Val Phe Ala Cys Lys Asp Leu Leu Lys His Leu Ser Lys
 150 155 160

gaa cgc tta caa agt gaa ttg aat aag ctt ctt atg ggg aaa aac gcc 585
 Glu Arg Leu Gln Ser Glu Leu Asn Lys Leu Leu Met Gly Lys Asn Ala
 165 170 175

tat gaa gtg gct aaa gaa tat caa gaa att tta gag ttg gtt att caa 633
 Tyr Glu Val Ala Lys Glu Tyr Gln Glu Ile Leu Glu Leu Val Ile Gln

180	185	190	195	
gaa aaa ata gaa aat tta ggg ttt tta aaa aac gcg cct ttc aat ctg				681
Glu Lys Ile Glu Asn Leu Gly Phe Leu Lys Asn Ala Pro Phe Asn Leu	200	205	210	
gaa tta aga ttg tta ggg ttt ttt aag cat caa aaa agt tta gaa agt				729
Glu Leu Arg Leu Leu Gly Phe Phe Lys His Gln Lys Ser Leu Glu Ser	215	220	225	
tta cgc tac cct aaa aaa acg atc gtt tta ttt tcc aaa gct aaa gaa				777
Leu Arg Tyr Pro Lys Lys Thr Ile Val Leu Phe Ser Lys Ala Lys Glu	230	235	240	
tgc cat aaa tct ttt tta aat att cat aac aaa aca gag tta aaa ttt				825
Cys His Lys Ser Phe Leu Asn Ile His Asn Lys Thr Glu Leu Lys Phe	245	250	255	
tta ttg aaa aac tac gat tta gag cct ttt aat ttg gct tta gat ttt				873
Leu Leu Lys Asn Tyr Asp Leu Glu Pro Phe Asn Leu Ala Leu Asp Phe	260	265	270	275
tat gcg ctc aaa aac ccc aaa cat gct tta aaa att aaa ggc ttg tta				921
Tyr Ala Leu Lys Asn Pro Lys His Ala Leu Lys Ile Lys Gly Leu Leu	280	285	290	
aaa gaa atc ttt gat tct aac gag cct ttt aaa aaa gaa cac ttg gcc				969
Lys Glu Ile Phe Asp Ser Asn Glu Pro Phe Lys Lys Glu His Leu Ala	295	300	305	
ctt aag ggc ggt gcg ctt caa agc ttg ggt tac cag cac caa aaa atc				1017
Leu Lys Gly Gly Ala Leu Gln Ser Leu Gly Tyr Gln His Gln Lys Ile	310	315	320	
ggc gaa att tta aac gca tgc tta gat tta gtc atc gct aac cct aaa				1065
Gly Glu Ile Leu Asn Ala Cys Leu Asp Leu Val Ile Ala Asn Pro Lys	325	330	335	
aat aac gct tta gaa tgg ctg att gaa tgg gtt aag ggt cat tat tta				1113
Asn Asn Ala Leu Glu Trp Leu Ile Glu Trp Val Lys Gly His Tyr Leu	340	345	350	355
cct aat gat act ata aat ctt tcg cca ata ggc aga aga aat				1155
Pro Asn Asp Thr Ile Asn Leu Ser Pro Ile Gly Arg Arg Asn	360	365		
taaaaacaga gaaaacatga taacgatgaa tgcgattcaa tggcct				1201
<210> 46				
<211> 369				
<212> PRT				
<213> Helicobacter pylori				
<400> 46				
Met Gly Ile Thr Pro Lys Asp Tyr Asp Leu Thr Ser Asn Ala Leu Val				
1 5 10 15				
Asn Glu Ser Lys Glu Leu Leu Leu Lys Arg His Phe Arg Val Leu Glu				
20 25 30				
Thr Gly Ile Lys His Gly Thr Ile Thr Ala Leu Lys Asn His Gln Ser				

		35					40				45						
Tyr	Glu	Ile	Thr	Thr	Phe	Arg	Ile	Glu	Lys	Gly	His	Ile	Lys	His	Arg		
	50					55					60						
Lys	Pro	Lys	Glu	Leu	Val	Phe	Ser	Val	His	Leu	Thr	Asp	Asp	Leu	Lys		
65					70					75				80			
Arg	Arg	Asp	Phe	Ser	Met	Asn	Ala	Ile	Ala	Tyr	Ser	Pro	Thr	Lys	Gly		
				85					90					95			
Leu	Ile	Asp	Pro	Phe	Lys	Gly	Gln	Asn	Ala	Ile	Glu	Asn	Gln	Met	Ile		
			100					105					110				
Glu	Cys	Val	Gly	Glu	Ala	Arg	Leu	Arg	Phe	Phe	Glu	Asp	Ala	Leu	Arg		
		115					120					125					
Ile	Leu	Arg	Ser	Leu	Arg	Phe	Ser	Ala	Thr	Leu	Gly	Phe	Lys	Ile	Ala		
	130					135					140						
Pro	Asn	Thr	Lys	Glu	Ala	Val	Phe	Ala	Cys	Lys	Asp	Leu	Leu	Lys	His		
145					150					155					160		
Leu	Ser	Lys	Glu	Arg	Leu	Gln	Ser	Glu	Leu	Asn	Lys	Leu	Leu	Met	Gly		
				165					170					175			
Lys	Asn	Ala	Tyr	Glu	Val	Ala	Lys	Glu	Tyr	Gln	Glu	Ile	Leu	Glu	Leu		
		180						185					190				
Val	Ile	Gln	Glu	Lys	Ile	Glu	Asn	Leu	Gly	Phe	Leu	Lys	Asn	Ala	Pro		
		195					200					205					
Phe	Asn	Leu	Glu	Leu	Arg	Leu	Leu	Gly	Phe	Phe	Lys	His	Gln	Lys	Ser		
	210					215					220						
Leu	Glu	Ser	Leu	Arg	Tyr	Pro	Lys	Lys	Thr	Ile	Val	Leu	Phe	Ser	Lys		
225					230					235					240		
Ala	Lys	Glu	Cys	His	Lys	Ser	Phe	Leu	Asn	Ile	His	Asn	Lys	Thr	Glu		
				245					250					255			
Leu	Lys	Phe	Leu	Leu	Lys	Asn	Tyr	Asp	Leu	Glu	Pro	Phe	Asn	Leu	Ala		
		260						265					270				
Leu	Asp	Phe	Tyr	Ala	Leu	Lys	Asn	Pro	Lys	His	Ala	Leu	Lys	Ile	Lys		
		275					280					285					
Gly	Leu	Leu	Lys	Glu	Ile	Phe	Asp	Ser	Asn	Glu	Pro	Phe	Lys	Lys	Glu		
	290					295					300						
His	Leu	Ala	Leu	Lys	Gly	Gly	Ala	Leu	Gln	Ser	Leu	Gly	Tyr	Gln	His		
305					310					315					320		
Gln	Lys	Ile	Gly	Glu	Ile	Leu	Asn	Ala	Cys	Leu	Asp	Leu	Val	Ile	Ala		
				325					330					335			
Asn	Pro	Lys	Asn	Asn	Ala	Leu	Glu	Trp	Leu	Ile	Glu	Trp	Val	Lys	Gly		
			340					345					350				
His	Tyr	Leu	Pro	Asn	Asp	Thr	Ile	Asn	Leu	Ser	Pro	Ile	Gly	Arg	Arg		
		355					360					365					

Asn

<210> 47
 <211> 360
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (50)...(340)

<400> 47
 ttttccccta tatccaaagc catcatcaag aagttttaag gctcaaagc atg att ttt 58
 Met Ile Phe
 1

tcc act ctt att aat gcg ata gcg gtg att tta agc tcg ctc att acg	106
Ser Thr Leu Ile Asn Ala Ile Ala Val Ile Leu Ser Ser Leu Ile Thr	
5 10 15	
att tat atg tgg ata gta atc att tat tcg ctt atc agt ttc gtg cag	154
Ile Tyr Met Trp Ile Val Ile Ile Tyr Ser Leu Ile Ser Phe Val Gln	
20 25 30 35	
cct aac ccc aat aac ccc atc atg caa att ctc gct cgc ttg tgt gag	202
Pro Asn Pro Asn Asn Pro Ile Met Gln Ile Leu Ala Arg Leu Cys Glu	
40 45 50	
ccg gtg ttt tat ttt tta cgc tct aga ttc aag ctg gtg ttt aac ggg	250
Pro Val Phe Tyr Phe Leu Arg Ser Arg Phe Lys Leu Val Phe Asn Gly	
55 60 65	
ttg gat ttc tct cct tta gtg gtg gtc att gtt ttg aaa ttc ttg gat	298
Leu Asp Phe Ser Pro Leu Val Val Val Ile Val Leu Lys Phe Leu Asp	
70 75 80	
ctc acg ctc att cag tgg ctt ttc atg ctc gct aaa aac ctt	340
Leu Thr Leu Ile Gln Trp Leu Phe Met Leu Ala Lys Asn Leu	
85 90 95	
taaagaaaat catgcgtttt	360

<210> 48
 <211> 97
 <212> PRT
 <213> *Helicobacter pylori*

<400> 48

Met Ile Phe Ser Thr Leu Ile Asn Ala Ile Ala Val Ile Leu Ser Ser	
1 5 10 15	
Leu Ile Thr Ile Tyr Met Trp Ile Val Ile Ile Tyr Ser Leu Ile Ser	
20 25 30	
Phe Val Gln Pro Asn Pro Asn Asn Pro Ile Met Gln Ile Leu Ala Arg	
35 40 45	
Leu Cys Glu Pro Val Phe Tyr Phe Leu Arg Ser Arg Phe Lys Leu Val	
50 55 60	
Phe Asn Gly Leu Asp Phe Ser Pro Leu Val Val Val Ile Val Leu Lys	
65 70 75 80	
Phe Leu Asp Leu Thr Leu Ile Gln Trp Leu Phe Met Leu Ala Lys Asn	
85 90 95	

Leu

<210> 49
 <211> 1740
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (22)...(1701)

<400> 49
 taaaaacctt taaagaaaat c atg cgt ttt ttt acc ttg ttt ttt atc ggt 51

	Met	Arg	Phe	Phe	Thr	Leu	Phe	Phe	Ile	Gly	
	1				5					10	
atg ctt ggc gtt ggt ttt tct caa acc gag tta aat tta aaa gat tta	99										
Met Leu Gly Val Gly Phe Ser Gln Thr Glu Leu Asn Leu Lys Asp Leu											
	15 20 25										
gaa aaa aag ccc gcc ggg atc gtt agg gat tat tat ttg tgg cgt tat	147										
Glu Lys Lys Pro Ala Gly Ile Val Arg Asp Tyr Tyr Leu Trp Arg Tyr											
	30 35 40										
att agc gat aaa aaa acc agt tta gaa aac gct aaa aaa gcc tat gaa	195										
Ile Ser Asp Lys Lys Thr Ser Leu Glu Asn Ala Lys Lys Ala Tyr Glu											
	45 50 55										
ttg act caa aat aaa aac aac gcc cta caa aag gcc atg caa gaa aaa	243										
Leu Thr Gln Asn Lys Asn Asn Ala Leu Gln Lys Ala Met Gln Glu Lys											
	60 65 70										
ggc tca gac aat gca gaa aaa aac cct gat gtt aaa ttg cct gaa gat	291										
Gly Ser Asp Asn Ala Glu Lys Asn Pro Asp Val Lys Leu Pro Glu Asp											
	75 80 85 90										
att tat tgc aag caa acg gct tta gaa agc atg cta gaa aca aca gac	339										
Ile Tyr Cys Lys Gln Thr Ala Leu Glu Ser Met Leu Glu Thr Thr Asp											
	95 100 105										
act ttc caa gca agc tgc atc gct atc gct tta aaa tca aag atc aga	387										
Thr Phe Gln Ala Ser Cys Ile Ala Ile Ala Leu Lys Ser Lys Ile Arg											
	110 115 120										
gat ttt gat aaa atc cct att gaa acc ctt aag ccc tta caa att aaa	435										
Asp Phe Asp Lys Ile Pro Ile Glu Thr Leu Lys Pro Leu Gln Ile Lys											
	125 130 135										
atc aaa gag gct tac ccc gtt ctt tat gaa gaa tta gaa att ttg caa	483										
Ile Lys Glu Ala Tyr Pro Val Leu Tyr Glu Glu Leu Glu Ile Leu Gln											
	140 145 150										
agt aag cat gtg agc gct tct ttg ttt aag gct aac gcg caa gtg ttt	531										
Ser Lys His Val Ser Ala Ser Leu Phe Lys Ala Asn Ala Gln Val Phe											
	155 160 165 170										
agc gcg ctt ttc aat cat ttg agt tat gaa aaa aag ctc caa att ttt	579										
Ser Ala Leu Phe Asn His Leu Ser Tyr Glu Lys Lys Leu Gln Ile Phe											
	175 180 185										
gaa aag cat atc ccc att aaa gag tta aac cgt ctt tta gac gaa aat	627										
Glu Lys His Ile Pro Ile Lys Glu Leu Asn Arg Leu Leu Asp Glu Asn											
	190 195 200										
tat ccg gcg ttt aac cgc ttg atc tat cag gtt att tta gat cct aaa	675										
Tyr Pro Ala Phe Asn Arg Leu Ile Tyr Gln Val Ile Leu Asp Pro Lys											
	205 210 215										
ttg gat cat ttt aaa gac gct ctc act aaa agt aac gct acc cac agc	723										
Leu Asp His Phe Lys Asp Ala Leu Thr Lys Ser Asn Ala Thr His Ser											
	220 225 230										

aac gcg caa acc ttt ttt att cta ggg att aat gaa atc ttg cgc aaa	771
Asn Ala Gln Thr Phe Phe Ile Leu Gly Ile Asn Glu Ile Leu Arg Lys	
235 240 245 250	
aaa ccc tct aaa gcg ctc aag tat ttt gaa cga tca gaa gcg gtt gtc	819
Lys Pro Ser Lys Ala Leu Lys Tyr Phe Glu Arg Ser Glu Ala Val Val	
255 260 265	
aaa gac gat gat ttt tca aaa gac aga gcg att ttt tgg cag tat tta	867
Lys Asp Asp Asp Phe Ser Lys Asp Arg Ala Ile Phe Trp Gln Tyr Leu	
270 275 280	
gtt tct aaa aag aaa aaa act tta gaa cgc ctt tca caa agc cca gct	915
Val Ser Lys Lys Lys Lys Thr Leu Glu Arg Leu Ser Gln Ser Pro Ala	
285 290 295	
tta aat ctc tat agt ctt tat gcg agc cgc aaa ctc aaa acc acg ccc	963
Leu Asn Leu Tyr Ser Leu Tyr Ala Ser Arg Lys Leu Lys Thr Thr Pro	
300 305 310	
agt tac cgc atc att tca cgc atc cag aat tta agc caa gaa gat cct	1011
Ser Tyr Arg Ile Ile Ser Arg Ile Gln Asn Leu Ser Gln Glu Asp Pro	
315 320 325 330	
cct ttt aac act tat gac cct ttt tcg tgg caa att ttt aag gaa aaa	1059
Pro Phe Asn Thr Tyr Asp Pro Phe Ser Trp Gln Ile Phe Lys Glu Lys	
335 340 345	
acc ttg agt ttg aaa gat gag ggc gcg ttt aat gcg atg cta aaa agc	1107
Thr Leu Ser Leu Lys Asp Glu Gly Ala Phe Asn Ala Met Leu Lys Ser	
350 355 360	
ctg tat tat gaa aaa agc gct cct gaa ttg acc tat ctt tta agc caa	1155
Leu Tyr Tyr Glu Lys Ser Ala Pro Glu Leu Thr Tyr Leu Leu Ser Gln	
365 370 375	
cgc aat aaa gac aag att tat tat tat tta tcc cct tat gag ggc att	1203
Arg Asn Lys Asp Lys Ile Tyr Tyr Tyr Leu Ser Pro Tyr Glu Gly Ile	
380 385 390	
att gaa tgg caa aat act gat gaa aag gct atg gcg tat gcg atc gct	1251
Ile Glu Trp Gln Asn Thr Asp Glu Lys Ala Met Ala Tyr Ala Ile Ala	
395 400 405 410	
agg caa gaa agc ttt ttg ctc ccg gca gtc att tcg cgc tcg ttc gct	1299
Arg Gln Glu Ser Phe Leu Leu Pro Ala Val Ile Ser Arg Ser Phe Ala	
415 420 425	
ctg ggg ctt atg caa atc atg ccc ttt aat gta ggg cct ttc gct aaa	1347
Leu Gly Leu Met Gln Ile Met Pro Phe Asn Val Gly Pro Phe Ala Lys	
430 435 440	
agc ctt ggc atg gat aac att gat cta aac gac atg ttt aac ccc aac	1395
Ser Leu Gly Met Asp Asn Ile Asp Leu Asn Asp Met Phe Asn Pro Asn	
445 450 455	
atc gct ctc aaa ttt ggc aat tat tac ttg aac cat ttg aaa aaa gaa	1443
Ile Ala Leu Lys Phe Gly Asn Tyr Tyr Leu Asn His Leu Lys Lys Glu	
460 465 470	

ttc aac cac ccc ctt ttt gtc gcc tac gct tat aac gct ggg cct ggg	1491
Phe Asn His Pro Leu Phe Val Ala Tyr Ala Tyr Asn Ala Gly Pro Gly	
475 480 485 490	

ttt tta agg agg tgg tta gaa agt tcc aaa cga ttt aaa gaa aaa aat	1539
Phe Leu Arg Arg Trp Leu Glu Ser Ser Lys Arg Phe Lys Glu Lys Asn	
495 500 505	

cat ttt gag cca tgg ctt agc atg gag ctt atg cct tat agc gag act	1587
His Phe Glu Pro Trp Leu Ser Met Glu Leu Met Pro Tyr Ser Glu Thr	
510 515 520	

cgc atg tat ggc ttt agg gtc atg ctc aat tac ttg att tat caa gaa	1635
Arg Met Tyr Gly Phe Arg Val Met Leu Asn Tyr Leu Ile Tyr Gln Glu	
525 530 535	

att ttt ggg aat ttc atc cct att gat gga ttt tta gaa caa act ctt	1683
Ile Phe Gly Asn Phe Ile Pro Ile Asp Gly Phe Leu Glu Gln Thr Leu	
540 545 550	

aac tca aag gac aaa cca tgattaaaaa atgccttttt cctgctgcgg	1731
Asn Ser Lys Asp Lys Pro	
555 560	

gctatggca	1740
-----------	------

<210> 50
 <211> 560
 <212> PRT
 <213> Helicobacter pylori

<400> 50	
Met Arg Phe Phe Thr Leu Phe Phe Ile Gly Met Leu Gly Val Gly Phe	
1 5 10 15	
Ser Gln Thr Glu Leu Asn Leu Lys Asp Leu Glu Lys Lys Pro Ala Gly	
20 25 30	
Ile Val Arg Asp Tyr Tyr Leu Trp Arg Tyr Ile Ser Asp Lys Lys Thr	
35 40 45	
Ser Leu Glu Asn Ala Lys Lys Ala Tyr Glu Leu Thr Gln Asn Lys Asn	
50 55 60	
Asn Ala Leu Gln Lys Ala Met Gln Glu Lys Gly Ser Asp Asn Ala Glu	
65 70 75 80	
Lys Asn Pro Asp Val Lys Leu Pro Glu Asp Ile Tyr Cys Lys Gln Thr	
85 90 95	
Ala Leu Glu Ser Met Leu Glu Thr Thr Asp Thr Phe Gln Ala Ser Cys	
100 105 110	
Ile Ala Ile Ala Leu Lys Ser Lys Ile Arg Asp Phe Asp Lys Ile Pro	
115 120 125	
Ile Glu Thr Leu Lys Pro Leu Gln Ile Lys Ile Lys Glu Ala Tyr Pro	
130 135 140	
Val Leu Tyr Glu Glu Leu Glu Ile Leu Gln Ser Lys His Val Ser Ala	
145 150 155 160	
Ser Leu Phe Lys Ala Asn Ala Gln Val Phe Ser Ala Leu Phe Asn His	
165 170 175	
Leu Ser Tyr Glu Lys Lys Leu Gln Ile Phe Glu Lys His Ile Pro Ile	
180 185 190	
Lys Glu Leu Asn Arg Leu Leu Asp Glu Asn Tyr Pro Ala Phe Asn Arg	
195 200 205	

Leu	Ile	Tyr	Gln	Val	Ile	Leu	Asp	Pro	Lys	Leu	Asp	His	Phe	Lys	Asp
210						215				220					
Ala	Leu	Thr	Lys	Ser	Asn	Ala	Thr	His	Ser	Asn	Ala	Gln	Thr	Phe	Phe
225					230					235					240
Ile	Leu	Gly	Ile	Asn	Glu	Ile	Leu	Arg	Lys	Lys	Pro	Ser	Lys	Ala	Leu
				245					250					255	
Lys	Tyr	Phe	Glu	Arg	Ser	Glu	Ala	Val	Lys	Asp	Asp	Asp	Asp	Phe	Ser
			260					265					270		
Lys	Asp	Arg	Ala	Ile	Phe	Trp	Gln	Tyr	Leu	Val	Ser	Lys	Lys	Lys	Lys
		275					280					285			
Thr	Leu	Glu	Arg	Leu	Ser	Gln	Ser	Pro	Ala	Leu	Asn	Leu	Tyr	Ser	Leu
		290				295					300				
Tyr	Ala	Ser	Arg	Lys	Leu	Lys	Thr	Thr	Pro	Ser	Tyr	Arg	Ile	Ile	Ser
305					310					315					320
Arg	Ile	Gln	Asn	Leu	Ser	Gln	Glu	Asp	Pro	Pro	Phe	Asn	Thr	Tyr	Asp
			325						330					335	
Pro	Phe	Ser	Trp	Gln	Ile	Phe	Lys	Glu	Lys	Thr	Leu	Ser	Leu	Lys	Asp
			340					345					350		
Glu	Gly	Ala	Phe	Asn	Ala	Met	Leu	Lys	Ser	Leu	Tyr	Tyr	Glu	Lys	Ser
		355				360						365			
Ala	Pro	Glu	Leu	Thr	Tyr	Leu	Leu	Ser	Gln	Arg	Asn	Lys	Asp	Lys	Ile
		370				375					380				
Tyr	Tyr	Tyr	Leu	Ser	Pro	Tyr	Glu	Gly	Ile	Ile	Glu	Trp	Gln	Asn	Thr
385					390					395					400
Asp	Glu	Lys	Ala	Met	Ala	Tyr	Ala	Ile	Ala	Arg	Gln	Glu	Ser	Phe	Leu
			405						410					415	
Leu	Pro	Ala	Val	Ile	Ser	Arg	Ser	Phe	Ala	Leu	Gly	Leu	Met	Gln	Ile
			420					425					430		
Met	Pro	Phe	Asn	Val	Gly	Pro	Phe	Ala	Lys	Ser	Leu	Gly	Met	Asp	Asn
			435				440					445			
Ile	Asp	Leu	Asn	Asp	Met	Phe	Asn	Pro	Asn	Ile	Ala	Leu	Lys	Phe	Gly
	450				455					460					
Asn	Tyr	Tyr	Leu	Asn	His	Leu	Lys	Lys	Glu	Phe	Asn	His	Pro	Leu	Phe
465					470					475					480
Val	Ala	Tyr	Ala	Tyr	Asn	Ala	Gly	Pro	Gly	Phe	Leu	Arg	Arg	Trp	Leu
			485						490					495	
Glu	Ser	Ser	Lys	Arg	Phe	Lys	Glu	Lys	Asn	His	Phe	Glu	Pro	Trp	Leu
			500					505					510		
Ser	Met	Glu	Leu	Met	Pro	Tyr	Ser	Glu	Thr	Arg	Met	Tyr	Gly	Phe	Arg
		515					520					525			
Val	Met	Leu	Asn	Tyr	Leu	Ile	Tyr	Gln	Glu	Ile	Phe	Gly	Asn	Phe	Ile
	530				535						540				
Pro	Ile	Asp	Gly	Phe	Leu	Glu	Gln	Thr	Leu	Asn	Ser	Lys	Asp	Lys	Pro
545					550					555					560

<210> 51
 <211> 770
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (16)...(738)

<400> 51
 taaaaagaag gacaa atg atg cca ttt gaa gct gta atc ggg cta gaa gtc 51
 Met Met Pro Phe Glu Ala Val Ile Gly Leu Glu Val
 1 5 10

cat gtc caa ctc aac acc aaa acc aaa atc ttt tgc tct tgc tct aca	99
His Val Gln Leu Asn Thr Lys Thr Lys Ile Phe Cys Ser Cys Ser Thr	
15 20 25	
agc ttt gga gaa tcc cct aat tct aac acc tgc cct gtg tgt ttg ggt	147
Ser Phe Gly Glu Ser Pro Asn Ser Asn Thr Cys Pro Val Cys Leu Gly	
30 35 40	
tta ccg gga gct ttg ccg gta ttg aat aaa gaa gtg gtt aaa aaa gcc	195
Leu Pro Gly Ala Leu Pro Val Leu Asn Lys Glu Val Val Lys Lys Ala	
45 50 55 60	
atc caa tta ggc aca gcc att gaa gcc aat atc aac caa tat tct att	243
Ile Gln Leu Gly Thr Ala Ile Glu Ala Asn Ile Asn Gln Tyr Ser Ile	
65 70 75	
ttt gcg agg aaa aat tat ttt tac cct gat ttg cct aag gct tat caa	291
Phe Ala Arg Lys Asn Tyr Phe Tyr Pro Asp Leu Pro Lys Ala Tyr Gln	
80 85 90	
att tcg cag ttt gaa gtc cct att gtg agc gat ggg aaa tta gag att	339
Ile Ser Gln Phe Glu Val Pro Ile Val Ser Asp Gly Lys Leu Glu Ile	
95 100 105	
gac act aaa gag ggt gca aaa atc gtg cgt att gaa agg gcc cac atg	387
Asp Thr Lys Glu Gly Ala Lys Ile Val Arg Ile Glu Arg Ala His Met	
110 115 120	
gaa gaa gac gcc ggt aaa aat atc cat gag ggc agt tat tct tta gtg	435
Glu Glu Asp Ala Gly Lys Asn Ile His Glu Gly Ser Tyr Ser Leu Val	
125 130 135 140	
gat ttg aac cgc gct tgc acc cct tta tta gaa att gtc agt aag ccg	483
Asp Leu Asn Arg Ala Cys Thr Pro Leu Leu Glu Ile Val Ser Lys Pro	
145 150 155	
gac atg cga aat agt gaa gaa gct ata gcg tat ttg aaa aag ctc cat	531
Asp Met Arg Asn Ser Glu Glu Ala Ile Ala Tyr Leu Lys Lys Leu His	
160 165 170	
gct atc gtg cgt ttt ata ggg att tct gat gcg aac atg caa gag ggg	579
Ala Ile Val Arg Phe Ile Gly Ile Ser Asp Ala Asn Met Gln Glu Gly	
175 180 185	
aat ttc agg tgc gat gcg aac gtg tcc att aga ccc aaa ggc gat gaa	627
Asn Phe Arg Cys Asp Ala Asn Val Ser Ile Arg Pro Lys Gly Asp Glu	
190 195 200	
aag ctt tat acg aga gta gag att aaa aat cta aat agc ttt aga ttc	675
Lys Leu Tyr Thr Arg Val Glu Ile Lys Asn Leu Asn Ser Phe Arg Phe	
205 210 215 220	
att gct aaa gcg att gaa tac gag ata gag cgc caa agc gcg gac gtg	723
Ile Ala Lys Ala Ile Glu Tyr Glu Ile Glu Arg Gln Ser Ala Asp Val	
225 230 235	
gga gaa cgg gcg cta taatgaagag gtggttcaag aaacgcgcct tt	770
Gly Glu Arg Ala Leu	

240

<210> 52
 <211> 241
 <212> PRT
 <213> Helicobacter pylori

<400> 52
 Met Met Pro Phe Glu Ala Val Ile Gly Leu Glu Val His Val Gln Leu
 1 5 10 15
 Asn Thr Lys Thr Lys Ile Phe Cys Ser Cys Ser Thr Ser Phe Gly Glu
 20 25 30
 Ser Pro Asn Ser Asn Thr Cys Pro Val Cys Leu Gly Leu Pro Gly Ala
 35 40 45
 Leu Pro Val Leu Asn Lys Glu Val Val Lys Lys Ala Ile Gln Leu Gly
 50 55 60
 Thr Ala Ile Glu Ala Asn Ile Asn Gln Tyr Ser Ile Phe Ala Arg Lys
 65 70 75 80
 Asn Tyr Phe Tyr Pro Asp Leu Pro Lys Ala Tyr Gln Ile Ser Gln Phe
 85 90 95
 Glu Val Pro Ile Val Ser Asp Gly Lys Leu Glu Ile Asp Thr Lys Glu
 100 105 110
 Gly Ala Lys Ile Val Arg Ile Glu Arg Ala His Met Glu Glu Asp Ala
 115 120 125
 Gly Lys Asn Ile His Glu Gly Ser Tyr Ser Leu Val Asp Leu Asn Arg
 130 135 140
 Ala Cys Thr Pro Leu Leu Glu Ile Val Ser Lys Pro Asp Met Arg Asn
 145 150 155 160
 Ser Glu Glu Ala Ile Ala Tyr Leu Lys Lys Leu His Ala Ile Val Arg
 165 170 175
 Phe Ile Gly Ile Ser Asp Ala Asn Met Gln Glu Gly Asn Phe Arg Cys
 180 185 190
 Asp Ala Asn Val Ser Ile Arg Pro Lys Gly Asp Glu Lys Leu Tyr Thr
 195 200 205
 Arg Val Glu Ile Lys Asn Leu Asn Ser Phe Arg Phe Ile Ala Lys Ala
 210 215 220
 Ile Glu Tyr Glu Ile Glu Arg Gln Ser Ala Asp Val Gly Glu Arg Ala
 225 230 235 240
 Leu

<210> 53
 <211> 487
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (16)...(444)

<400> 53
 atgggagtgg attga atg caa gaa att gaa att ttt tgc gat ggc tct tct 51
 Met Gln Glu Ile Glu Ile Phe Cys Asp Gly Ser Ser
 1 5 10
 tta ggc aat ccc ggg cca ggc ggt tat gcg gcg att tta cgc tat aaa 99
 Leu Gly Asn Pro Gly Pro Gly Gly Tyr Ala Ala Ile Leu Arg Tyr Lys

15	20	25	
gat aaa gaa aaa acc atc agt ggg ggc gaa gaa ttc acc acg aat aac			147
Asp Lys Glu Lys Thr Ile Ser Gly Gly Glu Glu Phe Thr Thr Asn Asn			
30	35	40	
cgc atg gaa tta aga gcg ctc aat gaa gcg tta aaa att ttg aaa cgc			195
Arg Met Glu Leu Arg Ala Leu Asn Glu Ala Leu Lys Ile Leu Lys Arg			
45	50	55	60
cca tgc cgt atc acg ctt tat agc gat tgc caa tac gtg tgc caa gcg			243
Pro Cys Arg Ile Thr Leu Tyr Ser Asp Ser Gln Tyr Val Cys Gln Ala			
65	70	75	
atc aat gtg tgg cta gct aac tgg caa aaa aag aat ttt tct aaa gtt			291
Ile Asn Val Trp Leu Ala Asn Trp Gln Lys Lys Asn Phe Ser Lys Val			
80	85	90	
aaa aat gtg gat tta tgg aaa gaa ttt tta gaa gtc tct aaa ggg cat			339
Lys Asn Val Asp Leu Trp Lys Glu Phe Leu Glu Val Ser Lys Gly His			
95	100	105	
tct att gtg gct gtt tgg atc aag ggg cat aac ggg cat gcc gag aat			387
Ser Ile Val Ala Val Trp Ile Lys Gly His Asn Gly His Ala Glu Asn			
110	115	120	
gaa cga tgc gat agc ctc gct aaa tta gag gcg caa aaa cgg gtc aaa			435
Glu Arg Cys Asp Ser Leu Ala Lys Leu Glu Ala Gln Lys Arg Val Lys			
125	130	135	140
acg acc act taaagggaaa aatgatgaaa aacaaacgct ctcaaaacag			484
Thr Thr Thr			
ccc			487
<210> 54			
<211> 143			
<212> PRT			
<213> Helicobacter pylori			
<400> 54			
Met Gln Glu Ile Glu Ile Phe Cys Asp Gly Ser Ser Leu Gly Asn Pro			
1 5 10 15			
Gly Pro Gly Gly Tyr Ala Ala Ile Leu Arg Tyr Lys Asp Lys Glu Lys			
20 25 30			
Thr Ile Ser Gly Gly Glu Glu Phe Thr Thr Asn Asn Arg Met Glu Leu			
35 40 45			
Arg Ala Leu Asn Glu Ala Leu Lys Ile Leu Lys Arg Pro Cys Arg Ile			
50 55 60			
Thr Leu Tyr Ser Asp Ser Gln Tyr Val Cys Gln Ala Ile Asn Val Trp			
65 70 75 80			
Leu Ala Asn Trp Gln Lys Lys Asn Phe Ser Lys Val Lys Asn Val Asp			
85 90 95			
Leu Trp Lys Glu Phe Leu Glu Val Ser Lys Gly His Ser Ile Val Ala			
100 105 110			
Val Trp Ile Lys Gly His Asn Gly His Ala Glu Asn Glu Arg Cys Asp			
115 120 125			
Ser Leu Ala Lys Leu Glu Ala Gln Lys Arg Val Lys Thr Thr Thr			

140

<400> 55																
atgtatg																56
cgctaaagg caaaagcaaa aaagaagccg aacagca atg cgc tta																
Met Arg Leu																
1																
tca agc gct tca aaa act gaa gga agc caa atg aac act ttg ggg cgt																104
Ser Ser 5 Ala Ser Lys Thr 10 Glu Gly Ser Gln Met Asn 15 Thr Leu Gly Arg																
ttt tta agg ctc acg act ttt ggg gaa tcg cat ggg gat gtg ata ggg																152
Phe Leu Arg Leu Thr 25 Phe Gly Glu Ser His 30 Gly Asp Val Ile Gly 35																
20																
ggg gta tta gac ggc atg cct agc ggg att aaa ata gac tat gcg cta																200
Gly Val Leu Asp 40 Gly Met Pro Ser Gly 45 Ile Lys Ile Asp Tyr Ala Leu 50																
tta gaa aat gaa atg aag cgc cgc caa ggg ggg agg aac gtt ttc att																248
Leu Glu Asn 55 Glu Met Lys Arg Arg Gln 60 Gly Gly Arg Asn Val Phe Ile 65																
acg cca cga aaa gaa gac gat aaa gtg gaa ata aca agc ggg gtt ttt																296
Thr Pro 70 Lys Glu Asp Asp 75 Val Glu Ile Thr 80 Ser Gly Val Phe 85																
gaa gat ttt agc aca ggg act cct ata ggg ttt tta atc cac aac caa																344
Glu Asp 85 Phe Ser Thr Gly 90 Thr Pro Ile Gly Phe Leu 95 Ile His Asn Gln 100																
agg gct agg agc aag gat tac gat aac att aaa aac ctt ttt agg cct																392
Arg Ala Arg Ser Lys 105 Tyr Asp Asn Ile Lys 110 Asn Leu Phe Arg Pro 115																
100																
agc cat gcg gat ttc act tat ttt cat aaa tac ggc att agg gat ttt																440
Ser His Ala Asp 120 Thr Tyr Phe His Lys 125 Tyr Gly Ile Arg Asp Phe 130																
agg ggt ggg ggg agg agt tcg gcc aga gag agt gct ata aga gtg gct																488
Arg Gly Gly 135 Arg Ser Ser Ala Arg 140 Glu Ser Ala Ile 145 Arg Val Ala 150																
gct ggg gcg ttt gct aaa atg ctt tta aga gaa atc ggt att gtt tgt																536
Ala Gly Ala Phe Ala Lys Met 155 Leu Leu Arg Glu Ile 160 Gly Ile Val Cys 165																
gaa agc ggg att ata gaa att ggg ggt att aaa gcc aaa aat tat gat																584
Glu Ser Gly Ile Ile Glu Ile Gly Gly Ile Lys Ala Lys Asn Tyr Asp 170																

165	170	175	
ttt aat cac gcc tta	aaa agc gag att ttt	gcc cta gat gaa gaa caa	632
Phe Asn His Ala Leu	Lys Ser Glu Ile Phe	Ala Leu Asp Glu Glu Gln	
180	185	190	195
gaa gaa gcg caa aaa	aca gcc att caa aac	gct atc aaa aac cac gat	680
Glu Glu Ala Gln Lys	Thr Ala Ile Gln Asn	Ala Ile Lys Asn His Asp	
	200	205	210
agc ata ggg ggt gtg	gct ttg att aga gcg	agg agc ata aaa acc aat	728
Ser Ile Gly Gly Val	Ala Leu Ile Arg Ala	Arg Ser Ile Lys Thr Asn	
	215	220	225
caa aag ctc ccc att	ggc tta ggt caa ggg	cta tac gct aaa tta gac	776
Gln Lys Leu Pro Ile	Gly Leu Gly Gln Gly	Leu Tyr Ala Lys Leu Asp	
	230	235	240
gct aaa atc gct gaa	gcg atg atg ggg ctt	aat ggg gtg aaa gcg gtt	824
Ala Lys Ile Ala Glu	Ala Met Met Gly Leu	Asn Gly Val Lys Ala Val	
	245	250	255
gaa ata ggc aag ggg	gta gaa agc tct tta	tta aaa ggc tca gag tat	872
Glu Ile Gly Lys Gly	Val Glu Ser Ser Leu	Leu Lys Gly Ser Glu Tyr	
	260	265	270
aat gat tta atg gat	caa aag ggg ttt ttg	agc aat cgt agc gga ggg	920
Asn Asp Leu Met Asp	Gln Lys Gly Phe Leu	Ser Asn Arg Ser Gly Gly	
	280	285	290
gtt tta ggg ggc atg	agc aat ggg gaa gaa	atc att gtt aga gtg cat	968
Val Leu Gly Gly Met	Ser Asn Gly Glu Glu	Ile Ile Val Arg Val His	
	295	300	305
ttc aaa ccc acg cca	agc att ttc caa cct	caa cga acc ata gac att	1016
Phe Lys Pro Thr Pro	Ser Ile Phe Gln Pro	Gln Arg Thr Ile Asp Ile	
	310	315	320
aat ggc aat gag tgc	gaa tgc ttg tta aag	ggc agg cat gat cct tgc	1064
Asn Gly Asn Glu Cys	Glu Cys Leu Leu Lys	Gly Arg His Asp Pro Cys	
	325	330	335
att gcg att aga ggg	agc gtg gtg tgc gag	agt ttg tta gcg ttg gtg	1112
Ile Ala Ile Arg Gly	Ser Val Val Cys Glu	Ser Leu Leu Ala Leu Val	
	340	345	350
ttg gct gat atg gta	tta ctc aat ttg act	tca aaa ata gag tat tta	1160
Leu Ala Asp Met Val	Leu Leu Asn Leu Thr	Ser Lys Ile Glu Tyr Leu	
	360	365	370
aaa acg att tat aat	gag aat taaacgaaat	tgatacaat cagcttaaaa	1211
Lys Thr Ile Tyr Asn	Glu Asn		
	375		
aggata			1217
<210> 56			
<211> 378			
<212> PRT			

<213> Helicobacter pylori

<400> 56

Met	Arg	Leu	Ser	Ser	Ala	Ser	Lys	Thr	Glu	Gly	Ser	Gln	Met	Asn	Thr
1				5					10					15	
Leu	Gly	Arg	Phe	Leu	Arg	Leu	Thr	Thr	Phe	Gly	Glu	Ser	His	Gly	Asp
			20					25					30		
Val	Ile	Gly	Gly	Val	Leu	Asp	Gly	Met	Pro	Ser	Gly	Ile	Lys	Ile	Asp
		35					40					45			
Tyr	Ala	Leu	Leu	Glu	Asn	Glu	Met	Lys	Arg	Arg	Gln	Gly	Gly	Arg	Asn
	50					55					60				
Val	Phe	Ile	Thr	Pro	Arg	Lys	Glu	Asp	Asp	Lys	Val	Glu	Ile	Thr	Ser
65					70					75					80
Gly	Val	Phe	Glu	Asp	Phe	Ser	Thr	Gly	Thr	Pro	Ile	Gly	Phe	Leu	Ile
				85					90					95	
His	Asn	Gln	Arg	Ala	Arg	Ser	Lys	Asp	Tyr	Asp	Asn	Ile	Lys	Asn	Leu
			100					105					110		
Phe	Arg	Pro	Ser	His	Ala	Asp	Phe	Thr	Tyr	Phe	His	Lys	Tyr	Gly	Ile
		115					120					125			
Arg	Asp	Phe	Arg	Gly	Gly	Gly	Arg	Ser	Ser	Ala	Arg	Glu	Ser	Ala	Ile
	130					135					140				
Arg	Val	Ala	Ala	Gly	Ala	Phe	Ala	Lys	Met	Leu	Leu	Arg	Glu	Ile	Gly
145					150					155					160
Ile	Val	Cys	Glu	Ser	Gly	Ile	Ile	Glu	Ile	Gly	Gly	Ile	Lys	Ala	Lys
				165					170					175	
Asn	Tyr	Asp	Phe	Asn	His	Ala	Leu	Lys	Ser	Glu	Ile	Phe	Ala	Leu	Asp
			180					185					190		
Glu	Glu	Gln	Glu	Glu	Ala	Gln	Lys	Thr	Ala	Ile	Gln	Asn	Ala	Ile	Lys
			195				200					205			
Asn	His	Asp	Ser	Ile	Gly	Gly	Val	Ala	Leu	Ile	Arg	Ala	Arg	Ser	Ile
	210				215						220				
Lys	Thr	Asn	Gln	Lys	Leu	Pro	Ile	Gly	Leu	Gly	Gln	Gly	Leu	Tyr	Ala
225					230					235					240
Lys	Leu	Asp	Ala	Lys	Ile	Ala	Glu	Ala	Met	Met	Gly	Leu	Asn	Gly	Val
				245					250					255	
Lys	Ala	Val	Glu	Ile	Gly	Lys	Gly	Val	Glu	Ser	Ser	Leu	Leu	Lys	Gly
			260					265					270		
Ser	Glu	Tyr	Asn	Asp	Leu	Met	Asp	Gln	Lys	Gly	Phe	Leu	Ser	Asn	Arg
		275					280					285			
Ser	Gly	Gly	Val	Leu	Gly	Gly	Met	Ser	Asn	Gly	Glu	Glu	Ile	Ile	Val
	290				295						300				
Arg	Val	His	Phe	Lys	Pro	Thr	Pro	Ser	Ile	Phe	Gln	Pro	Gln	Arg	Thr
305					310					315					320
Ile	Asp	Ile	Asn	Gly	Asn	Glu	Cys	Glu	Cys	Leu	Leu	Lys	Gly	Arg	His
				325					330					335	
Asp	Pro	Cys	Ile	Ala	Ile	Arg	Gly	Ser	Val	Val	Cys	Glu	Ser	Leu	Leu
			340					345					350		
Ala	Leu	Val	Leu	Ala	Asp	Met	Val	Leu	Leu	Asn	Leu	Thr	Ser	Lys	Ile
		355					360						365		
Glu	Tyr	Leu	Lys	Thr	Ile	Tyr	Asn	Glu	Asn						
	370					375									

<210> 57

<211> 588

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS
 <222> (20)...(535)

<400> 57

```

tcattgtgcc tgaagccac atg cgc tac atg ctc atc aac gat tat tac aag 52
      Met Arg Tyr Met Leu Ile Asn Asp Tyr Tyr Lys
      1             5             10

gtg ttt ttg ggc gaa aaa gat aag gat ttg tat gtg aag cgc ttg gaa 100
Val Phe Leu Gly Glu Lys Asp Lys Asp Leu Tyr Val Lys Arg Leu Glu
      15             20             25

aaa atc acg cct aaa atc tat ctg gcg agc gtg ttt tta gag aaa cac 148
Lys Ile Thr Pro Lys Ile Tyr Leu Ala Ser Val Phe Leu Glu Lys His
      30             35             40

acc cct tta aaa agt ctt tta gaa aaa atc cct aag gga aaa aaa gag 196
Thr Pro Leu Lys Ser Leu Leu Glu Lys Ile Pro Lys Gly Lys Lys Glu
      45             50             55

act atc acc tat cat aac cct tgt cat gcc aaa aaa acc cta aac gct 244
Thr Ile Thr Tyr His Asn Pro Cys His Ala Lys Lys Thr Leu Asn Ala
      60             65             70             75

cac aaa gaa gtg cgc aac ttg ctc aat ttg cat tat gaa att aaa gaa 292
His Lys Glu Val Arg Asn Leu Leu Asn Leu His Tyr Glu Ile Lys Glu
      80             85             90

atg ccg gac aat tgt tgc ggt ttt ggg ggg att acg atg caa aca caa 340
Met Pro Asp Asn Cys Cys Gly Phe Gly Gly Ile Thr Met Gln Thr Gln
      95             100             105

aag gcg gga ttt tct tta aaa gtg ggg ctt ctt agg gct aaa gaa atc 388
Lys Ala Gly Phe Ser Leu Lys Val Gly Leu Leu Arg Ala Lys Glu Ile
      110             115             120

ata gac acc aaa gct gca att ttg agc gct gaa tgc ggg gca tgc cat 436
Ile Asp Thr Lys Ala Ala Ile Leu Ser Ala Glu Cys Gly Ala Cys His
      125             130             135

atg caa tta aac aac gct tta aag tct tta gac gac cct aac act ccg 484
Met Gln Leu Asn Asn Ala Leu Lys Ser Leu Asp Asp Pro Asn Thr Pro
      140             145             150             155

cca ttt ttg cac cct tta gaa ctc atc gct aaa gcc tta aaa agc gct 532
Pro Phe Leu His Pro Leu Glu Leu Ile Ala Lys Ala Leu Lys Ser Ala
      160             165             170

gaa taaaaagcct ttttaacccc attctccaac atcttttttat ataatacaga 585
Glu

gct 588

```

<210> 58
 <211> 172
 <212> PRT
 <213> Helicobacter pylori

<400> 58
Met Arg Tyr Met Leu Ile Asn Asp Tyr Tyr Lys Val Phe Leu Gly Glu
1 5 10 15
Lys Asp Lys Asp Leu Tyr Val Lys Arg Leu Glu Lys Ile Thr Pro Lys
20 25 30
Ile Tyr Leu Ala Ser Val Phe Leu Glu Lys His Thr Pro Leu Lys Ser
35 40 45
Leu Leu Glu Lys Ile Pro Lys Gly Lys Lys Glu Thr Ile Thr Tyr His
50 55 60
Asn Pro Cys His Ala Lys Lys Thr Leu Asn Ala His Lys Glu Val Arg
65 70 75 80
Asn Leu Leu Asn Leu His Tyr Glu Ile Lys Glu Met Pro Asp Asn Cys
85 90 95
Cys Gly Phe Gly Gly Ile Thr Met Gln Thr Gln Lys Ala Gly Phe Ser
100 105 110
Leu Lys Val Gly Leu Leu Arg Ala Lys Glu Ile Ile Asp Thr Lys Ala
115 120 125
Ala Ile Leu Ser Ala Glu Cys Gly Ala Cys His Met Gln Leu Asn Asn
130 135 140
Ala Leu Lys Ser Leu Asp Asp Pro Asn Thr Pro Pro Phe Leu His Pro
145 150 155 160
Leu Glu Leu Ile Ala Lys Ala Leu Lys Ser Ala Glu
165 170

<210> 59
<211> 350
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (30)...(317)

<400> 59
ggcgtttaaag ctctgtatta tataaaaag atg ttg gag aat ggg gtt aaa aag 53
Met Leu Glu Asn Gly Val Lys Lys
1 5
gct ttt tat tca gcg ctt ttt aag gct tta gcg atg agt tct aaa ggg 101
Ala Phe Tyr Ser Ala Leu Phe Lys Ala Leu Ala Met Ser Ser Lys Gly
10 15 20
tgc aaa aat ggc gga gtg tta ggg tcg tct aaa gac ttt aaa gcg ttg 149
Cys Lys Asn Gly Gly Val Leu Gly Ser Ser Lys Asp Phe Lys Ala Leu
25 30 35 40
ttt aat tgc ata tgg cat gcc ccg cat tca gcg ctc aaa att gca gct 197
Phe Asn Cys Ile Trp His Ala Pro His Ser Ala Leu Lys Ile Ala Ala
45 50 55
ttg gtg tct atg att tct tta gcc cta aga agc ccc act ttt aaa gaa 245
Leu Val Ser Met Ile Ser Leu Ala Leu Arg Ser Pro Thr Phe Lys Glu
60 65 70
aat ccc gcc ttt tgt gtt tgc atc gta atc ccc cca aaa ccg caa caa 293
Asn Pro Ala Phe Cys Val Cys Ile Val Ile Pro Pro Lys Pro Gln Gln
75 80 85

ttg tcc ggc att tct tta att tca taatgcaaatt tgagcaacct tttgcattct 347
 Leu Ser Gly Ile Ser Leu Ile Ser
 90 95

tac 350

<210> 60
 <211> 96
 <212> PRT
 <213> Helicobacter pylori

<400> 60
 Met Leu Glu Asn Gly Val Lys Lys Ala Phe Tyr Ser Ala Leu Phe Lys
 1 5 10 15
 Ala Leu Ala Met Ser Ser Lys Gly Cys Lys Asn Gly Gly Val Leu Gly
 20 25 30
 Ser Ser Lys Asp Phe Lys Ala Leu Phe Asn Cys Ile Trp His Ala Pro
 35 40 45
 His Ser Ala Leu Lys Ile Ala Ala Leu Val Ser Met Ile Ser Leu Ala
 50 55 60
 Leu Arg Ser Pro Thr Phe Lys Glu Asn Pro Ala Phe Cys Val Cys Ile
 65 70 75 80
 Val Ile Pro Pro Lys Pro Gln Gln Leu Ser Gly Ile Ser Leu Ile Ser
 85 90 95

<210> 61
 <211> 1800
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (69)...(1718)

<400> 61
 tcattcatctc cacttctaatt ttaacctcta acgcccttaa cgcaattgag caaatcagaa 60
 gcacagga atg ggg att gac att gat gaa atc act gaa gag gat ttt atc 110
 Met Gly Ile Asp Ile Asp Glu Ile Thr Glu Glu Asp Phe Ile
 1 5 10

 tat tct cgc att gat tgg gaa aag ttt gat ccc aca aaa acg caa gac 158
 Tyr Ser Arg Ile Asp Trp Glu Lys Phe Asp Pro Thr Lys Thr Gln Asp
 15 20 25 30

 gaa atc ccc tta tgc gat aag aaa aag ccg cgc tcg cat caa aca gaa 206
 Glu Ile Pro Leu Cys Asp Lys Lys Lys Pro Arg Ser His Gln Thr Glu
 35 40 45

 gcc ata aac gcc act aaa gag tat ttt tct gac cct aaa aac gct aga 254
 Ala Ile Asn Ala Thr Lys Glu Tyr Phe Ser Asp Pro Lys Asn Ala Arg
 50 55 60

 ggc aag ctc att atg gca tgc ggg aca ggc aaa acc tac act tct tta 302
 Gly Lys Leu Ile Met Ala Cys Gly Thr Gly Lys Thr Tyr Thr Ser Leu
 65 70 75

 aaa atc atg gaa gct tta gac tct aag atc acg ctt ttt cta gca ccc 350
 Lys Ile Met Glu Ala Leu Asp Ser Lys Ile Thr Leu Phe Leu Ala Pro

80	85	90	
agc atc gct ttg ctt tct caa act ttt aga gaa tac gcg caa gaa aaa			398
Ser Ile Ala Leu Leu Ser Gln Thr Phe Arg Glu Tyr Ala Gln Glu Lys			
95	100	105	110
agt gag ccg ttt tac gct tct atc gtg tgc agc gat gat aaa gtc ggg			446
Ser Glu Pro Phe Tyr Ala Ser Ile Val Cys Ser Asp Asp Lys Val Gly			
	115	120	125
aaa agt aaa gac gaa gac aat gat gat att aaa ttt tct gag ctc cct			494
Lys Ser Lys Asp Glu Asp Asn Asp Asp Ile Lys Phe Ser Glu Leu Pro			
	130	135	140
tta aag ccc tcc act cgc ctt gaa gac att tta agc gtt cga aaa aaa			542
Leu Lys Pro Ser Thr Arg Leu Glu Asp Ile Leu Ser Val Arg Lys Lys			
	145	150	155
gcg caa aaa gaa aac aag cgc ttc att att ttt tca acc tat caa agc			590
Ala Gln Lys Glu Asn Lys Arg Phe Ile Ile Phe Ser Thr Tyr Gln Ser			
	160	165	170
gcg ttg cgt att aaa gaa gcg caa gaa gcg ggt ttg ggc gga atc gat			638
Ala Leu Arg Ile Lys Glu Ala Gln Glu Ala Gly Leu Gly Gly Ile Asp			
	175	180	185
ctt att att tgc gat gaa gcc cac aga acg gta ggg gct atg tat tct			686
Leu Ile Ile Cys Asp Glu Ala His Arg Thr Val Gly Ala Met Tyr Ser			
	195	200	205
agt aat gaa agg gac gat aaa aac gct ttc acg ctt tgc cat agc gat			734
Ser Asn Glu Arg Asp Asp Lys Asn Ala Phe Thr Leu Cys His Ser Asp			
	210	215	220
aaa aat atc aaa gcg aaa aaa cgc ctg tat atg acc gcc acg cct aaa			782
Lys Asn Ile Lys Ala Lys Lys Arg Leu Tyr Met Thr Ala Thr Pro Lys			
	225	230	235
gtt tat agc gaa agc tcc aaa gct aaa gcc aaa gag agc gat aat gtt			830
Val Tyr Ser Glu Ser Ser Lys Ala Lys Ala Lys Glu Ser Asp Asn Val			
	240	245	250
atc tat tct atg gac gat gca gag att ttt ggc gaa gaa atc tat acg			878
Ile Tyr Ser Met Asp Asp Ala Glu Ile Phe Gly Glu Glu Ile Tyr Thr			
	255	260	265
ctc aat ttt tca aaa gcg atc gct ttg gat ctc tta acc gat tat aaa			926
Leu Asn Phe Ser Lys Ala Ile Ala Leu Asp Leu Leu Thr Asp Tyr Lys			
	275	280	285
gtc atc att tta gcg gtg cga aaa gaa aat tta agc ggc gtt act aac			974
Val Ile Ile Leu Ala Val Arg Lys Glu Asn Leu Ser Gly Val Thr Asn			
	290	295	300
agc gtg aat aaa aag atc agc cag ctc aaa gcc gaa ggc act aaa tta			1022
Ser Val Asn Lys Lys Ile Ser Gln Leu Lys Ala Glu Gly Thr Lys Leu			
	305	310	315
gat aaa aag ctc atc aat aac gaa ttt gtt tgt aag atc atc ggc act			1070

Asp	Lys	Lys	Leu	Ile	Asn	Asn	Glu	Phe	Val	Cys	Lys	Ile	Ile	Gly	Thr		
320						325					330						
cat	aaa	ggg	tta	gcc	aag	cag	gat	tta	atc	gtt	tta	aac	gag	aaa	aac	1118	
His	Lys	Gly	Leu	Ala	Lys	Gln	Asp	Leu	Ile	Val	Leu	Asn	Glu	Lys	Asn	335	
335					340					345					350		
aaa	gaa	gat	cac	aac	ttg	caa	aac	caa	tac	gac	acc	gct	ccc	tct	caa	1166	
Lys	Glu	Asp	His	Asn	Leu	Gln	Asn	Gln	Tyr	Asp	Thr	Ala	Pro	Ser	Gln		
				355					360					365			
aga	gcc	ata	aac	ttt	tgt	aaa	agc	att	aac	acg	agc	aag	aac	att	aaa	1214	
Arg	Ala	Ile	Asn	Phe	Cys	Lys	Ser	Ile	Asn	Thr	Ser	Lys	Asn	Ile	Lys		
			370					375					380				
gac	tcc	ttt	gaa	acg	att	atg	gaa	tgc	tat	gat	gaa	gag	ttg	aag	aaa	1262	
Asp	Ser	Phe	Glu	Thr	Ile	Met	Glu	Cys	Tyr	Asp	Glu	Glu	Leu	Lys	Lys		
	385						390					395					
aag	agt	ttt	aaa	aac	cta	aaa	atc	agc	atc	gat	cac	att	gat	ggc	acc	1310	
Lys	Ser	Phe	Lys	Asn	Leu	Lys	Ile	Ser	Ile	Asp	His	Ile	Asp	Gly	Thr		
400						405					410						
atg	aat	tgt	aag	gat	agg	ctt	gaa	aaa	tta	gaa	gag	ctc	aat	caa	ttt	1358	
Met	Asn	Cys	Lys	Asp	Arg	Leu	Glu	Lys	Leu	Glu	Glu	Leu	Asn	Gln	Phe		
415					420					425					430		
gag	ccc	aac	act	tgc	aag	gtt	tta	agc	aac	gcc	agg	tgt	ttg	agc	gaa	1406	
Glu	Pro	Asn	Thr	Cys	Lys	Val	Leu	Ser	Asn	Ala	Arg	Cys	Leu	Ser	Glu		
				435					440					445			
ggg	gtg	gat	gtc	cca	gcg	tta	gat	agc	atc	gtc	ttt	ttt	gat	ggc	aaa	1454	
Gly	Val	Asp	Val	Pro	Ala	Leu	Asp	Ser	Ile	Val	Phe	Phe	Asp	Gly	Lys		
			450					455					460				
agc	gct	atg	gtg	gat	att	atc	caa	gcg	gtg	ggt	agg	gtg	atg	cga	aaa	1502	
Ser	Ala	Met	Val	Asp	Ile	Ile	Gln	Ala	Val	Gly	Arg	Val	Met	Arg	Lys		
		465					470					475					
gcc	aaa	cgc	aag	aaa	aga	ggc	tat	atc	att	ttg	cct	atc	gct	tta	gaa	1550	
Ala	Lys	Arg	Lys	Lys	Arg	Gly	Tyr	Ile	Ile	Leu	Pro	Ile	Ala	Leu	Glu		
480						485					490						
gag	agt	gaa	atc	caa	aac	ctg	gat	gaa	gcc	gtc	aat	aac	acc	aat	ttc	1598	
Glu	Ser	Glu	Ile	Gln	Asn	Leu	Asp	Glu	Ala	Val	Asn	Asn	Thr	Asn	Phe		
495					500					505					510		
aaa	aac	att	tgg	aaa	gtg	ata	aaa	gcc	tta	aga	agc	cat	gac	cca	agc	1646	
Lys	Asn	Ile	Trp	Lys	Val	Ile	Lys	Ala	Leu	Arg	Ser	His	Asp	Pro	Ser		
				515					520					525			
ctg	gtt	gat	gaa	gcc	act	ttt	aaa	gaa	aaa	atc	aaa	atc	ttt	gga	agc	1694	
Leu	Val	Asp	Glu	Ala	Thr	Phe	Lys	Glu	Lys	Ile	Lys	Ile	Phe	Gly	Ser		
			530					535					540				
gat	gat	ggc	aac	caa	tca	caa	cga	tgaaaaaac	ctttttgacg	ctatcttact	1748						
Asp	Asp	Gly	Asn	Gln	Ser	Gln	Arg										
		545					550										

gcaagatcta gcggacgcta tgtataatgt catgcccact aaattagggg ac

1800

<210> 62

<211> 550

<212> PRT

<213> Helicobacter pylori

<400> 62

Met	Gly	Ile	Asp	Ile	Asp	Glu	Ile	Thr	Glu	Glu	Asp	Phe	Ile	Tyr	Ser	1	5	10	15
Arg	Ile	Asp	Trp	Glu	Lys	Phe	Asp	Pro	Thr	Lys	Thr	Gln	Asp	Glu	Ile	20	25	30	
Pro	Leu	Cys	Asp	Lys	Lys	Lys	Pro	Arg	Ser	His	Gln	Thr	Glu	Ala	Ile	35	40	45	
Asn	Ala	Thr	Lys	Glu	Tyr	Phe	Ser	Asp	Pro	Lys	Asn	Ala	Arg	Gly	Lys	50	55	60	
Leu	Ile	Met	Ala	Cys	Gly	Thr	Gly	Lys	Thr	Tyr	Thr	Ser	Leu	Lys	Ile	65	70	75	80
Met	Glu	Ala	Leu	Asp	Ser	Lys	Ile	Thr	Leu	Phe	Leu	Ala	Pro	Ser	Ile	85	90	95	
Ala	Leu	Leu	Ser	Gln	Thr	Phe	Arg	Glu	Tyr	Ala	Gln	Glu	Lys	Ser	Glu	100	105	110	
Pro	Phe	Tyr	Ala	Ser	Ile	Val	Cys	Ser	Asp	Asp	Lys	Val	Gly	Lys	Ser	115	120	125	
Lys	Asp	Glu	Asp	Asn	Asp	Asp	Ile	Lys	Phe	Ser	Glu	Leu	Pro	Leu	Lys	130	135	140	
Pro	Ser	Thr	Arg	Leu	Glu	Asp	Ile	Leu	Ser	Val	Arg	Lys	Lys	Ala	Gln	145	150	155	160
Lys	Glu	Asn	Lys	Arg	Phe	Ile	Ile	Phe	Ser	Thr	Tyr	Gln	Ser	Ala	Leu	165	170	175	
Arg	Ile	Lys	Glu	Ala	Gln	Glu	Ala	Gly	Leu	Gly	Gly	Ile	Asp	Leu	Ile	180	185	190	
Ile	Cys	Asp	Glu	Ala	His	Arg	Thr	Val	Gly	Ala	Met	Tyr	Ser	Ser	Asn	195	200	205	
Glu	Arg	Asp	Asp	Lys	Asn	Ala	Phe	Thr	Leu	Cys	His	Ser	Asp	Lys	Asn	210	215	220	
Ile	Lys	Ala	Lys	Lys	Arg	Leu	Tyr	Met	Thr	Ala	Thr	Pro	Lys	Val	Tyr	225	230	235	240
Ser	Glu	Ser	Ser	Lys	Ala	Lys	Ala	Lys	Glu	Ser	Asp	Asn	Val	Ile	Tyr	245	250	255	
Ser	Met	Asp	Asp	Ala	Glu	Ile	Phe	Gly	Glu	Glu	Ile	Tyr	Thr	Leu	Asn	260	265	270	
Phe	Ser	Lys	Ala	Ile	Ala	Leu	Asp	Leu	Leu	Thr	Asp	Tyr	Lys	Val	Ile	275	280	285	
Ile	Leu	Ala	Val	Arg	Lys	Glu	Asn	Leu	Ser	Gly	Val	Thr	Asn	Ser	Val	290	295	300	
Asn	Lys	Lys	Ile	Ser	Gln	Leu	Lys	Ala	Glu	Gly	Thr	Lys	Leu	Asp	Lys	305	310	315	320
Lys	Leu	Ile	Asn	Asn	Glu	Phe	Val	Cys	Lys	Ile	Ile	Gly	Thr	His	Lys	325	330	335	
Gly	Leu	Ala	Lys	Gln	Asp	Leu	Ile	Val	Leu	Asn	Glu	Lys	Asn	Lys	Glu	340	345	350	
Asp	His	Asn	Leu	Gln	Asn	Gln	Tyr	Asp	Thr	Ala	Pro	Ser	Gln	Arg	Ala	355	360	365	
Ile	Asn	Phe	Cys	Lys	Ser	Ile	Asn	Thr	Ser	Lys	Asn	Ile	Lys	Asp	Ser	370	375	380	
Phe	Glu	Thr	Ile	Met	Glu	Cys	Tyr	Asp	Glu	Glu	Leu	Lys	Lys	Lys	Ser	385	390	395	400
Phe	Lys	Asn	Leu	Lys	Ile	Ser	Ile	Asp	His	Ile	Asp	Gly	Thr	Met	Asn				

				405					410					415			
Cys	Lys	Asp	Arg	Leu	Glu	Lys	Leu	Glu	Glu	Leu	Asn	Gln	Phe	Glu	Pro		
			420					425					430				
Asn	Thr	Cys	Lys	Val	Leu	Ser	Asn	Ala	Arg	Cys	Leu	Ser	Glu	Gly	Val		
		435					440					445					
Asp	Val	Pro	Ala	Leu	Asp	Ser	Ile	Val	Phe	Phe	Asp	Gly	Lys	Ser	Ala		
	450				455					460							
Met	Val	Asp	Ile	Ile	Gln	Ala	Val	Gly	Arg	Val	Met	Arg	Lys	Ala	Lys		
465					470					475					480		
Arg	Lys	Lys	Arg	Gly	Tyr	Ile	Ile	Leu	Pro	Ile	Ala	Leu	Glu	Glu	Ser		
			485					490						495			
Glu	Ile	Gln	Asn	Leu	Asp	Glu	Ala	Val	Asn	Asn	Thr	Asn	Phe	Lys	Asn		
		500					505					510					
Ile	Trp	Lys	Val	Ile	Lys	Ala	Leu	Arg	Ser	His	Asp	Pro	Ser	Leu	Val		
	515				520						525						
Asp	Glu	Ala	Thr	Phe	Lys	Glu	Lys	Ile	Lys	Ile	Phe	Gly	Ser	Asp	Asp		
	530				535					540							
Gly	Asn	Gln	Ser	Gln	Arg												
545				550													

<210> 63
 <211> 2880
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (16)...(2814)

<400> 63																	
aagccttaag	aagcc	atg	acc	caa	gcc	tgg	ttg	atg	aag	cca	ctt	tta	aag			51	
		Met	Thr	Gln	Ala	Trp	Leu	Met	Lys	Pro	Leu	Leu	Lys				
		1				5					10						
aaa	aaa	tca	aaa	tct	ttg	gaa	gcg	atg	atg	gca	acc	aat	cac	aac	gat	99	
Lys	Lys	Ser	Lys	Ser	Leu	Glu	Ala	Met	Met	Ala	Thr	Asn	His	Asn	Asp		
		15				20					25						
gaa	aaa	acc	ctt	ttt	gac	gct	atc	tta	ctg	caa	gat	cta	gcg	gac	gct	147	
Glu	Lys	Thr	Leu	Phe	Asp	Ala	Ile	Leu	Leu	Gln	Asp	Leu	Ala	Asp	Ala		
	30				35					40							
atg	tat	aat	gtc	atg	ccc	act	aaa	tta	ggg	gac	agg	aat	tat	tgg	gaa	195	
Met	Tyr	Asn	Val	Met	Pro	Thr	Lys	Leu	Gly	Asp	Arg	Asn	Tyr	Trp	Glu		
	45				50				55					60			
aat	ttc	act	aaa	aaa	acg	ggc	aac	atc	gca	agg	acc	ttg	aac	aac	cgc	243	
Asn	Phe	Thr	Lys	Lys	Thr	Gly	Asn	Ile	Ala	Arg	Thr	Leu	Asn	Asn	Arg		
			65			70							75				
cta	aaa	att	att	ttt	gac	aaa	aac	cct	gaa	ttt	ttc	cac	ggc	ttt	ttg	291	
Leu	Lys	Ile	Ile	Phe	Asp	Lys	Asn	Pro	Glu	Phe	Phe	His	Gly	Phe	Leu		
		80				85						90					
gat	tcc	tta	agg	gaa	aat	atc	cat	caa	aac	att	aaa	gaa	gat	gaa	gcc	339	
Asp	Ser	Leu	Arg	Glu	Asn	Ile	His	Gln	Asn	Ile	Lys	Glu	Asp	Glu	Ala		
		95				100						105					

tta gac atg atc act tct cac atc atc act aag ccc att ttt gat gca	387
Leu Asp Met Ile Thr Ser His Ile Ile Thr Lys Pro Ile Phe Asp Ala	
110 115 120	
ctt ttt ggg gac aac atc aaa aac cct atc gct aaa gcc ttg gat aaa	435
Leu Phe Gly Asp Asn Ile Lys Asn Pro Ile Ala Lys Ala Leu Asp Lys	
125 130 135 140	
atg gta gaa aaa ctc tcc act tta gga tta gaa gga gaa act aaa gat	483
Met Val Glu Lys Leu Ser Thr Leu Gly Leu Glu Gly Glu Thr Lys Asp	
145 150 155	
ctg aaa aac ctc tat gaa agc gtg aaa acc gaa gcc ttg cac gcc aaa	531
Leu Lys Asn Leu Tyr Glu Ser Val Lys Thr Glu Ala Leu His Ala Lys	
160 165 170	
agc caa aaa agc caa caa gaa ctc att aaa aac ctc tac aac act ttc	579
Ser Gln Lys Ser Gln Gln Glu Leu Ile Lys Asn Leu Tyr Asn Thr Phe	
175 180 185	
ttt aaa gaa gcc ttt aaa aag caa agc gaa aaa cta ggg atc gtt tat	627
Phe Lys Glu Ala Phe Lys Lys Gln Ser Glu Lys Leu Gly Ile Val Tyr	
190 195 200	
acg ccc ata gag gtg gtg gat ttc att tta aga gcc act aac ggc att	675
Thr Pro Ile Glu Val Val Asp Phe Ile Leu Arg Ala Thr Asn Gly Ile	
205 210 215 220	
ttg aaa aag cat ttc aac acg gat ttt aac gat caa agc atc acg att	723
Leu Lys Lys His Phe Asn Thr Asp Phe Asn Asp Gln Ser Ile Thr Ile	
225 230 235	
ttt gac cca ttc acc ggc acc ggg agt ttt atc gct cgt ttg ctt tct	771
Phe Asp Pro Phe Thr Gly Thr Gly Ser Phe Ile Ala Arg Leu Leu Ser	
240 245 250	
aaa gaa aac gcg ctc att agc gat gaa gcc tta aaa gag aag ttt caa	819
Lys Glu Asn Ala Leu Ile Ser Asp Glu Ala Leu Lys Glu Lys Phe Gln	
255 260 265	
aaa aat ttg ttc gct ttt gac atc gtg ctt ttg tct tat tat atc gct	867
Lys Asn Leu Phe Ala Phe Asp Ile Val Leu Leu Ser Tyr Tyr Ile Ala	
270 275 280	
tta atc aat atc acc caa gcc gcg caa aat agg gat ggc tcg tta aac	915
Leu Ile Asn Ile Thr Gln Ala Ala Gln Asn Arg Asp Gly Ser Leu Asn	
285 290 295 300	
aat ttc aaa aac atc gcg ctc acg gac agc ctg gat tat tta gaa gaa	963
Asn Phe Lys Asn Ile Ala Leu Thr Asp Ser Leu Asp Tyr Leu Glu Glu	
305 310 315	
aaa acc aat aaa ggg gtg ctc cct tta tat gag gat ttg aaa gaa aac	1011
Lys Thr Asn Lys Gly Val Leu Pro Leu Tyr Glu Asp Leu Lys Glu Asn	
320 325 330	
aaa ggc atc aaa gac act cta gcc aac caa aat att aga gtc atc atc	1059
Lys Gly Ile Lys Asp Thr Leu Ala Asn Gln Asn Ile Arg Val Ile Ile	
335 340 345	

ggc aac ccg cct tat tca gcc ggc gca aag agc caa aac gat aac aac	1107
Gly Asn Pro Pro Tyr Ser Ala Gly Ala Lys Ser Gln Asn Asp Asn Asn	
350 355 360	
caa aac ctc tca cac cca aag ctt gaa aaa tta gtt tat gaa aaa tac	1155
Gln Asn Leu Ser His Pro Lys Leu Glu Lys Leu Val Tyr Glu Lys Tyr	
365 370 375 380	
gga aaa aat tcc aca tct aga agt gtg gga aaa acc aca cga gac acg	1203
Gly Lys Asn Ser Thr Ser Arg Ser Val Gly Lys Thr Thr Arg Asp Thr	
385 390 395	
ctc att caa agc atc cgc atg gcg agc gat gtt gtt aaa gat agg ggg	1251
Leu Ile Gln Ser Ile Arg Met Ala Ser Asp Val Val Lys Asp Arg Gly	
400 405 410	
gtg ata ggc ttt gtg gtg aac ggg ggt ttt att gac tct aaa agc gcg	1299
Val Ile Gly Phe Val Val Asn Gly Gly Phe Ile Asp Ser Lys Ser Ala	
415 420 425	
gat ggg ttc aga aaa tgc gtg gcc aaa gaa ttt tcg cat ctt tat gta	1347
Asp Gly Phe Arg Lys Cys Val Ala Lys Glu Phe Ser His Leu Tyr Val	
430 435 440	
ttg aat ttg aga ggc aat cag cgc act tct ggg gaa gtg tca aaa aaa	1395
Leu Asn Leu Arg Gly Asn Gln Arg Thr Ser Gly Glu Val Ser Lys Lys	
445 450 455 460	
gag gga ggg aaa atc ttt gat agc gga tcg agg gcg acg gta gcg att	1443
Glu Gly Gly Lys Ile Phe Asp Ser Gly Ser Arg Ala Thr Val Ala Ile	
465 470 475	
atc ttt ttt gtg aaa gat aag agc act cct gat aat acg att ttt tat	1491
Ile Phe Phe Val Lys Asp Lys Ser Thr Pro Asp Asn Thr Ile Phe Tyr	
480 485 490	
tat gaa gtg gaa gat tac ttg aaa aga gaa gcc aaa ctc aac tgg ctc	1539
Tyr Glu Val Glu Asp Tyr Leu Lys Arg Glu Ala Lys Leu Asn Trp Leu	
495 500 505	
gcc aat ttt gaa aat ttg gat ttt gtg cct ttt gag aaa atc acc ccg	1587
Ala Asn Phe Glu Asn Leu Asp Phe Val Pro Phe Glu Lys Ile Thr Pro	
510 515 520	
aat gat aaa ggc gat tgg atc aac caa agg aat gac gct ttt gaa aaa	1635
Asn Asp Lys Gly Asp Trp Ile Asn Gln Arg Asn Asp Ala Phe Glu Lys	
525 530 535 540	
ctc atc cct tta aaa aga gac aaa aca ctc caa aac gac agc gtt ttt	1683
Leu Ile Pro Leu Lys Arg Asp Lys Thr Leu Gln Asn Asp Ser Val Phe	
545 550 555	
gac atc aat tct ctt ggc gtg gtg agc ggt cgt gat cct tgg gtg tat	1731
Asp Ile Asn Ser Leu Gly Val Val Ser Gly Arg Asp Pro Trp Val Tyr	
560 565 570	
aac ttt tct cca aac att tta acc caa tcg gtg caa aaa tgc att gac	1779
Asn Phe Ser Pro Asn Ile Leu Thr Gln Ser Val Gln Lys Cys Ile Asp	

575					580					585						
act	tat	aac	gct	gat	ttg	aag	cgc	ttc	aat	gcg	cgt	ttt	agg	gaa	gct	1827
Thr	Tyr	Asn	Ala	Asp	Leu	Lys	Arg	Phe	Asn	Ala	Arg	Phe	Arg	Glu	Ala	
	590					595					600					
ttc	aaa	caa	cgc	gct	caa	agc	gtc	aaa	gca	ggc	gat	ctt	tac	aaa	caa	1875
Phe	Lys	Gln	Arg	Ala	Gln	Ser	Val	Lys	Ala	Gly	Asp	Leu	Tyr	Lys	Gln	
605					610					615					620	
ctt	aat	gat	aaa	gaa	atc	acc	acc	gat	aaa	acg	aaa	atc	gct	tgg	act	1923
Leu	Asn	Asp	Lys	Glu	Ile	Thr	Thr	Asp	Lys	Thr	Lys	Ile	Ala	Trp	Thr	
				625					630					635		
gat	ggt	ttg	aaa	aac	aaa	ctc	att	aaa	aat	aaa	tct	gca	aga	gaa	agc	1971
Asp	Gly	Leu	Lys	Asn	Lys	Leu	Ile	Lys	Asn	Lys	Ser	Ala	Arg	Glu	Ser	
			640					645					650			
agt	gag	gag	cgt	gta	agg	ttg	gcc	ttg	tat	cgc	cct	ttt	aac	aaa	caa	2019
Ser	Glu	Glu	Arg	Val	Arg	Leu	Ala	Leu	Tyr	Arg	Pro	Phe	Asn	Lys	Gln	
	655						660					665				
tgg	ctt	tat	tgg	gat	aag	gat	tgg	ata	aac	agg	caa	aga	gaa	ttt	tca	2067
Trp	Leu	Tyr	Trp	Asp	Lys	Asp	Trp	Ile	Asn	Arg	Gln	Arg	Glu	Phe	Ser	
	670					675					680					
aaa	att	ttc	ccg	gat	aaa	gac	gct	cag	aat	gtg	gtg	att	aat	acc	ggt	2115
Lys	Ile	Phe	Pro	Asp	Lys	Asp	Ala	Gln	Asn	Val	Val	Ile	Asn	Thr	Gly	
685					690					695					700	
gtg	gga	aat	ggt	aaa	gat	ttt	agc	gct	ttg	gta	agc	gat	ttt	att	tct	2163
Val	Gly	Asn	Gly	Lys	Asp	Phe	Ser	Ala	Leu	Val	Ser	Asp	Phe	Ile	Ser	
				705					710					715		
gat	tat	agt	ttg	atc	tca	ccc	aat	caa	gct	tac	ccc	ttg	tat	tat	tac	2211
Asp	Tyr	Ser	Leu	Ile	Ser	Pro	Asn	Gln	Ala	Tyr	Pro	Leu	Tyr	Tyr	Tyr	
			720					725					730			
gat	gat	ttg	ggg	aat	cgc	cat	tac	gcc	atc	agc	ggc	tat	tgc	tta	aac	2259
Asp	Asp	Leu	Gly	Asn	Arg	His	Tyr	Ala	Ile	Ser	Gly	Tyr	Cys	Leu	Asn	
		735				740					745					
ctc	ttc	agg	agg	cat	tat	ggg	gat	aat	ctg	atc	gct	gaa	gaa	gag	att	2307
Leu	Phe	Arg	Arg	His	Tyr	Gly	Asp	Asn	Leu	Ile	Ala	Glu	Glu	Glu	Ile	
	750					755					760					
ttt	tat	tac	att	tat	gcg	att	ttc	cac	cat	aaa	ggc	tat	tta	gaa	aaa	2355
Phe	Tyr	Tyr	Ile	Tyr	Ala	Ile	Phe	His	His	Lys	Gly	Tyr	Leu	Glu	Lys	
765					770					775					780	
tac	aaa	aat	tcc	ctc	gcc	aaa	gaa	gcg	ccg	cgc	atc	gct	ttg	agc	gaa	2403
Tyr	Lys	Asn	Ser	Leu	Ala	Lys	Glu	Ala	Pro	Arg	Ile	Ala	Leu	Ser	Glu	
				785					790					795		
gat	ttt	aaa	gaa	ctc	tct	gtg	ctt	ggc	aaa	gaa	ttg	gcc	gaa	ttg	cac	2451
Asp	Phe	Lys	Glu	Leu	Ser	Val	Leu	Gly	Lys	Glu	Leu	Ala	Glu	Leu	His	
			800					805					810			
ctg	aac	tat	gag	agt	ggg	gaa	atg	cat	gat	aat	att	aaa	tac	acc	aca	2499

Leu	Asn	Tyr	Glu	Ser	Gly	Glu	Met	His	Asp	Asn	Ile	Lys	Tyr	Thr	Thr		
	815						820					825					
ctg	atg	aac	gcc	gaa	ata	gag	ggg	tat	tat	gat	gtg	gat	aaa	atg	acc	2547	
Leu	Met	Asn	Ala	Glu	Ile	Glu	Gly	Tyr	Tyr	Asp	Val	Asp	Lys	Met	Thr		
	830					835					840						
aaa	aaa	ggg	gat	tgc	atc	atc	tat	aac	caa	aac	atc	gct	atc	act	aag	2595	
Lys	Lys	Gly	Asp	Cys	Ile	Ile	Tyr	Asn	Gln	Asn	Ile	Ala	Ile	Thr	Lys		
	845				850					855					860		
atc	cct	aaa	aaa	gcc	ttt	gac	tat	gtc	att	aat	ggc	aag	agc	gcg	att	2643	
Ile	Pro	Lys	Lys	Ala	Phe	Asp	Tyr	Val	Ile	Asn	Gly	Lys	Ser	Ala	Ile		
				865					870					875			
gac	tgg	gtg	atc	gaa	cgc	tat	caa	aaa	act	atg	gat	aaa	gaa	agc	ctg	2691	
Asp	Trp	Val	Ile	Glu	Arg	Tyr	Gln	Lys	Thr	Met	Asp	Lys	Glu	Ser	Leu		
				880				885						890			
att	gaa	aac	aac	ccg	aac	gat	tac	gcc	ggc	gga	aaa	tac	gtt	ttt	gaa	2739	
Ile	Glu	Asn	Asn	Pro	Asn	Asp	Tyr	Ala	Gly	Gly	Lys	Tyr	Val	Phe	Glu		
	895						900					905					
ctc	ctt	tgt	agg	gtc	atc	aca	ctt	tcg	gta	aaa	agc	gtg	gat	ttg	ata	2787	
Leu	Leu	Cys	Arg	Val	Ile	Thr	Leu	Ser	Val	Lys	Ser	Val	Asp	Leu	Ile		
	910					915					920						
gaa	aag	atc	agc	gaa	aag	agg	ttt	gag	tgattacatc	gcttgggggt						2834	
Glu	Lys	Ile	Ser	Glu	Lys	Arg	Phe	Glu									
	925					930											
gtggaatatt	ttgaaaggca	atgtcttgct	ttcttaaaaa	atccac												2880	

<210> 64
 <211> 933
 <212> PRT
 <213> Helicobacter pylori

<400> 64

Met	Thr	Gln	Ala	Trp	Leu	Met	Lys	Pro	Leu	Leu	Lys	Lys	Lys	Ser	Lys
1				5					10					15	
Ser	Leu	Glu	Ala	Met	Met	Ala	Thr	Asn	His	Asn	Asp	Glu	Lys	Thr	Leu
			20					25					30		
Phe	Asp	Ala	Ile	Leu	Leu	Gln	Asp	Leu	Ala	Asp	Ala	Met	Tyr	Asn	Val
		35				40						45			
Met	Pro	Thr	Lys	Leu	Gly	Asp	Arg	Asn	Tyr	Trp	Glu	Asn	Phe	Thr	Lys
	50				55						60				
Lys	Thr	Gly	Asn	Ile	Ala	Arg	Thr	Leu	Asn	Asn	Arg	Leu	Lys	Ile	Ile
	65				70					75				80	
Phe	Asp	Lys	Asn	Pro	Glu	Phe	Phe	His	Gly	Phe	Leu	Asp	Ser	Leu	Arg
			85						90					95	
Glu	Asn	Ile	His	Gln	Asn	Ile	Lys	Glu	Asp	Glu	Ala	Leu	Asp	Met	Ile
			100					105					110		
Thr	Ser	His	Ile	Ile	Thr	Lys	Pro	Ile	Phe	Asp	Ala	Leu	Phe	Gly	Asp
		115					120					125			
Asn	Ile	Lys	Asn	Pro	Ile	Ala	Lys	Ala	Leu	Asp	Lys	Met	Val	Glu	Lys
	130					135					140				
Leu	Ser	Thr	Leu	Gly	Leu	Glu	Gly	Glu	Thr	Lys	Asp	Leu	Lys	Asn	Leu
	145				150					155					160

Tyr	Glu	Ser	Val	Lys	Thr	Glu	Ala	Leu	His	Ala	Lys	Ser	Gln	Lys	Ser
				165					170					175	
Gln	Gln	Glu	Leu	Ile	Lys	Asn	Leu	Tyr	Asn	Thr	Phe	Phe	Lys	Glu	Ala
			180					185					190		
Phe	Lys	Lys	Gln	Ser	Glu	Lys	Leu	Gly	Ile	Val	Tyr	Thr	Pro	Ile	Glu
		195					200				205				
Val	Val	Asp	Phe	Ile	Leu	Arg	Ala	Thr	Asn	Gly	Ile	Leu	Lys	Lys	His
	210					215				220					
Phe	Asn	Thr	Asp	Phe	Asn	Asp	Gln	Ser	Ile	Thr	Ile	Phe	Asp	Pro	Phe
225					230					235					240
Thr	Gly	Thr	Gly	Ser	Phe	Ile	Ala	Arg	Leu	Leu	Ser	Lys	Glu	Asn	Ala
				245					250					255	
Leu	Ile	Ser	Asp	Glu	Ala	Leu	Lys	Glu	Lys	Phe	Gln	Lys	Asn	Leu	Phe
			260					265					270		
Ala	Phe	Asp	Ile	Val	Leu	Leu	Ser	Tyr	Tyr	Ile	Ala	Leu	Ile	Asn	Ile
		275					280					285			
Thr	Gln	Ala	Ala	Gln	Asn	Arg	Asp	Gly	Ser	Leu	Asn	Asn	Phe	Lys	Asn
	290					295					300				
Ile	Ala	Leu	Thr	Asp	Ser	Leu	Asp	Tyr	Leu	Glu	Glu	Lys	Thr	Asn	Lys
305					310					315					320
Gly	Val	Leu	Pro	Leu	Tyr	Glu	Asp	Leu	Lys	Glu	Asn	Lys	Gly	Ile	Lys
				325					330					335	
Asp	Thr	Leu	Ala	Asn	Gln	Asn	Ile	Arg	Val	Ile	Ile	Gly	Asn	Pro	Pro
			340					345					350		
Tyr	Ser	Ala	Gly	Ala	Lys	Ser	Gln	Asn	Asp	Asn	Asn	Gln	Asn	Leu	Ser
		355					360					365			
His	Pro	Lys	Leu	Glu	Lys	Leu	Val	Tyr	Glu	Lys	Tyr	Gly	Lys	Asn	Ser
	370					375					380				
Thr	Ser	Arg	Ser	Val	Gly	Lys	Thr	Thr	Arg	Asp	Thr	Leu	Ile	Gln	Ser
385					390					395					400
Ile	Arg	Met	Ala	Ser	Asp	Val	Val	Lys	Asp	Arg	Gly	Val	Ile	Gly	Phe
				405					410					415	
Val	Val	Asn	Gly	Phe	Ile	Asp	Ser	Lys	Ser	Ala	Asp	Gly	Phe	Arg	
			420				425					430			
Lys	Cys	Val	Ala	Lys	Glu	Phe	Ser	His	Leu	Tyr	Val	Leu	Asn	Leu	Arg
		435					440					445			
Gly	Asn	Gln	Arg	Thr	Ser	Gly	Glu	Val	Ser	Lys	Lys	Glu	Gly	Gly	Lys
	450					455					460				
Ile	Phe	Asp	Ser	Gly	Ser	Arg	Ala	Thr	Val	Ala	Ile	Ile	Phe	Phe	Val
465					470					475					480
Lys	Asp	Lys	Ser	Thr	Pro	Asp	Asn	Thr	Ile	Phe	Tyr	Tyr	Glu	Val	Glu
				485					490					495	
Asp	Tyr	Leu	Lys	Arg	Glu	Ala	Lys	Leu	Asn	Trp	Leu	Ala	Asn	Phe	Glu
			500					505					510		
Asn	Leu	Asp	Phe	Val	Pro	Phe	Glu	Lys	Ile	Thr	Pro	Asn	Asp	Lys	Gly
		515					520					525			
Asp	Trp	Ile	Asn	Gln	Arg	Asn	Asp	Ala	Phe	Glu	Lys	Leu	Ile	Pro	Leu
	530					535					540				
Lys	Arg	Asp	Lys	Thr	Leu	Gln	Asn	Asp	Ser	Val	Phe	Asp	Ile	Asn	Ser
545					550					555					560
Leu	Gly	Val	Val	Ser	Gly	Arg	Asp	Pro	Trp	Val	Tyr	Asn	Phe	Ser	Pro
				565					570					575	
Asn	Ile	Leu	Thr	Gln	Ser	Val	Gln	Lys	Cys	Ile	Asp	Thr	Tyr	Asn	Ala
			580					585					590		
Asp	Leu	Lys	Arg	Phe	Asn	Ala	Arg	Phe	Arg	Glu	Ala	Phe	Lys	Gln	Arg
		595					600					605			
Ala	Gln	Ser	Val	Lys	Ala	Gly	Asp	Leu	Tyr	Lys	Gln	Leu	Asn	Asp	Lys
	610					615					620				
Glu	Ile	Thr	Thr	Asp	Lys	Thr	Lys	Ile	Ala	Trp	Thr	Asp	Gly	Leu	Lys

625					630					635					640
Asn	Lys	Leu	Ile	Lys	Asn	Lys	Ser	Ala	Arg	Glu	Ser	Ser	Glu	Glu	Arg
				645					650					655	
Val	Arg	Leu	Ala	Leu	Tyr	Arg	Pro	Phe	Asn	Lys	Gln	Trp	Leu	Tyr	Trp
			660					665					670		
Asp	Lys	Asp	Trp	Ile	Asn	Arg	Gln	Arg	Glu	Phe	Ser	Lys	Ile	Phe	Pro
		675					680					685			
Asp	Lys	Asp	Ala	Gln	Asn	Val	Val	Ile	Asn	Thr	Gly	Val	Gly	Asn	Gly
	690					695					700				
Lys	Asp	Phe	Ser	Ala	Leu	Val	Ser	Asp	Phe	Ile	Ser	Asp	Tyr	Ser	Leu
705					710					715					720
Ile	Ser	Pro	Asn	Gln	Ala	Tyr	Pro	Leu	Tyr	Tyr	Tyr	Asp	Asp	Leu	Gly
			725						730					735	
Asn	Arg	His	Tyr	Ala	Ile	Ser	Gly	Tyr	Cys	Leu	Asn	Leu	Phe	Arg	Arg
		740					745						750		
His	Tyr	Gly	Asp	Asn	Leu	Ile	Ala	Glu	Glu	Glu	Ile	Phe	Tyr	Tyr	Ile
	755						760					765			
Tyr	Ala	Ile	Phe	His	His	Lys	Gly	Tyr	Leu	Glu	Lys	Tyr	Lys	Asn	Ser
	770					775					780				
Leu	Ala	Lys	Glu	Ala	Pro	Arg	Ile	Ala	Leu	Ser	Glu	Asp	Phe	Lys	Glu
785					790					795					800
Leu	Ser	Val	Leu	Gly	Lys	Glu	Leu	Ala	Glu	Leu	His	Leu	Asn	Tyr	Glu
			805						810					815	
Ser	Gly	Glu	Met	His	Asp	Asn	Ile	Lys	Tyr	Thr	Thr	Leu	Met	Asn	Ala
		820						825					830		
Glu	Ile	Glu	Gly	Tyr	Tyr	Asp	Val	Asp	Lys	Met	Thr	Lys	Lys	Gly	Asp
	835						840					845			
Cys	Ile	Ile	Tyr	Asn	Gln	Asn	Ile	Ala	Ile	Thr	Lys	Ile	Pro	Lys	Lys
	850					855					860				
Ala	Phe	Asp	Tyr	Val	Ile	Asn	Gly	Lys	Ser	Ala	Ile	Asp	Trp	Val	Ile
865					870					875					880
Glu	Arg	Tyr	Gln	Lys	Thr	Met	Asp	Lys	Glu	Ser	Leu	Ile	Glu	Asn	Asn
			885						890					895	
Pro	Asn	Asp	Tyr	Ala	Gly	Gly	Lys	Tyr	Val	Phe	Glu	Leu	Leu	Cys	Arg
		900					905						910		
Val	Ile	Thr	Leu	Ser	Val	Lys	Ser	Val	Asp	Leu	Ile	Glu	Lys	Ile	Ser
	915						920					925			
Glu	Lys	Arg	Phe	Glu											
	930														

<210> 65
 <211> 1440
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (24)...(1370)

<400> 65
 aagatcagcgcg aaaagagggtt tga gtg att aca tcg ctt ggg ggt gtg gaa tat 53
 Val Ile Thr Ser Leu Gly Gly Val Glu Tyr
 1 5 10

ttt gaa agg caa tgt ctt gct ttc tta aaa aat cca caa act aat cca 101
 Phe Glu Arg Gln Cys Leu Ala Phe Leu Lys Asn Pro Gln Thr Asn Pro
 15 20 25

caa aat gag caa tac att cca gga gtg ttt tcg tat caa gaa aac aaa	149
Gln Asn Glu Gln Tyr Ile Pro Gly Val Phe Ser Tyr Gln Glu Asn Lys	
30 35 40	
att tct ttt tct ttt ttg gtt tta gga gaa att gaa gag atc cac tct	197
Ile Ser Phe Ser Phe Leu Val Leu Gly Glu Ile Glu Glu Ile His Ser	
45 50 55	
ttg caa tac caa acg ctc tat att gtg gat aac aaa aaa aga tac act	245
Leu Gln Tyr Gln Thr Leu Tyr Ile Val Asp Asn Lys Lys Arg Tyr Thr	
60 65 70	
ctt tac aag ctt tat gat cgc att att ttg ggt cat act tta ggg tat	293
Leu Tyr Lys Leu Tyr Asp Arg Ile Ile Leu Gly His Thr Leu Gly Tyr	
75 80 85 90	
tct gca cca atc acg ctc tat tat gaa tgg ctg ttt gat gat tgg atc	341
Ser Ala Pro Ile Thr Leu Tyr Tyr Glu Trp Leu Phe Asp Asp Trp Ile	
95 100 105	
gat cca gaa aaa att atg ggc gat cgt ttt gtt tgt agg aca aat tat	389
Asp Pro Glu Lys Ile Met Gly Asp Arg Phe Val Cys Arg Thr Asn Tyr	
110 115 120	
tta gaa agt ttt ttt acg acc aag aag cat ttg cta cct gat aca tta	437
Leu Glu Ser Phe Phe Thr Thr Lys Lys His Leu Leu Pro Asp Thr Leu	
125 130 135	
ttt aaa gta gat gaa agt ggg tgt gaa agt tat cat gag aat aac gat	485
Phe Lys Val Asp Glu Ser Gly Cys Glu Ser Tyr His Glu Asn Asn Asp	
140 145 150	
aag gac ttt atc cta caa tca ttt tat att caa aat gat ttt tta tcc	533
Lys Asp Phe Ile Leu Gln Ser Phe Tyr Ile Gln Asn Asp Phe Leu Ser	
155 160 165 170	
caa aga tat gaa aaa gac aag ata aaa gca aaa tct aat ttg att cct	581
Gln Arg Tyr Glu Lys Asp Lys Ile Lys Ala Lys Ser Asn Leu Ile Pro	
175 180 185	
aaa aga cag aat cgt tta tta act tat caa ttt gat ttg tct ttg gaa	629
Lys Arg Gln Asn Arg Leu Leu Thr Tyr Gln Phe Asp Leu Ser Leu Glu	
190 195 200	
tgc aat ata att ttt gaa acc ctt gaa aaa tta gca ctt att gct gga	677
Cys Asn Ile Ile Phe Glu Thr Leu Glu Lys Leu Ala Leu Ile Ala Gly	
205 210 215	
gcg att aaa aac ttt ttt att ttg att tat gct cat tct aat ttt gac	725
Ala Ile Lys Asn Phe Phe Ile Leu Ile Tyr Ala His Ser Asn Phe Asp	
220 225 230	
atc caa att gac tat atc caa ttc aag ctt tct aat aaa gac att aca	773
Ile Gln Ile Asp Tyr Ile Gln Phe Lys Leu Ser Asn Lys Asp Ile Thr	
235 240 245 250	
gca ata aga aac act tac aaa aaa gat aaa aag tct atg gag ata gat	821
Ala Ile Arg Asn Thr Tyr Lys Lys Asp Lys Lys Ser Met Glu Ile Asp	
255 260 265	

ctt tat ggg att gct ata aat ttc caa cgg ata gac aat ttt tct gta	869
Leu Tyr Gly Ile Ala Ile Asn Phe Gln Arg Ile Asp Asn Phe Ser Val	
270 275 280	
ata ctt gaa aaa tgg att gtt ttt tat atc aaa gac aat aga gat ttc	917
Ile Leu Glu Lys Trp Ile Val Phe Tyr Ile Lys Asp Asn Arg Asp Phe	
285 290 295	
caa ctt gca agt att tta gac att att aat aaa aaa gat cca att att	965
Gln Leu Ala Ser Ile Leu Asp Ile Ile Asn Lys Lys Asp Pro Ile Ile	
300 305 310	
cac ttg tat ttg gac atg ttt gta ttg att agc atg att gaa agt ttt	1013
His Leu Tyr Leu Asp Met Phe Val Leu Ile Ser Met Ile Glu Ser Phe	
315 320 325 330	
tta aag aaa cca caa caa aca aaa ctc cat gaa aaa ctc tct gaa ttt	1061
Leu Lys Lys Pro Gln Gln Thr Lys Leu His Glu Lys Leu Ser Glu Phe	
335 340 345	
ttt aaa att tca tta tct agg aca aaa tgc gat caa acg aaa aat tat	1109
Phe Lys Ile Ser Leu Ser Arg Thr Lys Cys Asp Gln Thr Lys Asn Tyr	
350 355 360	
ttt aat gat aaa tgt caa gaa gat cta atc caa cag att gtt gac tgc	1157
Phe Asn Asp Lys Cys Gln Glu Asp Leu Ile Gln Gln Ile Val Asp Cys	
365 370 375	
cgt aac tct cta gcg cac gga aga agt tta aag ctt gat aca aac aaa	1205
Arg Asn Ser Leu Ala His Gly Arg Ser Leu Lys Leu Asp Thr Asn Lys	
380 385 390	
gct aca gac att agc cat gct ttt ata gat ttc aag caa att gtc att	1253
Ala Thr Asp Ile Ser His Ala Phe Ile Asp Phe Lys Gln Ile Val Ile	
395 400 405 410	
gaa ttt ttc ttt ggc gag ata gga ttg agc gat ttt att aca aac aat	1301
Glu Phe Phe Phe Gly Glu Ile Gly Leu Ser Asp Phe Ile Thr Asn Asn	
415 420 425	
ttt ggt ttt ctt aac aaa gtt aaa tta aga aac ccc cca aaa aca gaa	1349
Phe Gly Phe Leu Asn Lys Val Lys Leu Arg Asn Pro Pro Lys Thr Glu	
430 435 440	
aaa atc acc gag cca aac cgc taaaaccct tagaaaattt aaaatttta	1400
Lys Ile Thr Glu Pro Asn Arg	
445	
gttttagggg tgtttttctt aagaatttag gttttttata	1440
<210> 66	
<211> 449	
<212> PRT	
<213> Helicobacter pylori	
<400> 66	
Val Ile Thr Ser Leu Gly Gly Val Glu Tyr Phe Glu Arg Gln Cys Leu	
1 5 10 15	

Ala	Phe	Leu	Lys	Asn	Pro	Gln	Thr	Asn	Pro	Gln	Asn	Glu	Gln	Tyr	Ile		
			20					25					30				
Pro	Gly	Val	Phe	Ser	Tyr	Gln	Glu	Asn	Lys	Ile	Ser	Phe	Ser	Phe	Leu		
		35					40					45					
Val	Leu	Gly	Glu	Ile	Glu	Glu	Ile	His	Ser	Leu	Gln	Tyr	Gln	Thr	Leu		
	50				55						60						
Tyr	Ile	Val	Asp	Asn	Lys	Lys	Arg	Tyr	Thr	Leu	Tyr	Lys	Leu	Tyr	Asp		
65				70						75					80		
Arg	Ile	Ile	Leu	Gly	His	Thr	Leu	Gly	Tyr	Ser	Ala	Pro	Ile	Thr	Leu		
			85					90						95			
Tyr	Tyr	Glu	Trp	Leu	Phe	Asp	Asp	Trp	Ile	Asp	Pro	Glu	Lys	Ile	Met		
		100						105					110				
Gly	Asp	Arg	Phe	Val	Cys	Arg	Thr	Asn	Tyr	Leu	Glu	Ser	Phe	Phe	Thr		
	115						120					125					
Thr	Lys	Lys	His	Leu	Leu	Pro	Asp	Thr	Leu	Phe	Lys	Val	Asp	Glu	Ser		
	130				135						140						
Gly	Cys	Glu	Ser	Tyr	His	Glu	Asn	Asn	Asp	Lys	Asp	Phe	Ile	Leu	Gln		
145				150						155					160		
Ser	Phe	Tyr	Ile	Gln	Asn	Asp	Phe	Leu	Ser	Gln	Arg	Tyr	Glu	Lys	Asp		
			165					170						175			
Lys	Ile	Lys	Ala	Lys	Ser	Asn	Leu	Ile	Pro	Lys	Arg	Gln	Asn	Arg	Leu		
		180					185						190				
Leu	Thr	Tyr	Gln	Phe	Asp	Leu	Ser	Leu	Glu	Cys	Asn	Ile	Ile	Phe	Glu		
	195					200						205					
Thr	Leu	Glu	Lys	Leu	Ala	Leu	Ile	Ala	Gly	Ala	Ile	Lys	Asn	Phe	Phe		
	210				215						220						
Ile	Leu	Ile	Tyr	Ala	His	Ser	Asn	Phe	Asp	Ile	Gln	Ile	Asp	Tyr	Ile		
225				230						235					240		
Gln	Phe	Lys	Leu	Ser	Asn	Lys	Asp	Ile	Thr	Ala	Ile	Arg	Asn	Thr	Tyr		
			245					250						255			
Lys	Lys	Asp	Lys	Lys	Ser	Met	Glu	Ile	Asp	Leu	Tyr	Gly	Ile	Ala	Ile		
		260					265						270				
Asn	Phe	Gln	Arg	Ile	Asp	Asn	Phe	Ser	Val	Ile	Leu	Glu	Lys	Trp	Ile		
		275				280						285					
Val	Phe	Tyr	Ile	Lys	Asp	Asn	Arg	Asp	Phe	Gln	Leu	Ala	Ser	Ile	Leu		
	290				295						300						
Asp	Ile	Ile	Asn	Lys	Lys	Asp	Pro	Ile	Ile	His	Leu	Tyr	Leu	Asp	Met		
305				310						315					320		
Phe	Val	Leu	Ile	Ser	Met	Ile	Glu	Ser	Phe	Leu	Lys	Lys	Pro	Gln	Gln		
			325					330						335			
Thr	Lys	Leu	His	Glu	Lys	Leu	Ser	Glu	Phe	Phe	Lys	Ile	Ser	Leu	Ser		
		340						345					350				
Arg	Thr	Lys	Cys	Asp	Gln	Thr	Lys	Asn	Tyr	Phe	Asn	Asp	Lys	Cys	Gln		
	355					360						365					
Glu	Asp	Leu	Ile	Gln	Gln	Ile	Val	Asp	Cys	Arg	Asn	Ser	Leu	Ala	His		
	370				375						380						
Gly	Arg	Ser	Leu	Lys	Leu	Asp	Thr	Asn	Lys	Ala	Thr	Asp	Ile	Ser	His		
385				390						395					400		
Ala	Phe	Ile	Asp	Phe	Lys	Gln	Ile	Val	Ile	Glu	Phe	Phe	Phe	Gly	Glu		
			405					410						415			
Ile	Gly	Leu	Ser	Asp	Phe	Ile	Thr	Asn	Asn	Phe	Gly	Phe	Leu	Asn	Lys		
		420					425						430				
Val	Lys	Leu	Arg	Asn	Pro	Pro	Lys	Thr	Glu	Lys	Ile	Thr	Glu	Pro	Asn		
		435					440					445					
Arg																	

<210> 67

```
<220>  
<221> CDS  
<222> (25) ... (1302)
```

-75-

190										195					200					
tgt	ttt	att	gac	tgc	cca	att	aca	att	gag	gat	tat	tta	att	tta	gat	675				
Cys	Phe	Ile	Asp	Cys	Pro	Ile	Thr	Ile	Glu	Asp	Tyr	Leu	Ile	Leu	Asp					
			205					210					215							
aat	cta	aaa	agc	tgt	ttt	gta	atc	caa	aat	aag	cca	aat	gta	aca	tta	723				
Asn	Leu	Lys	Ser	Cys	Phe	Val	Ile	Gln	Asn	Lys	Pro	Asn	Val	Thr	Leu					
			220				225					230								
ttt	gat	aac	gac	gag	aac	gat	aga	cca	ttc	aat	tta	aag	cga	tac	ttg	771				
Phe	Asp	Asn	Asp	Glu	Asn	Asp	Arg	Pro	Phe	Asn	Leu	Lys	Arg	Tyr	Leu					
			235				240					245								
tta	gga	ttg	aaa	gaa	aag	tta	ggg	ttt	gag	cca	acg	ggg	att	ttc	tat	819				
Leu	Gly	Leu	Lys	Glu	Lys	Leu	Gly	Phe	Glu	Pro	Thr	Gly	Ile	Phe	Tyr					
250							255				260				265					
tgc	gaa	aac	gca	aac	aca	cac	aaa	att	gaa	ttg	att	ggg	aat	gat	tct	867				
Cys	Glu	Asn	Ala	Asn	Thr	His	Lys	Ile	Glu	Leu	Ile	Gly	Asn	Asp	Ser					
			270					275					280							
gat	ttc	aga	gag	gta	tta	ctt	gaa	ttt	tca	gag	aat	ata	cca	aaa	gcc	915				
Asp	Phe	Arg	Glu	Val	Leu	Leu	Glu	Phe	Ser	Glu	Asn	Ile	Pro	Lys	Ala					
			285					290					295							
cct	aat	gaa	cta	cca	caa	ttt	ctt	aca	aac	ttt	aaa	aat	tca	aaa	atc	963				
Pro	Asn	Glu	Leu	Pro	Gln	Phe	Leu	Thr	Asn	Phe	Lys	Asn	Ser	Lys	Ile					
			300				305					310								
ccc	aat	gga	aac	att	tca	ttt	tcg	cca	cca	aaa	aat	tct	cca	tca	att	1011				
Pro	Asn	Gly	Asn	Ile	Ser	Phe	Ser	Pro	Pro	Lys	Asn	Ser	Pro	Ser	Ile					
			315				320					325								
tct	tca	tat	gct	tta	tct	gat	aag	att	aaa	aga	gaa	gta	aga	gat	acc	1059				
Ser	Ser	Tyr	Ala	Leu	Ser	Asp	Lys	Ile	Lys	Arg	Glu	Val	Arg	Asp	Thr					
330							335				340				345					
ttt	gat	cgc	tat	ttg	tgg	cat	ggg	tat	tct	aaa	att	cca	cag	gag	aaa	1107				
Phe	Asp	Arg	Tyr	Leu	Trp	His	Gly	Tyr	Ser	Lys	Ile	Pro	Gln	Glu	Lys					
			350					355					360							
agg	ata	gcc	aaa	ata	aaa	gag	caa	gtg	aag	gaa	gaa	att	aaa	cta	aat	1155				
Arg	Ile	Ala	Lys	Ile	Lys	Glu	Gln	Val	Lys	Glu	Glu	Ile	Lys	Leu	Asn					
			365					370					375							
cct	tct	ttt	cgt	aat	tat	aga	gta	gac	tct	gaa	caa	aac	cgc	aag	atc	1203				
Pro	Ser	Phe	Arg	Asn	Tyr	Arg	Val	Asp	Ser	Glu	Gln	Asn	Arg	Lys	Ile					
			380				385					390								
aat	gaa	att	gct	gag	ggg	tta	aaa	agt	ggg	aag	ata	att	ggg	aaa	aag	1251				
Asn	Glu	Ile	Ala	Glu	Gly	Leu	Lys	Ser	Gly	Lys	Ile	Ile	Gly	Lys	Lys					
			395				400					405								
gtt	att	gct	aat	gcg	ttc	gat	cta	aat	gct	agc	tta	ttg	ttt	tat	tac	1299				
Val	Ile	Ala	Asn	Ala	Phe	Asp	Leu	Asn	Ala	Ser	Leu	Leu	Phe	Tyr	Tyr					
410							415				420				425					
tcc	tgatgattta	aagaatttaa	aggaacgatt	atttatagat	att											1345				

Ser

<210> 68
<211> 426
<212> PRT
<213> *Helicobacter pylori*

<400> 68

Met	Ala	Val	Arg	Phe	Gly	Ile	Ile	Phe	Ile	Ser	Asp	Ser	Ile	Asp	Asp
1				5				10					15		
Tyr	Lys	Ala	Lys	Gln	Leu	Arg	Ser	Ile	Leu	Glu	Arg	Lys	Lys	Glu	Cys
			20				25					30			
Asn	Phe	Ile	Trp	Phe	Asn	Glu	Ser	Ser	Ala	Ile	Ile	His	Asn	Thr	Pro
		35				40						45			
Lys	Val	Phe	Glu	Gly	Glu	Ser	Phe	Phe	Asp	His	Leu	Phe	Val	Ser	Ala
	50				55					60					
Lys	Ile	Thr	Ala	Phe	Val	Val	Ser	Thr	Asn	Glu	Ser	Asp	Thr	Ile	Phe
65				70					75					80	
Asn	Leu	Lys	Asn	Tyr	Leu	Leu	Val	Leu	Ala	Lys	Asn	Leu	Asn	Asn	Arg
			85					90					95		
Asp	Ile	Trp	Tyr	Cys	Glu	Asn	Thr	Ile	Cys	Asp	Lys	Lys	Gly	Thr	Tyr
		100					105						110		
Asn	Ile	Glu	Ile	Glu	Leu	Val	Ser	Asn	Ala	Asn	Asp	Phe	Arg	Gly	Val
		115				120					125				
Phe	Gly	Glu	Val	Leu	Gly	Ile	Val	Lys	Asp	Thr	Phe	Gly	Asp	Leu	Leu
	130				135						140				
Gln	Leu	Leu	Thr	Asn	Leu	Lys	Asn	Lys	Glu	Ile	Glu	Phe	Asn	Phe	His
145				150					155					160	
Lys	Lys	Ile	Asn	Tyr	Gly	Leu	Pro	Phe	Gly	Ile	Ile	Phe	Ile	Ala	Ser
			165					170						175	
Asn	Ser	Asp	Asn	Pro	Ile	Asp	Ile	Asp	Asn	Lys	Thr	Lys	Lys	Leu	Lys
			180				185					190			
Ser	Cys	Phe	Arg	Asp	Asp	Glu	Ser	Asn	Cys	Phe	Ile	Asp	Cys	Pro	Ile
		195				200						205			
Thr	Ile	Glu	Asp	Tyr	Leu	Ile	Leu	Asp	Asn	Leu	Lys	Ser	Cys	Phe	Val
	210				215						220				
Ile	Gln	Asn	Lys	Pro	Asn	Val	Thr	Leu	Phe	Asp	Asn	Asp	Glu	Asn	Asp
225				230					235					240	
Arg	Pro	Phe	Asn	Leu	Lys	Arg	Tyr	Leu	Leu	Gly	Leu	Lys	Glu	Lys	Leu
			245					250					255		
Gly	Phe	Glu	Pro	Thr	Gly	Ile	Phe	Tyr	Cys	Glu	Asn	Ala	Asn	Thr	His
			260				265						270		
Lys	Ile	Glu	Leu	Ile	Gly	Asn	Asp	Ser	Asp	Phe	Arg	Glu	Val	Leu	Leu
		275				280						285			
Glu	Phe	Ser	Glu	Asn	Ile	Pro	Lys	Ala	Pro	Asn	Glu	Leu	Pro	Gln	Phe
	290				295					300					
Leu	Thr	Asn	Phe	Lys	Asn	Ser	Lys	Ile	Pro	Asn	Gly	Asn	Ile	Ser	Phe
305				310						315				320	
Ser	Pro	Pro	Lys	Asn	Ser	Pro	Ser	Ile	Ser	Ser	Tyr	Ala	Leu	Ser	Asp
			325					330					335		
Lys	Ile	Lys	Arg	Glu	Val	Arg	Asp	Thr	Phe	Asp	Arg	Tyr	Leu	Trp	His
			340				345						350		
Gly	Tyr	Ser	Lys	Ile	Pro	Gln	Glu	Lys	Arg	Ile	Ala	Lys	Ile	Lys	Glu
		355				360						365			
Gln	Val	Lys	Glu	Glu	Ile	Lys	Leu	Asn	Pro	Ser	Phe	Arg	Asn	Tyr	Arg
	370				375					380					
Val	Asp	Ser	Glu	Gln	Asn	Arg	Lys	Ile	Asn	Glu	Ile	Ala	Glu	Gly	Leu

385					390					395					400
Lys	Ser	Gly	Lys	Ile	Ile	Gly	Lys	Lys	Val	Ile	Ala	Asn	Ala	Phe	Asp
				405					410					415	
Leu	Asn	Ala	Ser	Leu	Leu	Phe	Tyr	Tyr	Ser						
			420					425							

<210> 69
 <211> 720
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (22)...(705)

<400> 69																
ttgcta	aatgc	gttcgat	cta	a	atg	cta	gct	tat	tgt	ttt	att	act	cct	gat		51
					Met	Leu	Ala	Tyr	Cys	Phe	Ile	Thr	Pro	Asp		
					1				5					10		
gat	tta	aag	aat	tta	aag	gaa	cga	tta	ttt	ata	gat	att	atc	aat	gct	99
Asp	Leu	Lys	Asn	Leu	Lys	Glu	Arg	Leu	Phe	Ile	Asp	Ile	Ile	Asn	Ala	
				15					20					25		
atc	aac	caa	aaa	aag	aga	gtc	gcg	ctc	gat	cat	gct	caa	ata	gat	gac	147
Ile	Asn	Gln	Lys	Lys	Arg	Val	Ala	Leu	Asp	His	Ala	Gln	Ile	Asp	Asp	
			30					35					40			
atc	cag	tat	aat	gtg	ctt	gat	aat	gcg	ttt	tat	ttt	atc	ttt	gat	gtt	195
Ile	Gln	Tyr	Asn	Val	Leu	Asp	Asn	Ala	Phe	Tyr	Phe	Ile	Phe	Asp	Val	
		45					50					55				
ggg	aac	cct	tct	caa	tta	gct	att	aaa	gtg	cct	aga	aaa	tct	tta	gaa	243
Gly	Asn	Pro	Ser	Gln	Leu	Ala	Ile	Lys	Val	Pro	Arg	Lys	Ser	Leu	Glu	
	60					65					70					
aat	gat	gag	ttg	ccc	aac	act	aaa	aaa	aac	ata	ttc	aat	gga	tta	ata	291
Asn	Asp	Glu	Leu	Pro	Asn	Thr	Lys	Lys	Asn	Ile	Phe	Asn	Gly	Leu	Ile	
	75				80					85					90	
aga	act	atc	tat	ggg	tgt	att	gat	gat	gaa	aat	tca	ttt	tta	tta	gaa	339
Arg	Thr	Ile	Tyr	Gly	Cys	Ile	Asp	Asp	Glu	Asn	Ser	Phe	Leu	Leu	Glu	
				95					100					105		
aac	gat	aaa	acc	atc	aag	gat	tta	aat	att	cag	gat	tta	ttg	ggg	cca	387
Asn	Asp	Lys	Thr	Ile	Lys	Asp	Leu	Asn	Ile	Gln	Asp	Leu	Leu	Gly	Pro	
			110					115					120			
tta	aaa	act	caa	gca	ttt	cca	tta	tca	tac	att	att	act	gac	gct	atc	435
Leu	Lys	Thr	Gln	Ala	Phe	Pro	Leu	Ser	Tyr	Ile	Ile	Thr	Asp	Ala	Ile	
			125				130					135				
aat	caa	aaa	gaa	ggg	gtg	gct	ctc	gat	tac	gct	cta	ata	aac	gat	att	483
Asn	Gln	Lys	Glu	Gly	Val	Ala	Leu	Asp	Tyr	Ala	Leu	Ile	Asn	Asp	Ile	
	140					145					150					
aag	tat	aat	ttg	ctt	gat	aac	aca	ttc	cat	ttt	atc	ttt	gat	gtt	ggg	531
Lys	Tyr	Asn	Leu	Leu	Asp	Asn	Thr	Phe	His	Phe	Ile	Phe	Asp	Val	Gly	

155	160	165	170	
aat cct ttg ttg aaa gag tca agt caa ttt att att gaa gtg cct aga				579
Asn Pro Leu Leu Lys Glu Ser Ser Gln Phe Ile Ile Glu Val Pro Arg				
	175	180	185	
gag gcg ttg gat cta gag aat gtt gat cgg ctt gtt gaa tat acg ctg				627
Glu Ala Leu Asp Leu Glu Asn Val Asp Arg Leu Val Glu Tyr Thr Leu				
	190	195	200	
tct cct aat aat cat agt caa agt tct tta gtg tat cat att tct gaa				675
Ser Pro Asn Asn His Ser Gln Ser Ser Leu Val Tyr His Ile Ser Glu				
	205	210	215	
ggc tct tat atc att cac tta ata gat gac taaacttaaaa tgaaa				720
Gly Ser Tyr Ile Ile His Leu Ile Asp Asp				
	220	225		

<210> 70
 <211> 228
 <212> PRT
 <213> Helicobacter pylori

<400> 70

Met	Leu	Ala	Tyr	Cys	Phe	Ile	Thr	Pro	Asp	Asp	Leu	Lys	Asn	Leu	Lys
1				5					10					15	
Glu	Arg	Leu	Phe	Ile	Asp	Ile	Ile	Asn	Ala	Ile	Asn	Gln	Lys	Lys	Arg
			20					25				30			
Val	Ala	Leu	Asp	His	Ala	Gln	Ile	Asp	Asp	Ile	Gln	Tyr	Asn	Val	Leu
		35				40					45				
Asp	Asn	Ala	Phe	Tyr	Phe	Ile	Phe	Asp	Val	Gly	Asn	Pro	Ser	Gln	Leu
	50					55					60				
Ala	Ile	Lys	Val	Pro	Arg	Lys	Ser	Leu	Glu	Asn	Asp	Glu	Leu	Pro	Asn
65					70					75					80
Thr	Lys	Lys	Asn	Ile	Phe	Asn	Gly	Leu	Ile	Arg	Thr	Ile	Tyr	Gly	Cys
			85						90					95	
Ile	Asp	Asp	Glu	Asn	Ser	Phe	Leu	Leu	Glu	Asn	Asp	Lys	Thr	Ile	Lys
			100					105					110		
Asp	Leu	Asn	Ile	Gln	Asp	Leu	Leu	Gly	Pro	Leu	Lys	Thr	Gln	Ala	Phe
		115				120						125			
Pro	Leu	Ser	Tyr	Ile	Ile	Thr	Asp	Ala	Ile	Asn	Gln	Lys	Glu	Gly	Val
		130				135					140				
Ala	Leu	Asp	Tyr	Ala	Leu	Ile	Asn	Asp	Ile	Lys	Tyr	Asn	Leu	Leu	Asp
145					150					155					160
Asn	Thr	Phe	His	Phe	Ile	Phe	Asp	Val	Gly	Asn	Pro	Leu	Leu	Lys	Glu
				165					170					175	
Ser	Ser	Gln	Phe	Ile	Ile	Glu	Val	Pro	Arg	Glu	Ala	Leu	Asp	Leu	Glu
			180					185					190		
Asn	Val	Asp	Arg	Leu	Val	Glu	Tyr	Thr	Leu	Ser	Pro	Asn	Asn	His	Ser
		195					200					205			
Gln	Ser	Ser	Leu	Val	Tyr	His	Ile	Ser	Glu	Gly	Ser	Tyr	Ile	Ile	His
	210					215					220				
Leu	Ile	Asp	Asp												
225															

<210> 71
 <211> 611

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (25)...(561)

<400> 71

tttgggcatg cttggtgatac ttaa atg agt caa ggt gat ggg gtg gaa gga	51
Met Ser Gln Gly Asp Gly Val Glu Gly	
1 5	
aat aat atg gat act acg aaa gag aac ttg aat ggc tca aaa gag cgt	99
Asn Asn Met Asp Thr Thr Lys Glu Asn Leu Asn Gly Ser Lys Glu Arg	
10 15 20 25	
ttg agc gat tgg gaa tat cga tgg gca atg gct cta gtc tat gga gga	147
Leu Ser Asp Trp Glu Tyr Arg Trp Ala Met Ala Leu Val Tyr Gly Gly	
30 35 40	
tgt atc tcc ata acc act agg att ttt tat gac ata aat ggt tca gct	195
Cys Ile Ser Ile Thr Thr Arg Ile Phe Tyr Asp Ile Asn Gly Ser Ala	
45 50 55	
agc gat ccg ctt ttt gac cct aaa tac agc tat tat gtg tgg tta gtg	243
Ser Asp Pro Leu Phe Asp Pro Lys Tyr Ser Tyr Tyr Val Trp Leu Val	
60 65 70	
gct cta ata gcg gct ttg ttg tct aat ctc ttg ttt aat cct aaa ggc	291
Ala Leu Ile Ala Ala Leu Leu Ser Asn Leu Leu Phe Asn Pro Lys Gly	
75 80 85	
agg tcg gta ggt tat tta atg att gaa act tgg caa ggg ttc ccc aag	339
Arg Ser Val Gly Tyr Leu Met Ile Glu Thr Trp Gln Gly Phe Pro Lys	
90 95 100 105	
ttt ttt aaa gcc att ttt aag gct agg ttt ttt ggt gcg ttt tat gac	387
Phe Phe Lys Ala Ile Phe Lys Ala Arg Phe Phe Gly Ala Phe Tyr Asp	
110 115 120	
gct gtg tta gga tca agg cta agg gat ttt tat gtg atg ctt tta acg	435
Ala Val Leu Gly Ser Arg Leu Arg Asp Phe Tyr Val Met Leu Leu Thr	
125 130 135	
atg ccc ttt att gcc gct atc cat gag gtt tcg gcg tat tgt ggg cat	483
Met Pro Phe Ile Ala Ala Ile His Glu Val Ser Ala Tyr Cys Gly His	
140 145 150	
cct agc aat ctc ctt gta gag ggt ttg gtc att ttg ggg ttt caa ggt	531
Pro Ser Asn Leu Leu Val Glu Gly Leu Val Ile Leu Gly Phe Gln Gly	
155 160 165	
ttt ctt aag ctt tgc gct aaa tgg ggg tgg tgatttaacc caaatgtcat	581
Phe Leu Lys Leu Cys Ala Lys Trp Gly Trp	
170 175	
taaatggagg gggtataaaa aaattaaaaa	611

<210> 72

<211> 179
 <212> PRT
 <213> Helicobacter pylori

<400> 72
 Met Ser Gln Gly Asp Gly Val Glu Gly Asn Asn Met Asp Thr Thr Lys
 1 5 10 15
 Glu Asn Leu Asn Gly Ser Lys Glu Arg Leu Ser Asp Trp Glu Tyr Arg
 20 25 30
 Trp Ala Met Ala Leu Val Tyr Gly Gly Cys Ile Ser Ile Thr Thr Arg
 35 40 45
 Ile Phe Tyr Asp Ile Asn Gly Ser Ala Ser Asp Pro Leu Phe Asp Pro
 50 55 60
 Lys Tyr Ser Tyr Tyr Val Trp Leu Val Ala Leu Ile Ala Ala Leu Leu
 65 70 75 80
 Ser Asn Leu Leu Phe Asn Pro Lys Gly Arg Ser Val Gly Tyr Leu Met
 85 90 95
 Ile Glu Thr Trp Gln Gly Phe Pro Lys Phe Phe Lys Ala Ile Phe Lys
 100 105 110
 Ala Arg Phe Phe Gly Ala Phe Tyr Asp Ala Val Leu Gly Ser Arg Leu
 115 120 125
 Arg Asp Phe Tyr Val Met Leu Leu Thr Met Pro Phe Ile Ala Ala Ile
 130 135 140
 His Glu Val Ser Ala Tyr Cys Gly His Pro Ser Asn Leu Leu Val Glu
 145 150 155 160
 Gly Leu Val Ile Leu Gly Phe Gln Gly Phe Leu Lys Leu Cys Ala Lys
 165 170 175
 Trp Gly Trp

<210> 73
 <211> 424
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (72)...(404)

<400> 73
 gttgtggtat aaatattctt atcaaggtgt gccaaacatg ccttgaatct caatttttga 60
 atctcaattt t atg aaa gga ttt gtt atg agt gga tta aga aca ttt agt 110
 Met Lys Gly Phe Val Met Ser Gly Leu Arg Thr Phe Ser
 1 5 10
 tgt gta gtg gtt tta tgc ggt gca atg gct aat gtg gct ata gct agt 158
 Cys Val Val Val Leu Cys Gly Ala Met Ala Asn Val Ala Ile Ala Ser
 15 20 25
 cct aaa ata gag gca agg ggt gaa tta ggc aaa ttt ata ggg ggt ggt 206
 Pro Lys Ile Glu Ala Arg Gly Glu Leu Gly Lys Phe Ile Gly Gly Gly
 30 35 40 45
 gtt ggg ggt ttt gtt ggt gat aaa atg ggc gga ttt gtt ggt ggt gca 254
 Val Gly Gly Phe Val Gly Asp Lys Met Gly Gly Phe Val Gly Gly Ala
 50 55 60
 ata gga gga tat att ggg tct gaa ata ggc gat agg gta gaa gat tat 302

Ile Gly Gly Tyr Ile Gly Ser Glu Ile Gly Asp Arg Val Glu Asp Tyr
65 70 75

atc cgt ggt gtt gat aga gag cca caa aac aaa gaa cca caa gcc cca 350
Ile Arg Gly Val Asp Arg Glu Pro Gln Asn Lys Glu Pro Gln Ala Pro
80 85 90

aga gaa cct atc cgt gat ctt tat gat tac ggc tat agt ttt ggg cat 398
Arg Glu Pro Ile Arg Asp Leu Tyr Asp Tyr Gly Tyr Ser Phe Gly His
95 100 105

gct tgg tgatcttaaa tgagtcaaga 424
Ala Trp
110

<210> 74
<211> 111
<212> PRT
<213> Helicobacter pylori

<400> 74
Met Lys Gly Phe Val Met Ser Gly Leu Arg Thr Phe Ser Cys Val Val
1 5 10 15
Val Leu Cys Gly Ala Met Ala Asn Val Ala Ile Ala Ser Pro Lys Ile
20 25 30
Glu Ala Arg Gly Glu Leu Gly Lys Phe Ile Gly Gly Gly Val Gly Gly
35 40 45
Phe Val Gly Asp Lys Met Gly Gly Phe Val Gly Gly Ala Ile Gly Gly
50 55 60
Tyr Ile Gly Ser Glu Ile Gly Asp Arg Val Glu Asp Tyr Ile Arg Gly
65 70 75 80
Val Asp Arg Glu Pro Gln Asn Lys Glu Pro Gln Ala Pro Arg Glu Pro
85 90 95
Ile Arg Asp Leu Tyr Asp Tyr Gly Tyr Ser Phe Gly His Ala Trp
100 105 110

<210> 75
<211> 630
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (132)...(569)

<400> 75
gatttttagtg atgacgagtt tcacccggtt gatcgtggtg ttttcttttt taaggaccgc 60
tttgggcacg caacaaaccc ccccccactc aaatttttagt ctcgctctct ttgatattga 120
cttttttcat c atg gaa cct agc cta aaa aag gcc tat gat aca ggg att 170
Met Glu Pro Ser Leu Lys Lys Ala Tyr Asp Thr Gly Ile
1 5 10

aag cct tat atg gat aaa aag att tct tac acc gaa gcg ttt gaa aaa 218
Lys Pro Tyr Met Asp Lys Lys Ile Ser Tyr Thr Glu Ala Phe Glu Lys
15 20 25

agc gct ctg ccc ttc aag gaa ttc atg ctt aaa aac aca cga gaa aag 266

Ser	Ala	Leu	Pro	Phe	Lys	Glu	Phe	Met	Leu	Lys	Asn	Thr	Arg	Glu	Lys		
30					35					40					45		
gat cta gcc ctt ttt ttt agg att aga aac ctc cct aac cct aaa acc 314																	
Asp	Leu	Ala	Leu	Phe	Phe	Arg	Ile	Arg	Asn	Leu	Pro	Asn	Pro	Lys	Thr		
				50					55					60			
cct gat gag gtg agt ttg agc gtt ttg atc ccg gca ttt atg ata agc 362																	
Pro	Asp	Glu	Val	Ser	Leu	Ser	Val	Leu	Ile	Pro	Ala	Phe	Met	Ile	Ser		
			65					70					75				
gag ttg aaa aca gcg ttt caa atc ggc ttt tta ctc tac ttg cct ttt 410																	
Glu	Leu	Lys	Thr	Ala	Phe	Gln	Ile	Gly	Phe	Leu	Leu	Tyr	Leu	Pro	Phe		
		80					85					90					
ttg gtg att gat atg gtg atc agc tct att tta atg gcg atg ggc atg 458																	
Leu	Val	Ile	Asp	Met	Val	Ile	Ser	Ser	Ile	Leu	Met	Ala	Met	Gly	Met		
		95				100					105						
atg atg ctc ccg cct gta atg att tct ctg cct ttt aaa att tta gtg 506																	
Met	Met	Leu	Pro	Pro	Val	Met	Ile	Ser	Leu	Pro	Phe	Lys	Ile	Leu	Val		
110						115				120					125		
ttt att ctg gta gat ggg ttt aat tta ttg acc gaa aat tta gtg gcg 554																	
Phe	Ile	Leu	Val	Asp	Gly	Phe	Asn	Leu	Leu	Thr	Glu	Asn	Leu	Val	Ala		
				130				135						140			
agt ttt aaa atg gtt tgatattaac aagcattcaa gcgataaaaag cttgaagcta 609																	
Ser	Phe	Lys	Met	Val													
			145														
gtttaaaact cataattcaa a 630																	
<210> 76																	
<211> 146																	
<212> PRT																	
<213> Helicobacter pylori																	
<400> 76																	
Met	Glu	Pro	Ser	Leu	Lys	Lys	Ala	Tyr	Asp	Thr	Gly	Ile	Lys	Pro	Tyr		
1				5					10					15			
Met	Asp	Lys	Lys	Ile	Ser	Tyr	Thr	Glu	Ala	Phe	Glu	Lys	Ser	Ala	Leu		
			20					25					30				
Pro	Phe	Lys	Glu	Phe	Met	Leu	Lys	Asn	Thr	Arg	Glu	Lys	Asp	Leu	Ala		
		35					40					45					
Leu	Phe	Phe	Arg	Ile	Arg	Asn	Leu	Pro	Asn	Pro	Lys	Thr	Pro	Asp	Glu		
		50				55					60						
Val	Ser	Leu	Ser	Val	Leu	Ile	Pro	Ala	Phe	Met	Ile	Ser	Glu	Leu	Lys		
65					70					75					80		
Thr	Ala	Phe	Gln	Ile	Gly	Phe	Leu	Leu	Tyr	Leu	Pro	Phe	Leu	Val	Ile		
			85						90					95			
Asp	Met	Val	Ile	Ser	Ser	Ile	Leu	Met	Ala	Met	Gly	Met	Met	Met	Leu		
			100					105					110				
Pro	Pro	Val	Met	Ile	Ser	Leu	Pro	Phe	Lys	Ile	Leu	Val	Phe	Ile	Leu		
			115					120					125				
Val	Asp	Gly	Phe	Asn	Leu	Leu	Thr	Glu	Asn	Leu	Val	Ala	Ser	Phe	Lys		
	130					135					140						
Met	Val																
145																	

<210> 77
 <211> 2352
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (13)...(2313)

<400> 77
 aaaaggtggt aa atg aaa aga att tta gtc tct ttg gct gtt ttg agt cat 51
 Met Lys Arg Ile Leu Val Ser Leu Ala Val Leu Ser His
 1 5 10

agc gcg cat gct gtc aaa act cat aat ttg gaa agg gtg gaa gct tca 99
 Ser Ala His Ala Val Lys Thr His Asn Leu Glu Arg Val Glu Ala Ser
 15 20 25

ggg gtg gct aac gat aag gaa gcg cct tta agc tgg agg agc aag gaa 147
 Gly Val Ala Asn Asp Lys Glu Ala Pro Leu Ser Trp Arg Ser Lys Glu
 30 35 40 45

gtg aga aac tat atg gga tct cgc acg gtg att tct aac aag caa ctc 195
 Val Arg Asn Tyr Met Gly Ser Arg Thr Val Ile Ser Asn Lys Gln Leu
 50 55 60

act aaa agc gcc aat cag agc att gaa gaa gct ttg caa aat gtg cca 243
 Thr Lys Ser Ala Asn Gln Ser Ile Glu Glu Ala Leu Gln Asn Val Pro
 65 70 75

ggc gtg cat att aga aac gct acg ggt att gga gct gtg cct agc ttt 291
 Gly Val His Ile Arg Asn Ala Thr Gly Ile Gly Ala Val Pro Ser Phe
 80 85 90

tct gtt agg ggc ttt ggt ggg gga agt tca ggg cat tcc aat acg gct 339
 Ser Val Arg Gly Phe Gly Gly Gly Ser Ser Gly His Ser Asn Thr Ala
 95 100 105

atg gtt tta gtc aat ggg atc cct att tat gtt gcg ccc tat gtt gat 387
 Met Val Leu Val Asn Gly Ile Pro Ile Tyr Val Ala Pro Tyr Val Asp
 110 115 120 125

att agc att cct att ttc cct gta acc ttt caa tct gta gat aga atc 435
 Ile Ser Ile Pro Ile Phe Pro Val Thr Phe Gln Ser Val Asp Arg Ile
 130 135 140

agc gta acc aag ggt ggg gag agc gtg cgt tat ggc cct aat gtt ttt 483
 Ser Val Thr Lys Gly Gly Glu Ser Val Arg Tyr Gly Pro Asn Val Phe
 145 150 155

ggc ggt gtg att aat gtg atc act aag ggc att cct acc aag tgg gag 531
 Gly Gly Val Ile Asn Val Ile Thr Lys Gly Ile Pro Thr Lys Trp Glu
 160 165 170

agt cag gtg agc gag agg gcc act ttt tgg ggc aaa tct gaa aat ggg 579
 Ser Gln Val Ser Glu Arg Ala Thr Phe Trp Gly Lys Ser Glu Asn Gly
 175 180 185

ggc ttt ttc aat caa aat tct aaa aac ctt gac aaa agc tta gcc aat	627
Gly Phe Phe Asn Gln Asn Ser Lys Asn Leu Asp Lys Ser Leu Ala Asn	
190 195 200 205	
aac atg ctt ttt gac act tac tta aga aca ggg ggc atg atg aat aag	675
Asn Met Leu Phe Asp Thr Tyr Leu Arg Thr Gly Gly Met Met Asn Lys	
210 215 220	
cat ttt gga atc caa gct caa gcc aac tgg ctt aaa ggg caa ggg ttt	723
His Phe Gly Ile Gln Ala Gln Ala Asn Trp Leu Lys Gly Gln Gly Phe	
225 230 235	
aga tac aac agc cct acg aac att caa aac tac atg cta gat tcc ttg	771
Arg Tyr Asn Ser Pro Thr Asn Ile Gln Asn Tyr Met Leu Asp Ser Leu	
240 245 250	
tat caa att aat gat agt aat aag atc act gct ttt ttc caa tac tat	819
Tyr Gln Ile Asn Asp Ser Asn Lys Ile Thr Ala Phe Phe Gln Tyr Tyr	
255 260 265	
aat tat ttt atg gca gac ccc gga tct tta ggc ata gaa gcg tat aat	867
Asn Tyr Phe Met Ala Asp Pro Gly Ser Leu Gly Ile Glu Ala Tyr Asn	
270 275 280 285	
caa aat cgt ttt caa aac aac cgc cct aat aac aat aaa agc ggg aga	915
Gln Asn Arg Phe Gln Asn Asn Arg Pro Asn Asn Asn Lys Ser Gly Arg	
290 295 300	
gcg aag cgr tgg gga gct gtg tat caa aac ttt ttt ggg gat acg gac	963
Ala Lys Xaa Trp Gly Ala Val Tyr Gln Asn Phe Phe Gly Asp Thr Asp	
305 310 315	
aaa ata ggt ggg gat ttc act ttt agt tac tat ggg cat gac atg tca	1011
Lys Ile Gly Gly Asp Phe Thr Phe Ser Tyr Tyr Gly His Asp Met Ser	
320 325 330	
agg gat ttt caa ttt gat tct aat ttt ttg aat gtc aat acc aat cct	1059
Arg Asp Phe Gln Phe Asp Ser Asn Phe Leu Asn Val Asn Thr Asn Pro	
335 340 345	
aaa tta ggc cct gtt tat acc gat caa aat tat cca gga ttt ttt att	1107
Lys Leu Gly Pro Val Tyr Thr Asp Gln Asn Tyr Pro Gly Phe Phe Ile	
350 355 360 365	
ttt gat cat tta agg cgt tac ata atg aac gct ttt gag cct aat ttg	1155
Phe Asp His Leu Arg Arg Tyr Ile Met Asn Ala Phe Glu Pro Asn Leu	
370 375 380	
aac tta gtt gtc aat acc aat aaa gtt aag caa act ttt aat gtg ggc	1203
Asn Leu Val Val Asn Thr Asn Lys Val Lys Gln Thr Phe Asn Val Gly	
385 390 395	
atg cgt ttt atg aca atg gat atg tat ttc aga ttg gat caa agc aca	1251
Met Arg Phe Met Thr Met Asp Met Tyr Phe Arg Leu Asp Gln Ser Thr	
400 405 410	
tgc gaa aaa acc gat att ttt aat ggg gtg tgc cgc atg cct cct ttt	1299
Cys Glu Lys Thr Asp Ile Phe Asn Gly Val Cys Arg Met Pro Pro Phe	
415 420 425	

gtt ctt tct aaa aaa ccc agc aac aat caa aac ctg ttt aac aac tat	1347
Val Leu Ser Lys Lys Pro Ser Asn Asn Gln Asn Leu Phe Asn Asn Tyr	
430 435 440 445	
aca gcg gta tgg ttg agc gat aaa ata gag ctt ttt gat tct aaa ttg	1395
Thr Ala Val Trp Leu Ser Asp Lys Ile Glu Leu Phe Asp Ser Lys Leu	
450 455 460	
gtg ata act cca ggg ctt aga tac act ttt ttg aac tat aac aac aaa	1443
Val Ile Thr Pro Gly Leu Arg Tyr Thr Phe Leu Asn Tyr Asn Asn Lys	
465 470 475	
gag cca gaa aag cat gat ttt tct gtg tgg aat att aca aaa aag cgt	1491
Glu Pro Glu Lys His Asp Phe Ser Val Trp Asn Ile Thr Lys Lys Arg	
480 485 490	
caa aac gaa tgg agt ccc gcc ctt aac att ggc tat aaa cct atg gaa	1539
Gln Asn Glu Trp Ser Pro Ala Leu Asn Ile Gly Tyr Lys Pro Met Glu	
495 500 505	
aat tgg ata tgg tat gcg aac tac cgc cgc agt ttt atc ccc cca caa	1587
Asn Trp Ile Trp Tyr Ala Asn Tyr Arg Arg Ser Phe Ile Pro Pro Gln	
510 515 520 525	
cat aca atg cta ggc att act agg act aat tac aac caa att ttt aat	1635
His Thr Met Leu Gly Ile Thr Arg Thr Asn Tyr Asn Gln Ile Phe Asn	
530 535 540	
gaa att gaa gtg ggg caa cgc tat agt tat aaa aat cta ttg agc ttt	1683
Glu Ile Glu Val Gly Gln Arg Tyr Ser Tyr Lys Asn Leu Leu Ser Phe	
545 550 555	
aac acg aat tat ttt gtg att ttt gcc aag cgt tac tat gcg gga ggc	1731
Asn Thr Asn Tyr Phe Val Ile Phe Ala Lys Arg Tyr Tyr Ala Gly Gly	
560 565 570	
tat agc cca cag cct att aac gct agg agt caa ggg gta gaa ttg gaa	1779
Tyr Ser Pro Gln Pro Ile Asn Ala Arg Ser Gln Gly Val Glu Leu Glu	
575 580 585	
ttg tat tac gcg ccg att agg ggt ttg caa ttc cat gtg gct tac acc	1827
Leu Tyr Tyr Ala Pro Ile Arg Gly Leu Gln Phe His Val Ala Tyr Thr	
590 595 600 605	
tat att gat gca cgc atc act tct aac gct gat gat att gct tat tat	1875
Tyr Ile Asp Ala Arg Ile Thr Ser Asn Ala Asp Asp Ile Ala Tyr Tyr	
610 615 620	
ttt aca ggc att gtc aat aaa ccc ttt gac att aaa ggg aag cgt ttg	1923
Phe Thr Gly Ile Val Asn Lys Pro Phe Asp Ile Lys Gly Lys Arg Leu	
625 630 635	
cct tat gtg agt cct aac caa ttc ata ttt gac atg atg tat act tac	1971
Pro Tyr Val Ser Pro Asn Gln Phe Ile Phe Asp Met Met Tyr Thr Tyr	
640 645 650	
aag cac acg act ttt ggt att agc agc tat ttt tat agc cgt gct tat	2019
Lys His Thr Thr Phe Gly Ile Ser Ser Tyr Phe Tyr Ser Arg Ala Tyr	

655	660	665	
agt tct atg ctc aat cag gcc aaa agc caa acc gtg tgc ctg ccc tta			2067
Ser Ser Met Leu Asn Gln Ala Lys Ser Gln Thr Val Cys Leu Pro Leu			
670	675	680	685
aac cca gaa tac aca ggg ggg cta gag tat ggt tgt aat tca gta ggg			2115
Asn Pro Glu Tyr Thr Gly Gly Leu Glu Tyr Gly Cys Asn Ser Val Gly			
	690	695	700
tta ttg ccc ttg tat ttt gtg ttg aac gtt caa gta agc tcg gtt tta			2163
Leu Leu Pro Leu Tyr Phe Val Leu Asn Val Gln Val Ser Ser Val Leu			
	705	710	715
tgg caa agc ggt agg cat aaa atc aca ggg agt ttg caa atc aat aat			2211
Trp Gln Ser Gly Arg His Lys Ile Thr Gly Ser Leu Gln Ile Asn Asn			
	720	725	730
ctt ttt aac atg aag tat tat ttt agg gga att ggc aca agc cct aca			2259
Leu Phe Asn Met Lys Tyr Tyr Phe Arg Gly Ile Gly Thr Ser Pro Thr			
	735	740	745
gga aga gag ccc gca cca ggg cga tcc att aca gcg tat ttg aat tat			2307
Gly Arg Glu Pro Ala Pro Gly Arg Ser Ile Thr Ala Tyr Leu Asn Tyr			
	750	755	760
gag ttt taaactagct tcaagctttt atcgcttgaa tgcttgtaa			2352
Glu Phe			

<210> 78
 <211> 767
 <212> PRT
 <213> Helicobacter pylori

<220>
 <221> VARIANT
 <222> 304
 <223> Xaa = Any Amino Acid

<400> 78

Met	Lys	Arg	Ile	Leu	Val	Ser	Leu	Ala	Val	Leu	Ser	His	Ser	Ala	His
1				5					10					15	
Ala	Val	Lys	Thr	His	Asn	Leu	Glu	Arg	Val	Glu	Ala	Ser	Gly	Val	Ala
			20					25					30		
Asn	Asp	Lys	Glu	Ala	Pro	Leu	Ser	Trp	Arg	Ser	Lys	Glu	Val	Arg	Asn
		35					40					45			
Tyr	Met	Gly	Ser	Arg	Thr	Val	Ile	Ser	Asn	Lys	Gln	Leu	Thr	Lys	Ser
	50					55					60				
Ala	Asn	Gln	Ser	Ile	Glu	Glu	Ala	Leu	Gln	Asn	Val	Pro	Gly	Val	His
65				70					75						80
Ile	Arg	Asn	Ala	Thr	Gly	Ile	Gly	Ala	Val	Pro	Ser	Phe	Ser	Val	Arg
			85					90						95	
Gly	Phe	Gly	Gly	Gly	Ser	Ser	Gly	His	Ser	Asn	Thr	Ala	Met	Val	Leu
			100				105					110			
Val	Asn	Gly	Ile	Pro	Ile	Tyr	Val	Ala	Pro	Tyr	Val	Asp	Ile	Ser	Ile
		115				120						125			
Pro	Ile	Phe	Pro	Val	Thr	Phe	Gln	Ser	Val	Asp	Arg	Ile	Ser	Val	Thr

130						135					140				
Lys	Gly	Gly	Glu	Ser	Val	Arg	Tyr	Gly	Pro	Asn	Val	Phe	Gly	Gly	Val
145					150					155					160
Ile	Asn	Val	Ile	Thr	Lys	Gly	Ile	Pro	Thr	Lys	Trp	Glu	Ser	Gln	Val
				165					170					175	
Ser	Glu	Arg	Ala	Thr	Phe	Trp	Gly	Lys	Ser	Glu	Asn	Gly	Gly	Phe	Phe
			180					185					190		
Asn	Gln	Asn	Ser	Lys	Asn	Leu	Asp	Lys	Ser	Leu	Ala	Asn	Asn	Met	Leu
		195					200					205			
Phe	Asp	Thr	Tyr	Leu	Arg	Thr	Gly	Gly	Met	Met	Asn	Lys	His	Phe	Gly
	210					215					220				
Ile	Gln	Ala	Gln	Ala	Asn	Trp	Leu	Lys	Gly	Gln	Gly	Phe	Arg	Tyr	Asn
225					230					235					240
Ser	Pro	Thr	Asn	Ile	Gln	Asn	Tyr	Met	Leu	Asp	Ser	Leu	Tyr	Gln	Ile
			245					250						255	
Asn	Asp	Ser	Asn	Lys	Ile	Thr	Ala	Phe	Phe	Gln	Tyr	Tyr	Asn	Tyr	Phe
		260						265					270		
Met	Ala	Asp	Pro	Gly	Ser	Leu	Gly	Ile	Glu	Ala	Tyr	Asn	Gln	Asn	Arg
		275					280					285			
Phe	Gln	Asn	Asn	Arg	Pro	Asn	Asn	Asn	Lys	Ser	Gly	Arg	Ala	Lys	Xaa
	290					295					300				
Trp	Gly	Ala	Val	Tyr	Gln	Asn	Phe	Phe	Gly	Asp	Thr	Asp	Lys	Ile	Gly
305					310					315					320
Gly	Asp	Phe	Thr	Phe	Ser	Tyr	Tyr	Gly	His	Asp	Met	Ser	Arg	Asp	Phe
				325					330					335	
Gln	Phe	Asp	Ser	Asn	Phe	Leu	Asn	Val	Asn	Thr	Asn	Pro	Lys	Leu	Gly
			340					345					350		
Pro	Val	Tyr	Thr	Asp	Gln	Asn	Tyr	Pro	Gly	Phe	Phe	Ile	Phe	Asp	His
	355						360					365			
Leu	Arg	Arg	Tyr	Ile	Met	Asn	Ala	Phe	Glu	Pro	Asn	Leu	Asn	Leu	Val
	370					375					380				
Val	Asn	Thr	Asn	Lys	Val	Lys	Gln	Thr	Phe	Asn	Val	Gly	Met	Arg	Phe
385					390					395					400
Met	Thr	Met	Asp	Met	Tyr	Phe	Arg	Leu	Asp	Gln	Ser	Thr	Cys	Glu	Lys
				405					410					415	
Thr	Asp	Ile	Phe	Asn	Gly	Val	Cys	Arg	Met	Pro	Pro	Phe	Val	Leu	Ser
		420					425					430			
Lys	Lys	Pro	Ser	Asn	Asn	Gln	Asn	Leu	Phe	Asn	Asn	Tyr	Thr	Ala	Val
	435					440						445			
Trp	Leu	Ser	Asp	Lys	Ile	Glu	Leu	Phe	Asp	Ser	Lys	Leu	Val	Ile	Thr
	450					455					460				
Pro	Gly	Leu	Arg	Tyr	Thr	Phe	Leu	Asn	Tyr	Asn	Asn	Lys	Glu	Pro	Glu
465					470					475					480
Lys	His	Asp	Phe	Ser	Val	Trp	Asn	Ile	Thr	Lys	Lys	Arg	Gln	Asn	Glu
			485						490					495	
Trp	Ser	Pro	Ala	Leu	Asn	Ile	Gly	Tyr	Lys	Pro	Met	Glu	Asn	Trp	Ile
		500						505					510		
Trp	Tyr	Ala	Asn	Tyr	Arg	Arg	Ser	Phe	Ile	Pro	Pro	Gln	His	Thr	Met
	515						520					525			
Leu	Gly	Ile	Thr	Arg	Thr	Asn	Tyr	Asn	Gln	Ile	Phe	Asn	Glu	Ile	Glu
	530					535					540				
Val	Gly	Gln	Arg	Tyr	Ser	Tyr	Lys	Asn	Leu	Leu	Ser	Phe	Asn	Thr	Asn
545					550					555					560
Tyr	Phe	Val	Ile	Phe	Ala	Lys	Arg	Tyr	Tyr	Ala	Gly	Gly	Tyr	Ser	Pro
			565						570					575	
Gln	Pro	Ile	Asn	Ala	Arg	Ser	Gln	Gly	Val	Glu	Leu	Glu	Leu	Tyr	Tyr
		580						585					590		
Ala	Pro	Ile	Arg	Gly	Leu	Gln	Phe	His	Val	Ala	Tyr	Thr	Tyr	Ile	Asp
	595						600					605			

Ala	Arg	Ile	Thr	Ser	Asn	Ala	Asp	Asp	Ile	Ala	Tyr	Tyr	Phe	Thr	Gly
610						615					620				
Ile	Val	Asn	Lys	Pro	Phe	Asp	Ile	Lys	Gly	Lys	Arg	Leu	Pro	Tyr	Val
625					630					635					640
Ser	Pro	Asn	Gln	Phe	Ile	Phe	Asp	Met	Met	Tyr	Thr	Tyr	Lys	His	Thr
				645					650					655	
Thr	Phe	Gly	Ile	Ser	Ser	Tyr	Phe	Tyr	Ser	Arg	Ala	Tyr	Ser	Ser	Met
			660					665					670		
Leu	Asn	Gln	Ala	Lys	Ser	Gln	Thr	Val	Cys	Leu	Pro	Leu	Asn	Pro	Glu
		675					680					685			
Tyr	Thr	Gly	Gly	Leu	Glu	Tyr	Gly	Cys	Asn	Ser	Val	Gly	Leu	Leu	Pro
	690					695					700				
Leu	Tyr	Phe	Val	Leu	Asn	Val	Gln	Val	Ser	Ser	Val	Leu	Trp	Gln	Ser
705					710					715					720
Gly	Arg	His	Lys	Ile	Thr	Gly	Ser	Leu	Gln	Ile	Asn	Asn	Leu	Phe	Asn
				725					730					735	
Met	Lys	Tyr	Tyr	Phe	Arg	Gly	Ile	Gly	Thr	Ser	Pro	Thr	Gly	Arg	Glu
			740					745					750		
Pro	Ala	Pro	Gly	Arg	Ser	Ile	Thr	Ala	Tyr	Leu	Asn	Tyr	Glu	Phe	
		755					760					765			

<210> 79
 <211> 888
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (19)...(837)

<400> 79																
agataggaat	gtaaagga	atg	gaa	ttt	atg	aaa	aag	ttt	gta	gct	tta	ggg			51	
		Met	Glu	Phe	Met	Lys	Lys	Phe	Val	Ala	Leu	Gly				
		1				5					10					
ctt	cta	tcc	gca	gtt	tta	agc	tct	tcg	ttg	tta	gcc	gaa	ggt	gat	ggt	99
Leu	Leu	Ser	Ala	Val	Leu	Ser	Ser	Ser	Leu	Leu	Ala	Glu	Gly	Asp	Gly	
			15					20					25			
gtt	tat	ata	ggg	act	aat	tat	cag	ctt	gga	caa	gcc	cgt	ttg	aat	agt	147
Val	Tyr	Ile	Gly	Thr	Asn	Tyr	Gln	Leu	Gly	Gln	Ala	Arg	Leu	Asn	Ser	
		30					35					40				
aat	att	tat	aat	aca	ggg	gat	tgc	aca	ggg	agt	gtt	gta	ggt	tgc	ccc	195
Asn	Ile	Tyr	Asn	Thr	Gly	Asp	Cys	Thr	Gly	Ser	Val	Val	Gly	Cys	Pro	
		45				50					55					
cca	ggt	ctt	acc	gct	aat	aag	cat	aat	cca	gga	ggc	acc	aat	atc	aat	243
Pro	Gly	Leu	Thr	Ala	Asn	Lys	His	Asn	Pro	Gly	Gly	Thr	Asn	Ile	Asn	
	60				65				70						75	
tgg	cat	gct	aaa	tac	gct	aat	ggg	gct	ttg	aat	ggt	ctt	ggg	ttg	aat	291
Trp	His	Ala	Lys	Tyr	Ala	Asn	Gly	Ala	Leu	Asn	Gly	Leu	Gly	Leu	Asn	
				80				85						90		
gtg	ggt	tat	aag	aag	ttc	ttc	cag	ttc	aag	tct	ttt	gat	atg	aca	agc	339
Val	Gly	Tyr	Lys	Lys	Phe	Phe	Gln	Phe	Lys	Ser	Phe	Asp	Met	Thr	Ser	
			95					100					105			

aag tgg ttt ggt ttt aga gtg tat ggg ctt ttt gat tat ggg cat gcc	387
Lys Trp Phe Gly Phe Arg Val Tyr Gly Leu Phe Asp Tyr Gly His Ala	
110 115 120	
act tta ggc aag caa gtt tat gca cct aat aaa atc cag ttg gat atg	435
Thr Leu Gly Lys Gln Val Tyr Ala Pro Asn Lys Ile Gln Leu Asp Met	
125 130 135	
gtc tct tgg ggt gtg ggg agc gat ttg tta gct gat att att gat aac	483
Val Ser Trp Gly Val Gly Ser Asp Leu Leu Ala Asp Ile Ile Asp Asn	
140 145 150 155	
gat aac gct tct ttt ggt att ttt ggt ggg gtc gct atc ggc ggt aac	531
Asp Asn Ala Ser Phe Gly Ile Phe Gly Gly Val Ala Ile Gly Gly Asn	
160 165 170	
act tgg aaa agc tca gcg gca aac tat tgg aaa gag caa atc att gaa	579
Thr Trp Lys Ser Ser Ala Ala Asn Tyr Trp Lys Glu Gln Ile Ile Glu	
175 180 185	
gct aag ggt cct gat gtt tgt acc cct act tat tgt aac cct aac gct	627
Ala Lys Gly Pro Asp Val Cys Thr Pro Thr Tyr Cys Asn Pro Asn Ala	
190 195 200	
cct tat agc acc aaa act tca acc gtc gct ttt cag gta tgg ttg aat	675
Pro Tyr Ser Thr Lys Thr Ser Thr Val Ala Phe Gln Val Trp Leu Asn	
205 210 215	
ttt ggg gtg aga gcc aat att tac aag cat aat ggc gta gag ttt ggc	723
Phe Gly Val Arg Ala Asn Ile Tyr Lys His Asn Gly Val Glu Phe Gly	
220 225 230 235	
gtg aga gtg ccg cta ctc atc aac aag ttt ttg agt gcg ggt cct aac	771
Val Arg Val Pro Leu Leu Ile Asn Lys Phe Leu Ser Ala Gly Pro Asn	
240 245 250	
gct act aat ctt tat tac cat ttg aaa cgg gat tat tcg ctt tat tta	819
Ala Thr Asn Leu Tyr Tyr His Leu Lys Arg Asp Tyr Ser Leu Tyr Leu	
255 260 265	
ggg tat aac tac act ttt taaacccttt aaaagggtgt ctttaagccc	867
Gly Tyr Asn Tyr Thr Phe	
270	
tttttagtcc ttataaaaag g	888
<210> 80	
<211> 273	
<212> PRT	
<213> Helicobacter pylori	
<400> 80	
Met Glu Phe Met Lys Lys Phe Val Ala Leu Gly Leu Leu Ser Ala Val	
1 5 10 15	
Leu Ser Ser Ser Leu Leu Ala Glu Gly Asp Gly Val Tyr Ile Gly Thr	
20 25 30	
Asn Tyr Gln Leu Gly Gln Ala Arg Leu Asn Ser Asn Ile Tyr Asn Thr	
35 40 45	

Gly	Asp	Cys	Thr	Gly	Ser	Val	Val	Gly	Cys	Pro	Pro	Gly	Leu	Thr	Ala		
50						55				60							
Asn	Lys	His	Asn	Pro	Gly	Gly	Thr	Asn	Ile	Asn	Trp	His	Ala	Lys	Tyr		
65					70					75					80		
Ala	Asn	Gly	Ala	Leu	Asn	Gly	Leu	Gly	Leu	Asn	Val	Gly	Tyr	Lys	Lys		
				85					90					95			
Phe	Phe	Gln	Phe	Lys	Ser	Phe	Asp	Met	Thr	Ser	Lys	Trp	Phe	Gly	Phe		
			100					105					110				
Arg	Val	Tyr	Gly	Leu	Phe	Asp	Tyr	Gly	His	Ala	Thr	Leu	Gly	Lys	Gln		
		115					120					125					
Val	Tyr	Ala	Pro	Asn	Lys	Ile	Gln	Leu	Asp	Met	Val	Ser	Trp	Gly	Val		
	130					135					140						
Gly	Ser	Asp	Leu	Leu	Ala	Asp	Ile	Ile	Asp	Asn	Asp	Asn	Ala	Ser	Phe		
145					150					155					160		
Gly	Ile	Phe	Gly	Gly	Val	Ala	Ile	Gly	Gly	Asn	Thr	Trp	Lys	Ser	Ser		
			165						170					175			
Ala	Ala	Asn	Tyr	Trp	Lys	Glu	Gln	Ile	Glu	Ala	Lys	Gly	Pro	Asp			
			180					185				190					
Val	Cys	Thr	Pro	Thr	Tyr	Cys	Asn	Pro	Asn	Ala	Pro	Tyr	Ser	Thr	Lys		
	195						200					205					
Thr	Ser	Thr	Val	Ala	Phe	Gln	Val	Trp	Leu	Asn	Phe	Gly	Val	Arg	Ala		
	210					215					220						
Asn	Ile	Tyr	Lys	His	Asn	Gly	Val	Glu	Phe	Gly	Val	Arg	Val	Pro	Leu		
225					230					235					240		
Leu	Ile	Asn	Lys	Phe	Leu	Ser	Ala	Gly	Pro	Asn	Ala	Thr	Asn	Leu	Tyr		
				245					250					255			
Tyr	His	Leu	Lys	Arg	Asp	Tyr	Ser	Leu	Tyr	Leu	Gly	Tyr	Asn	Tyr	Thr		
			260					265					270				
Phe																	

<210> 81
 <211> 560
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (37)...(522)

<400> 81																	
cacggtcatt	ttgtctgtgt	ttttagtcgc	gtattc	atg	caa	ctg	ctt	atg	gaa							54	
				Met	Gln	Leu	Leu	Met	Glu								
				1				5									
cgc	ctt	tct	ctt	gtc	ttc	agg	cat	ctt	ttc	cat	gcg	ctt	ttt	caa	ctc	102	
Arg	Leu	Ser	Leu	Val	Phe	Arg	His	Leu	Phe	His	Ala	Leu	Phe	Gln	Leu		
			10					15					20				
ttt	tgt	gta	atc	cac	aat	atc	ctg	cgg	agk	aca	acg	cca	gcc	att	tta	150	
Phe	Cys	Val	Ile	His	Asn	Ile	Leu	Arg	Xaa	Thr	Thr	Pro	Ala	Ile	Leu		
			25				30					35					
gcc	aaa	tct	tca	tcg	ctt	gtt	ttg	ctg	aaa	tct	ttg	gcg	ttc	aaa	gcc	198	
Ala	Lys	Ser	Ser	Ser	Leu	Val	Leu	Leu	Lys	Ser	Leu	Ala	Phe	Lys	Ala		
			40			45					50						
aca	aat	agc	aac	gcg	cta	aca	gaa	agt	att	ttc	aac	gct	ttt	ttc	att	246	

Thr	Asn	Ser	Asn	Ala	Leu	Thr	Glu	Ser	Ile	Phe	Asn	Ala	Phe	Phe	Ile	
55					60					65					70	
ttt	tat	cct	ttt	aaa	tta	aat	tta	tct	cac	tta	gga	gag	caa	tgc	tcg	294
Phe	Tyr	Pro	Phe	Lys	Leu	Asn	Leu	Ser	His	Leu	Gly	Glu	Gln	Cys	Ser	
				75					80					85		
tct	ttt	ttc	tta	aca	gcc	cta	cac	caa	act	ttt	ctc	gta	tcg	ccg	ctg	342
Ser	Phe	Phe	Leu	Thr	Ala	Leu	His	Gln	Thr	Phe	Leu	Val	Ser	Pro	Leu	
			90					95					100			
caa	acg	ctc	aca	tta	agt	cct	ttt	gcc	ttg	att	tct	tca	tcg	ctc	aaa	390
Gln	Thr	Leu	Thr	Leu	Ser	Pro	Phe	Ala	Leu	Ile	Ser	Ser	Ser	Leu	Lys	
		105					110					115				
cct	ttg	gtt	ttt	tct	tct	aat	tct	tta	cgc	act	tct	tca	cgc	att	ttt	438
Pro	Leu	Val	Phe	Ser	Ser	Asn	Ser	Leu	Arg	Thr	Ser	Ser	Arg	Ile	Phe	
	120					125					130					
ttg	aaa	tcc	ttc	gct	cat	ttt	gga	aag	att	ctt	cct	agc	gat	ccg	gct	486
Leu	Lys	Ser	Phe	Ala	His	Phe	Gly	Lys	Ile	Leu	Pro	Ser	Asp	Pro	Ala	
135				140					145						150	
gaa	att	cgc	gcg	gaa	ttt	ctt	agc	gtc	ctc	agc	gtt	taaagtttta				532
Glu	Ile	Arg	Ala	Glu	Phe	Leu	Ser	Val	Leu	Ser	Val					
				155				160								
aggcgtttag acacttccat gcgataat																560
<210> 82																
<211> 162																
<212> PRT																
<213> Helicobacter pylori																
<220>																
<221> VARIANT																
<222> 32																
<223> Xaa = Any Amino Acid																
<400> 82																
Met	Gln	Leu	Leu	Met	Glu	Arg	Leu	Ser	Leu	Val	Phe	Arg	His	Leu	Phe	
1				5					10					15		
His	Ala	Leu	Phe	Gln	Leu	Phe	Cys	Val	Ile	His	Asn	Ile	Leu	Arg	Xaa	
			20					25					30			
Thr	Thr	Pro	Ala	Ile	Leu	Ala	Lys	Ser	Ser	Ser	Leu	Val	Leu	Leu	Lys	
		35					40					45				
Ser	Leu	Ala	Phe	Lys	Ala	Thr	Asn	Ser	Asn	Ala	Leu	Thr	Glu	Ser	Ile	
	50					55					60					
Phe	Asn	Ala	Phe	Phe	Ile	Phe	Tyr	Pro	Phe	Lys	Leu	Asn	Leu	Ser	His	
65					70					75					80	
Leu	Gly	Glu	Gln	Cys	Ser	Ser	Phe	Phe	Leu	Thr	Ala	Leu	His	Gln	Thr	
			85						90					95		
Phe	Leu	Val	Ser	Pro	Leu	Gln	Thr	Leu	Thr	Leu	Ser	Pro	Phe	Ala	Leu	
			100					105						110		
Ile	Ser	Ser	Ser	Leu	Lys	Pro	Leu	Val	Phe	Ser	Ser	Asn	Ser	Leu	Arg	
		115				120						125				
Thr	Ser	Ser	Arg	Ile	Phe	Leu	Lys	Ser	Phe	Ala	His	Phe	Gly	Lys	Ile	
	130					135					140					
Leu	Pro	Ser	Asp	Pro	Ala	Glu	Ile	Arg	Ala	Glu	Phe	Leu	Ser	Val	Leu	

gct ttg aat tta tat aat gct gtg agc gta gcg ctc aat gaa aaa agt	583
Ala Leu Asn Leu Tyr Asn Ala Val Ser Val Ala Leu Asn Glu Lys Ser	
170 175 180	
gcg aat aaa ggc gtg tta gtg gtg atg gac gat aat att ttt agc gct	631
Ala Asn Lys Gly Val Leu Val Val Met Asp Asp Asn Ile Phe Ser Ala	
185 190 195	
aga gaa gtg att aaa acg cac acc acc cac act tcc acc ttt aaa gcc	679
Arg Glu Val Ile Lys Thr His Thr Thr His Thr Ser Thr Phe Lys Ala	
200 205 210	
tta aat agc ggc gcg ata ggg agc gtg tat tat ggc aaa acg cgc tat	727
Leu Asn Ser Gly Ala Ile Gly Ser Val Tyr Tyr Gly Lys Thr Arg Tyr	
215 220 225	
tac atg cag cct ttg aga aaa cac acc aca gag agc gaa ttt tcc ctt	775
Tyr Met Gln Pro Leu Arg Lys His Thr Thr Glu Ser Glu Phe Ser Leu	
230 235 240 245	
tca caa ctc aaa acc ccc ctg cct aaa gtg gat att att tac acg cat	823
Ser Gln Leu Lys Thr Pro Leu Pro Lys Val Asp Ile Ile Tyr Thr His	
250 255 260	
gct ggc atg acc cct gat tta ttc caa gcg agc cta aac tcg cat gca	871
Ala Gly Met Thr Pro Asp Leu Phe Gln Ala Ser Leu Asn Ser His Ala	
265 270 275	
aaa ggc gtt gtg ata gcc ggg gtg ggt aat ggg aat gtg agc gct ggg	919
Lys Gly Val Val Ile Ala Gly Val Gly Asn Gly Asn Val Ser Ala Gly	
280 285 290	
ttt tta aaa gcg atg caa gaa gcg agc caa atg ggg gtg gtt att gtt	967
Phe Leu Lys Ala Met Gln Glu Ala Ser Gln Met Gly Val Val Ile Val	
295 300 305	
cgt tct agc agg gta aat agc ggt gag att act tca ggc gag att gat	1015
Arg Ser Ser Arg Val Asn Ser Gly Glu Ile Thr Ser Gly Glu Ile Asp	
310 315 320 325	
gac aag gcc ttc atc aca agc gac aat tta aac ccc caa aaa gct agg	1063
Asp Lys Ala Phe Ile Thr Ser Asp Asn Leu Asn Pro Gln Lys Ala Arg	
330 335 340	
gtg ctt tta caa ctc gct tta act aaa aca aat aat aaa gaa aaa atc	1111
Val Leu Leu Gln Leu Ala Leu Thr Lys Thr Asn Asn Lys Glu Lys Ile	
345 350 355	
caa gaa atg ttt gaa gag tat tgaaagattc tcttaaatca cccaattatc	1162
Gln Glu Met Phe Glu Glu Tyr	
360	
aaagataatt ggggtgatttg gtttattttg tttt	1196
<210> 84	
<211> 364	
<212> PRT	
<213> Helicobacter pylori	

<400> 84
Met Phe Tyr Tyr Thr Ile Lys Ser Phe Asn Phe Lys Arg Trp Ser Ile
1 5 10 15
Met Arg Ile Phe Leu Lys Leu Leu Ile Leu Leu Phe Cys Leu Lys Gly
20 25 30
Gln Val Met Ala Gln Asn Leu Pro Thr Ile Ala Leu Leu Ala Thr Gly
35 40 45
Gly Thr Ile Ala Gly Ser Gly Ala Ser Ala Ser Leu Gly Ser Tyr Lys
50 55 60
Ser Gly Glu Leu Gly Ile Lys Glu Leu Leu Lys Ala Ile Pro Ser Leu
65 70 75 80
Asn Arg Leu Ala Arg Ile Gln Gly Glu Gln Ile Ser Asn Ile Gly Ser
85 90 95
Gln Asp Met Asn Glu Glu Val Trp Phe Lys Leu Ala Lys Arg Ala Gln
100 105 110
Glu Leu Leu Asp Asp Ser Arg Ile Gln Gly Val Val Ile Thr His Gly
115 120 125
Thr Asp Thr Leu Glu Glu Ser Ala Tyr Phe Leu Asn Leu Val Leu Arg
130 135 140
Ser Thr Lys Pro Val Val Leu Val Gly Ala Met Arg Asn Ala Ala Ser
145 150 155 160
Leu Ser Ala Asp Gly Ala Leu Asn Leu Tyr Asn Ala Val Ser Val Ala
165 170 175
Leu Asn Glu Lys Ser Ala Asn Lys Gly Val Leu Val Val Met Asp Asp
180 185 190
Asn Ile Phe Ser Ala Arg Glu Val Ile Lys Thr His Thr Thr His Thr
195 200 205
Ser Thr Phe Lys Ala Leu Asn Ser Gly Ala Ile Gly Ser Val Tyr Tyr
210 215 220
Gly Lys Thr Arg Tyr Tyr Met Gln Pro Leu Arg Lys His Thr Thr Glu
225 230 235 240
Ser Glu Phe Ser Leu Ser Gln Leu Lys Thr Pro Leu Pro Lys Val Asp
245 250 255
Ile Ile Tyr Thr His Ala Gly Met Thr Pro Asp Leu Phe Gln Ala Ser
260 265 270
Leu Asn Ser His Ala Lys Gly Val Val Ile Ala Gly Val Gly Asn Gly
275 280 285
Asn Val Ser Ala Gly Phe Leu Lys Ala Met Gln Glu Ala Ser Gln Met
290 295 300
Gly Val Val Ile Val Arg Ser Ser Arg Val Asn Ser Gly Glu Ile Thr
305 310 315 320
Ser Gly Glu Ile Asp Asp Lys Ala Phe Ile Thr Ser Asp Asn Leu Asn
325 330 335
Pro Gln Lys Ala Arg Val Leu Leu Gln Leu Ala Leu Thr Lys Thr Asn
340 345 350
Asn Lys Glu Lys Ile Gln Glu Met Phe Glu Glu Tyr
355 360

<210> 85
<211> 678
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (37)...(612)
<221> misc_feature

<222> 495

<223> n = A,T,C or G

<400> 85

```
agtaaaacat cgtaaata aatttaaaaa gggtta atg gtg gat gcc ttt ttc 54
              Met Val Asp Ala Phe Phe
              1 5

caa att gca gtg tta ctt ttt tcg ctt ttt tta ggg gca agg cta ggg 102
Gln Ile Ala Val Leu Leu Phe Ser Leu Phe Leu Gly Ala Arg Leu Gly
              10 15 20

ggc ttg gga gtg ggc tat gcg ggg ggc ttg ggc gtg ctt att tta tgc 150
Gly Leu Gly Val Gly Tyr Ala Gly Gly Leu Gly Val Leu Ile Leu Cys
              25 30 35

tta ttt ttg ggg cta aat ccg ggc aaa atc cct ttt gat gtg att tta 198
Leu Phe Leu Gly Leu Asn Pro Gly Lys Ile Pro Phe Asp Val Ile Leu
              40 45 50

atc atc atg gca gtc att agc gct att agc gcg atg caa aaa gcg ggg 246
Ile Ile Met Ala Val Ile Ser Ala Ile Ser Ala Met Gln Lys Ala Gly
              55 60 65 70

ggc ttg gat tac tta gtc aaa atc gct gaa aaa att tta agg aaa cac 294
Gly Leu Asp Tyr Leu Val Lys Ile Ala Glu Lys Ile Leu Arg Lys His
              75 80 85

ccc aag caa atc aat tac ctt gcg cca agc gtg gcg tat tgt tta acg 342
Pro Lys Gln Ile Asn Tyr Leu Ala Pro Ser Val Ala Tyr Cys Leu Thr
              90 95 100

ata cta gcc ggc acc ggg cat acg gtt ttt tcc ttg atc ccg gtg att 390
Ile Leu Ala Gly Thr Gly His Thr Val Phe Ser Leu Ile Pro Val Ile
              105 110 115

gtg gaa gtg agc cag agc caa aac atc aag cct aaa gcg cct tta agc 438
Val Glu Val Ser Gln Ser Gln Asn Ile Lys Pro Lys Ala Pro Leu Ser
              120 125 130

tta gcg gta gtc tct agt caa gtc gct att act gca agc ccg gtg agc 486
Leu Ala Val Val Ser Ser Gln Val Ala Ile Thr Ala Ser Pro Val Ser
              135 140 145 150

gca gcg gtn ggt gtt tat gag cgg cat ttt aga gcc ttt agg agc aaa 534
Ala Ala Val Gly Val Tyr Glu Arg His Phe Arg Ala Phe Arg Ser Lys
              155 160 165

tta ctt gac cct ttt aat ggt ttg gat ccc tac gac ttt ttt agc atg 582
Leu Leu Asp Pro Phe Asn Gly Leu Asp Pro Tyr Asp Phe Phe Ser Met
              170 175 180

cat gct cac ggc att tat tat ggg ttt tac tgatttgaaa ttagacagcg 632
His Ala His Gly Ile Tyr Tyr Gly Phe Tyr
              185 190

atccgcatta ttagagcgc ttgaaagcgg gcaaaatctc gcccc 678
```

<210> 86

<211> 192
 <212> PRT
 <213> Helicobacter pylori

<220>
 <221> VARIANT
 <222> 153
 <223> Xaa = Any Amino Acid

<400> 86
 Met Val Asp Ala Phe Phe Gln Ile Ala Val Leu Leu Phe Ser Leu Phe
 1 5 10 15
 Leu Gly Ala Arg Leu Gly Gly Leu Gly Val Gly Tyr Ala Gly Gly Leu
 20 25 30
 Gly Val Leu Ile Leu Cys Leu Phe Leu Gly Leu Asn Pro Gly Lys Ile
 35 40 45
 Pro Phe Asp Val Ile Leu Ile Ile Met Ala Val Ile Ser Ala Ile Ser
 50 55 60
 Ala Met Gln Lys Ala Gly Gly Leu Asp Tyr Leu Val Lys Ile Ala Glu
 65 70 75 80
 Lys Ile Leu Arg Lys His Pro Lys Gln Ile Asn Tyr Leu Ala Pro Ser
 85 90 95
 Val Ala Tyr Cys Leu Thr Ile Leu Ala Gly Thr Gly His Thr Val Phe
 100 105 110
 Ser Leu Ile Pro Val Ile Val Glu Val Ser Gln Ser Gln Asn Ile Lys
 115 120 125
 Pro Lys Ala Pro Leu Ser Leu Ala Val Val Ser Ser Gln Val Ala Ile
 130 135 140
 Thr Ala Ser Pro Val Ser Ala Ala Xaa Gly Val Tyr Glu Arg His Phe
 145 150 155 160
 Arg Ala Phe Arg Ser Lys Leu Leu Asp Pro Phe Asn Gly Leu Asp Pro
 165 170 175
 Tyr Asp Phe Phe Ser Met His Ala His Gly Ile Tyr Tyr Gly Phe Tyr
 180 185 190

<210> 87
 <211> 1038
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (22)...(1005)

<400> 87
 aaaactttga tatgagaata a atg gac ttt aaa aat aaa aaa tgg ctt ttt 51
 Met Asp Phe Lys Asn Lys Lys Trp Leu Phe 10
 1 5 10
 cta gcc cct tta gca ggc tat acg gat ttg cct ttc agg agc gtg gtg 99
 Leu Ala Pro Leu Ala Gly Tyr Thr Asp Leu Pro Phe Arg Ser Val Val 25
 15 20 25
 aaa aaa ttt ggc gtg gat gtt acc acg agc gaa atg gtg agc tcg cat 147
 Lys Lys Phe Gly Val Asp Val Thr Thr Ser Glu Met Val Ser Ser His 40
 30 35 40
 tcg ttg gtg tat gcg ttt gat aaa act tct aaa atg ttg gaa aaa tcc 195

Ser	Leu	Val	Tyr	Ala	Phe	Asp	Lys	Thr	Ser	Lys	Met	Leu	Glu	Lys	Ser		
		45					50					55					
cct	tta	gaa	gat	cat	ttc	atg	gcg	caa	att	tca	ggc	tct	aaa	gaa	agc	243	
Pro	Leu	Glu	Asp	His	Phe	Met	Ala	Gln	Ile	Ser	Gly	Ser	Lys	Glu	Ser		
	60					65					70						
gta	gtc	aaa	gaa	gcg	gtg	gag	aaa	atc	aac	gct	tta	gag	cat	gtg	aat	291	
Val	Val	Lys	Glu	Ala	Val	Glu	Lys	Ile	Asn	Ala	Leu	Glu	His	Val	Asn		
	75				80					85					90		
ggg	att	gat	ttt	aat	tgc	ggg	tgt	ccc	gct	cct	aaa	gtg	gct	aat	cat	339	
Gly	Ile	Asp	Phe	Asn	Cys	Gly	Cys	Pro	Ala	Pro	Lys	Val	Ala	Asn	His		
				95				100						105			
ggg	aat	ggg	agt	ggg	tta	ttg	aag	gat	tta	aac	cac	tta	gtg	aag	ctt	387	
Gly	Asn	Gly	Ser	Gly	Leu	Leu	Lys	Asp	Leu	Asn	His	Leu	Val	Lys	Leu		
			110					115					120				
tta	aaa	acc	atc	aga	gaa	aac	act	agt	aaa	aaa	atc	aca	agc	gtg	aaa	435	
Leu	Lys	Thr	Ile	Arg	Glu	Asn	Thr	Ser	Lys	Lys	Ile	Thr	Ser	Val	Lys		
		125					130					135					
gtg	cgt	tta	ggc	ttt	gaa	aag	aaa	atc	cct	aaa	gaa	atc	gct	cat	gcc	483	
Val	Arg	Leu	Gly	Phe	Glu	Lys	Lys	Ile	Pro	Lys	Glu	Ile	Ala	His	Ala		
	140					145					150						
cta	aat	gac	gca	ccg	gtg	gat	tat	gtg	gtg	gtg	cat	ggg	agg	aca	cga	531	
Leu	Asn	Asp	Ala	Pro	Val	Asp	Tyr	Val	Val	Val	His	Gly	Arg	Thr	Arg		
	155				160					165					170		
agc	gat	aaa	tac	caa	aaa	gac	aaa	ata	gat	tac	gaa	agc	atc	gct	tta	579	
Ser	Asp	Lys	Tyr	Gln	Lys	Asp	Lys	Ile	Asp	Tyr	Glu	Ser	Ile	Ala	Leu		
				175					180					185			
atg	aaa	aag	att	tta	aaa	aag	ccg	gtg	ata	gcc	aat	ggc	gaa	att	gac	627	
Met	Lys	Lys	Ile	Leu	Lys	Lys	Pro	Val	Ile	Ala	Asn	Gly	Glu	Ile	Asp		
			190					195					200				
agc	gtg	aaa	aag	gct	ttt	gaa	gtt	tta	caa	atc	act	caa	gcg	gat	ggg	675	
Ser	Val	Lys	Lys	Ala	Phe	Glu	Val	Leu	Gln	Ile	Thr	Gln	Ala	Asp	Gly		
		205					210					215					
cta	atg	ata	ggg	cga	gcg	gcc	tta	aga	gcc	cca	tgg	ata	ttt	tgg	caa	723	
Leu	Met	Ile	Gly	Arg	Ala	Ala	Leu	Arg	Ala	Pro	Trp	Ile	Phe	Trp	Gln		
	220					225					230						
atc	aga	aac	aac	acc	aca	aaa	tta	ccc	gca	gtc	gtg	aaa	aaa	gac	ctg	771	
Ile	Arg	Asn	Asn	Thr	Thr	Lys	Leu	Pro	Ala	Val	Val	Lys	Lys	Asp	Leu		
	235				240					245					250		
gtt	tta	gaa	cat	ttt	gat	aaa	atg	gtg	gag	ttt	tat	ggg	gat	atg	ggg	819	
Val	Leu	Glu	His	Phe	Asp	Lys	Met	Val	Glu	Phe	Tyr	Gly	Asp	Met	Gly		
				255					260					265			
gta	atc	atg	ttt	agg	aaa	aat	ttg	cat	gct	tac	gct	aag	ggc	gaa	atg	867	
Val	Ile	Met	Phe	Arg	Lys	Asn	Leu	His	Ala	Tyr	Ala	Lys	Gly	Glu	Met		
			270					275					280				

caa gcg agc gcg ttt cgt aac tgc gtc aat acc ctt aca gaa ata aag	915
Gln Ala Ser Ala Phe Arg Asn Cys Val Asn Thr Leu Thr Glu Ile Lys	
285 290 295	

agc atg cga gag agc ata gag gaa ttt ttt aat caa gaa atg ttg caa	963
Ser Met Arg Glu Ser Ile Glu Glu Phe Phe Asn Gln Glu Met Leu Gln	
300 305 310	

agt gaa gtg ccg tta tgg gta gaa ttg aat caa aaa agc gtt	1005
Ser Glu Val Pro Leu Trp Val Glu Leu Asn Gln Lys Ser Val	
315 320 325	

tgaaagcgct tgttttttta gccagcttgg ggg	1038
--------------------------------------	------

<210> 88
 <211> 328
 <212> PRT
 <213> Helicobacter pylori

<400> 88																	
Met	Asp	Phe	Lys	Asn	Lys	Lys	Trp	Leu	Phe	Leu	Ala	Pro	Leu	Ala	Gly		
1				5					10					15			
Tyr	Thr	Asp	Leu	Pro	Phe	Arg	Ser	Val	Val	Lys	Lys	Phe	Gly	Val	Asp		
			20					25					30				
Val	Thr	Thr	Ser	Glu	Met	Val	Ser	Ser	His	Ser	Leu	Val	Tyr	Ala	Phe		
			35				40					45					
Asp	Lys	Thr	Ser	Lys	Met	Leu	Glu	Lys	Ser	Pro	Leu	Glu	Asp	His	Phe		
	50					55					60						
Met	Ala	Gln	Ile	Ser	Gly	Ser	Lys	Glu	Ser	Val	Val	Lys	Glu	Ala	Val		
65					70					75					80		
Glu	Lys	Ile	Asn	Ala	Leu	Glu	His	Val	Asn	Gly	Ile	Asp	Phe	Asn	Cys		
			85						90					95			
Gly	Cys	Pro	Ala	Pro	Lys	Val	Ala	Asn	His	Gly	Asn	Gly	Ser	Gly	Leu		
			100					105					110				
Leu	Lys	Asp	Leu	Asn	His	Leu	Val	Lys	Leu	Leu	Lys	Thr	Ile	Arg	Glu		
			115				120					125					
Asn	Thr	Ser	Lys	Lys	Ile	Thr	Ser	Val	Lys	Val	Arg	Leu	Gly	Phe	Glu		
	130					135					140						
Lys	Lys	Ile	Pro	Lys	Glu	Ile	Ala	His	Ala	Leu	Asn	Asp	Ala	Pro	Val		
145					150					155					160		
Asp	Tyr	Val	Val	Val	His	Gly	Arg	Thr	Arg	Ser	Asp	Lys	Tyr	Gln	Lys		
				165					170					175			
Asp	Lys	Ile	Asp	Tyr	Glu	Ser	Ile	Ala	Leu	Met	Lys	Lys	Ile	Leu	Lys		
			180					185					190				
Lys	Pro	Val	Ile	Ala	Asn	Gly	Glu	Ile	Asp	Ser	Val	Lys	Lys	Ala	Phe		
			195				200					205					
Glu	Val	Leu	Gln	Ile	Thr	Gln	Ala	Asp	Gly	Leu	Met	Ile	Gly	Arg	Ala		
	210					215					220						
Ala	Leu	Arg	Ala	Pro	Trp	Ile	Phe	Trp	Gln	Ile	Arg	Asn	Asn	Thr	Thr		
225					230					235					240		
Lys	Leu	Pro	Ala	Val	Val	Lys	Lys	Asp	Leu	Val	Leu	Glu	His	Phe	Asp		
				245					250					255			
Lys	Met	Val	Glu	Phe	Tyr	Gly	Asp	Met	Gly	Val	Ile	Met	Phe	Arg	Lys		
			260					265					270				
Asn	Leu	His	Ala	Tyr	Ala	Lys	Gly	Glu	Met	Gln	Ala	Ser	Ala	Phe	Arg		
		275					280					285					
Asn	Cys	Val	Asn	Thr	Leu	Thr	Glu	Ile	Lys	Ser	Met	Arg	Glu	Ser	Ile		
	290					295					300						
Glu	Glu	Phe	Phe	Asn	Gln	Glu	Met	Leu	Gln	Ser	Glu	Val	Pro	Leu	Trp		

305 310 315 320
Val Glu Leu Asn Gln Lys Ser Val
 325

gaa ata acg cat gtt gat gcg ctc att gga ggg agt caa aaa gcg ttc Glu Ile Thr His Val Asp Ala Leu Ile Gly Gly Ser Gln Lys Ala Phe 175 180 185	581
atg ctg cct cct gcg atg agc cta gtc gca ttg agc cag aat gca att Met Leu Pro Pro Ala Met Ser Leu Val Ala Leu Ser Gln Asn Ala Ile 190 195 200	629
gag cgt ata gaa gaa cgc aat gtg ggg ttt tat ttc aat tta aag agc Glu Arg Ile Glu Glu Arg Asn Val Gly Phe Tyr Phe Asn Leu Lys Ser 205 210 215	677
gaa ttg aaa aac caa agg aat aac acc aca agc tac acc gct cct att Glu Leu Lys Asn Gln Arg Asn Asn Thr Thr Ser Tyr Thr Ala Pro Ile 220 225 230	725
tta cac act tta ggg ttg caa cgc tat ttt gaa ttg gtg caa aat tta Leu His Thr Leu Gly Leu Gln Arg Tyr Phe Glu Leu Val Gln Asn Leu 235 240 245 250	773
ggg ggc ttt gaa gcg ctc tat aga gag act aaa aaa gcc gct ttg gcc Gly Gly Phe Glu Ala Leu Tyr Arg Glu Thr Lys Lys Ala Ala Leu Ala 255 260 265	821
act caa aaa gcc gtt tta gct tta ggt tta aag att ttc cct aaa agc Thr Gln Lys Ala Val Leu Ala Leu Gly Leu Lys Ile Phe Pro Lys Ser 270 275 280	869
cca agc ttg agc atg aca acg att gtt aat gag cat gcc aaa gaa ttg Pro Ser Leu Ser Met Thr Thr Ile Val Asn Glu His Ala Lys Glu Leu 285 290 295	917
aga aac ctt tta aaa gaa aaa tac cag gtg caa ttt gcg ggc ggt caa Arg Asn Leu Leu Lys Glu Lys Tyr Gln Val Gln Phe Ala Gly Gly Gln 300 305 310	965
gag cct tat aaa gat gcg ctc att cgt atc aac cac atg ggg atc att Glu Pro Tyr Lys Asp Ala Leu Ile Arg Ile Asn His Met Gly Ile Ile 315 320 325 330	1013
cct gtt tat aaa agc gct tac gct tta aac gcc cta gag tta gcc cta Pro Val Tyr Lys Ser Ala Tyr Ala Leu Asn Ala Leu Glu Leu Ala Leu 335 340 345	1061
aac gac ttg gat tta agg gaa ttt gat ggc gtg gcg aac gca act ttt Asn Asp Leu Asp Leu Arg Glu Phe Asp Gly Val Ala Asn Ala Thr Phe 350 355 360	1109
tta aag caa tat tat gga att taaggatcac aatgcattat tcctatgaaa Leu Lys Gln Tyr Tyr Gly Ile 365	1160
ccttttttaaa	1170
<210> 90	
<211> 369	
<212> PRT	
<213> Helicobacter pylori	

<400> 90
Met Leu Leu Phe Thr Pro Gly Pro Val Ala Ile Asn Glu Glu Met Arg
1 5 10 15
Thr Ser Phe Ser Gln Pro Met Pro His His Arg Thr Lys Asp Phe Glu
20 25 30
Lys Ile Phe Gln Ser Val Arg Glu Asn Leu Lys Lys Met Thr Gly Leu
35 40 45
Glu Glu Val Leu Leu Leu Ser Ser Gly Thr Gly Ala Met Glu Ala
50 55 60
Ser Val Ile Ser Leu Cys Gln Lys Glu Leu Leu Phe Val Asn Ala Gly
65 70 75 80
Lys Phe Gly Glu Arg Phe Gly Lys Ile Ala Lys Ala His Ser Ile Lys
85 90 95
Ala His Glu Leu Val Tyr Glu Trp Asp Thr Pro Ala Gln Val Asp Glu
100 105 110
Ile Leu Ser Val Leu Lys Ala Asn Pro Asn Ile Asp Ala Phe Cys Ile
115 120 125
Gln Ala Cys Glu Ser Ser Gly Gly Leu Arg His Pro Val Glu Lys Ile
130 135 140
Ala Gln Ala Ile Lys Glu Thr Asn Pro Asn Val Phe Val Ile Val Asp
145 150 155 160
Ala Ile Thr Ala Leu Gly Val Glu Pro Leu Glu Ile Thr His Val Asp
165 170 175
Ala Leu Ile Gly Ser Gln Lys Ala Phe Met Leu Pro Pro Ala Met
180 185 190
Ser Leu Val Ala Leu Ser Gln Asn Ala Ile Glu Arg Ile Glu Glu Arg
195 200 205
Asn Val Gly Phe Tyr Phe Asn Leu Lys Ser Glu Leu Lys Asn Gln Arg
210 215 220
Asn Asn Thr Thr Ser Tyr Thr Ala Pro Ile Leu His Thr Leu Gly Leu
225 230 235 240
Gln Arg Tyr Phe Glu Leu Val Gln Asn Leu Gly Gly Phe Glu Ala Leu
245 250 255
Tyr Arg Glu Thr Lys Lys Ala Ala Leu Ala Thr Gln Lys Ala Val Leu
260 265 270
Ala Leu Gly Leu Lys Ile Phe Pro Lys Ser Pro Ser Leu Ser Met Thr
275 280 285
Thr Ile Val Asn Glu His Ala Lys Glu Leu Arg Asn Leu Leu Lys Glu
290 295 300
Lys Tyr Gln Val Gln Phe Ala Gly Gly Gln Glu Pro Tyr Lys Asp Ala
305 310 315 320
Leu Ile Arg Ile Asn His Met Gly Ile Ile Pro Val Tyr Lys Ser Ala
325 330 335
Tyr Ala Leu Asn Ala Leu Glu Leu Ala Leu Asn Asp Leu Asp Leu Arg
340 345 350
Glu Phe Asp Gly Val Ala Asn Ala Thr Phe Leu Lys Gln Tyr Tyr Gly
355 360 365
Ile

<210> 91
<211> 285
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (46)...(270)

<400> 91
aagaggcatg acagctctta cattgtgata gacgaattag tgggc atg tgg ttg gcg 57
Met Trp Leu Ala
1

atg gcg att agc ggg tta tcg tta gcg ggt gtg atc ttg agt ttt atc 105
Met Ala Ile Ser Gly Leu Ser Leu Ala Gly Val Ile Leu Ser Phe Ile
5 10 15 20

ttt ttt agg atc tat gat att act aaa ccc tca ctc att ggc aag ata 153
Phe Phe Arg Ile Tyr Asp Ile Thr Lys Pro Ser Leu Ile Gly Lys Ile
25 30 35

gat aaa gaa gtt aaa ggg ggc tta ggg gtt gtg gct gat gac gct tta 201
Asp Lys Glu Val Lys Gly Gly Leu Gly Val Val Ala Asp Asp Ala Leu
40 45 50

gcg ggt gtt tta gcc gga ttg agc gcg tta tta gtc atc cat att tta 249
Ala Gly Val Leu Ala Gly Leu Ser Ala Leu Leu Val Ile His Ile Leu
55 60 65

gga ttt ttt aac att aaa ctt taattttaag aaaat 285
Gly Phe Phe Asn Ile Lys Leu
70 75

<210> 92
<211> 75
<212> PRT
<213> Helicobacter pylori

<400> 92
Met Trp Leu Ala Met Ala Ile Ser Gly Leu Ser Leu Ala Gly Val Ile
1 5 10 15
Leu Ser Phe Ile Phe Phe Arg Ile Tyr Asp Ile Thr Lys Pro Ser Leu
20 25 30
Ile Gly Lys Ile Asp Lys Glu Val Lys Gly Gly Leu Gly Val Val Ala
35 40 45
Asp Asp Ala Leu Ala Gly Val Leu Ala Gly Leu Ser Ala Leu Leu Val
50 55 60
Ile His Ile Leu Gly Phe Phe Asn Ile Lys Leu
65 70 75

<210> 93
<211> 1021
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (70)...(957)

<400> 93
aaagatagga ttaaataattt tatttttttta gatgaaaacc atcattttta tttgattgaa 60
gaatccaac atg cat tca aaa tac ttc gct caa atc aaa gaa aaa aaa tta 111
Met His Ser Lys Tyr Phe Ala Gln Ile Lys Glu Lys Lys Leu
1 5 10

cct	ccc	cta	atc	ctc	aca	cac	aat	ggc	ttg	ctt	aaa	aac	tca	ttt	tta	159
Pro	Pro	Leu	Ile	Leu	Thr	His	Asn	Gly	Leu	Leu	Lys	Asn	Ser	Phe	Leu	
15					20				25						30	
ggc	gct	aag	att	ata	gaa	ttg	cct	tta	gtg	atc	aat	ctc	gtg	cat	ggg	207
Gly	Ala	Lys	Ile	Ile	Glu	Leu	Pro	Leu	Val	Ile	Asn	Leu	Val	His	Gly	
			35					40						45		
ggc	gat	ggc	gaa	gat	ggg	aaa	tta	gcg	agc	ttg	tta	gaa	ttt	tat	cgt	255
Gly	Asp	Gly	Glu	Asp	Gly	Lys	Leu	Ala	Ser	Leu	Leu	Glu	Phe	Tyr	Arg	
			50					55					60			
atc	gct	ttt	ata	ggc	cct	agg	att	gaa	gcg	agc	gtg	ctg	agt	tat	aac	303
Ile	Ala	Phe	Ile	Gly	Pro	Arg	Ile	Glu	Ala	Ser	Val	Leu	Ser	Tyr	Asn	
		65					70					75				
aaa	tat	tta	acc	aag	ctt	tac	gcc	aaa	gac	tta	ggg	gta	aag	act	tta	351
Lys	Tyr	Leu	Thr	Lys	Leu	Tyr	Ala	Lys	Asp	Leu	Gly	Val	Lys	Thr	Leu	
	80					85					90					
gat	cat	gtt	ctt	ttg	aat	gaa	aaa	aac	cgc	gct	aac	gcc	ttg	gat	ttg	399
Asp	His	Val	Leu	Leu	Asn	Glu	Lys	Asn	Arg	Ala	Asn	Ala	Leu	Asp	Leu	
95					100				105						110	
atg	aac	ttt	aat	ttc	cct	ttc	ata	atc	aag	cct	aat	aac	gcc	gga	agc	447
Met	Asn	Phe	Asn	Phe	Pro	Phe	Ile	Ile	Lys	Pro	Asn	Asn	Ala	Gly	Ser	
				115					120					125		
tct	tta	ggg	gtg	aat	gtt	gtg	aaa	gaa	gaa	aaa	gaa	ttg	gtt	tac	gct	495
Ser	Leu	Gly	Val	Asn	Val	Val	Lys	Glu	Glu	Lys	Glu	Leu	Val	Tyr	Ala	
			130					135					140			
tta	gac	ggc	gag	ttt	gaa	tat	tct	aaa	gag	gtc	ttg	ata	gag	cct	ttc	543
Leu	Asp	Gly	Ala	Phe	Glu	Tyr	Ser	Lys	Glu	Val	Leu	Ile	Glu	Pro	Phe	
		145					150					155				
att	cag	gga	gtg	aaa	gaa	tac	aat	ttg	gcc	ggt	tgc	aag	atc	aaa	aag	591
Ile	Gln	Gly	Val	Lys	Glu	Tyr	Asn	Leu	Ala	Gly	Cys	Lys	Ile	Lys	Lys	
	160					165					170					
gat	ttt	tgt	ttt	tcc	tat	gtg	gaa	gag	cct	aac	aaa	cag	gaa	ttt	tta	639
Asp	Phe	Cys	Phe	Ser	Tyr	Val	Glu	Glu	Pro	Asn	Lys	Gln	Glu	Phe	Leu	
175					180				185						190	
gat	ttc	aaa	caa	aaa	tat	ttg	gat	ttt	tca	cgc	aat	aaa	gcc	cct	aaa	687
Asp	Phe	Lys	Gln	Lys	Tyr	Leu	Asp	Phe	Ser	Arg	Asn	Lys	Ala	Pro	Lys	
				195					200					205		
gag	aat	ctt	tct	aac	gcc	cta	gaa	gag	caa	tta	aaa	gaa	aat	ttt	aaa	735
Ala	Asn	Leu	Ser	Asn	Ala	Leu	Glu	Glu	Gln	Leu	Lys	Glu	Asn	Phe	Lys	
			210				215						220			
aaa	ctc	tat	aac	gat	ttg	ttt	gat	ggc	gag	atc	att	cgt	tgc	gat	ttt	783
Lys	Leu	Tyr	Asn	Asp	Leu	Phe	Asp	Gly	Ala	Ile	Ile	Arg	Cys	Asp	Phe	
		225				230						235				
ttt	gtc	ata	aaa	aat	gaa	gtg	tat	ctt	aat	gag	atc	aac	ccc	att	cct	831
Phe	Val	Ile	Lys	Asn	Glu	Val	Tyr	Leu	Asn	Glu	Ile	Asn	Pro	Ile	Pro	
	240					245					250					

ggc agt ttg gcc aat tat ttg ttt gat gat ttt aaa aca acg cta gaa 879
 Gly Ser Leu Ala Asn Tyr Leu Phe Asp Asp Phe Lys Thr Thr Leu Glu
 255 260 265 270

aat tta gcg caa tca tta ccc aaa acc cct aag atc caa atc aaa aac 927
 Asn Leu Ala Gln Ser Leu Pro Lys Thr Pro Lys Ile Gln Ile Lys Asn
 275 280 285

tct tat ttg ttg caa atc caa aag aat aag taatggccaa acgcagtatc 977
 Ser Tyr Leu Leu Gln Ile Gln Lys Asn Lys
 290 295

gcttatttgg atagcggtttt tgacatttcc tacactttta taga 1021

<210> 94

<211> 296

<212> PRT

<213> Helicobacter pylori

<400> 94

Met His Ser Lys Tyr Phe Ala Gln Ile Lys Glu Lys Lys Leu Pro Pro
 1 5 10 15
 Leu Ile Leu Thr His Asn Gly Leu Leu Lys Asn Ser Phe Leu Gly Ala
 20 25 30
 Lys Ile Ile Glu Leu Pro Leu Val Ile Asn Leu Val His Gly Gly Asp
 35 40 45
 Gly Glu Asp Gly Lys Leu Ala Ser Leu Leu Glu Phe Tyr Arg Ile Ala
 50 55 60
 Phe Ile Gly Pro Arg Ile Glu Ala Ser Val Leu Ser Tyr Asn Lys Tyr
 65 70 75 80
 Leu Thr Lys Leu Tyr Ala Lys Asp Leu Gly Val Lys Thr Leu Asp His
 85 90 95
 Val Leu Leu Asn Glu Lys Asn Arg Ala Asn Ala Leu Asp Leu Met Asn
 100 105 110
 Phe Asn Phe Pro Phe Ile Ile Lys Pro Asn Asn Ala Gly Ser Ser Leu
 115 120 125
 Gly Val Asn Val Val Lys Glu Glu Lys Glu Leu Val Tyr Ala Leu Asp
 130 135 140
 Gly Ala Phe Glu Tyr Ser Lys Glu Val Leu Ile Glu Pro Phe Ile Gln
 145 150 155 160
 Gly Val Lys Glu Tyr Asn Leu Ala Gly Cys Lys Ile Lys Lys Asp Phe
 165 170 175
 Cys Phe Ser Tyr Val Glu Glu Pro Asn Lys Gln Glu Phe Leu Asp Phe
 180 185 190
 Lys Gln Lys Tyr Leu Asp Phe Ser Arg Asn Lys Ala Pro Lys Ala Asn
 195 200 205
 Leu Ser Asn Ala Leu Glu Glu Gln Leu Lys Glu Asn Phe Lys Lys Leu
 210 215 220
 Tyr Asn Asp Leu Phe Asp Gly Ala Ile Ile Arg Cys Asp Phe Phe Val
 225 230 235 240
 Ile Lys Asn Glu Val Tyr Leu Asn Glu Ile Asn Pro Ile Pro Gly Ser
 245 250 255
 Leu Ala Asn Tyr Leu Phe Asp Asp Phe Lys Thr Thr Leu Glu Asn Leu
 260 265 270
 Ala Gln Ser Leu Pro Lys Thr Pro Lys Ile Gln Ile Lys Asn Ser Tyr
 275 280 285
 Leu Leu Gln Ile Gln Lys Asn Lys
 290 295

```
<210> 95
<211> 686
<212> DNA
<213> Helicobacter pylori
```

<400> 95																
caaagcctat gcgagagtca attccgttgc attttcattt agaggc atg gaa gtc																55
Met Glu Val																
1																
ccc att gaa ggt tta gaa gaa ttg gta gat gaa acg aaa aaa tgc ttg	103															
Pro Ile Glu Gly Leu Glu Glu Leu Val Asp Glu Thr Lys Lys Cys Leu																
5 10 15																
ata gaa gct aag aaa aac aaa caa aac cat ttc ttg ctg att caa aaa	151															
Ile Glu Ala Lys Lys Asn Lys Gln Asn His Phe Leu Leu Ile Gln Lys																
20 25 30 35																
gct aac atc caa gca aga aaa caa gcc atg ata gat gaa agt aaa acc	199															
Ala Asn Ile Gln Ala Arg Lys Gln Ala Met Ile Asp Glu Ser Lys Thr																
40 45 50																
att atc cat gtt gca tca gga gcg gct gga gcg gcc ggg ctt atc ccc	247															
Ile Ile His Val Ala Ser Gly Ala Ala Gly Ala Ala Gly Leu Ile Pro																
55 60 65																
ata ccc ttt agc gat gca ctc gct atc gcg ccc att caa gca gga atg	295															
Ile Pro Phe Ser Asp Ala Leu Ala Ile Ala Pro Ile Gln Ala Gly Met																
70 75 80																
atc tac aaa atg aat gac gct ttt gga atg gat ttg gat aaa tct gta	343															
Ile Tyr Lys Met Asn Asp Ala Phe Gly Met Asp Leu Asp Lys Ser Val																
85 90 95																
gcc gca tca tta atc acc gga ttg tta ggc gta acc gct gtc gcg caa	391															
Ala Ala Ser Leu Ile Thr Gly Leu Leu Gly Val Thr Ala Val Ala Gln																
100 105 110 115																
gtg ggg aga acg ctt gtt aat ggt ttc ctt aaa ttc att cct gtt gtg	439															
Val Gly Arg Thr Leu Val Asn Gly Phe Leu Lys Phe Ile Pro Val Val																
120 125 130																
ggg agt gtt gca ggg ggc aca acc gct gta att atc aca gaa ggc att	487															
Gly Ser Val Ala Gly Gly Thr Thr Ala Val Ile Ile Thr Glu Gly Ile																
135 140 145																
ggg ttt gcg tat ttg aaa gtg cta gaa aag tgc ttt aat gat gag acg	535															
Gly Phe Ala Tyr Leu Lys Val Leu Glu Lys Cys Phe Asn Asp Glu Thr																
150 155 160																
ggc gaa gtc aat ttg cct gat gaa gtt ggc atg ata act tct ctc ttt	583															
Gly Glu Val Asn Leu Pro Asp Glu Val Gly Met Ile Thr Ser Leu Phe																
165 170 175																

aag gag aat tat ctc aac ttg gat aca atc aag aaa tta aca caa 628
 Lys Glu Asn Tyr Leu Asn Leu Asp Thr Ile Lys Lys Leu Thr Gln
 180 185 190

taagattagg gggttatgaaa aacgcatggc attagacaaa aggatttgga tgcatttt 686

<210> 96
 <211> 194
 <212> PRT
 <213> Helicobacter pylori

<400> 96
 Met Glu Val Pro Ile Glu Gly Leu Glu Glu Leu Val Asp Glu Thr Lys
 1 5 10 15
 Lys Cys Leu Ile Glu Ala Lys Lys Asn Lys Gln Asn His Phe Leu Leu
 20 25 30
 Ile Gln Lys Ala Asn Ile Gln Ala Arg Lys Gln Ala Met Ile Asp Glu
 35 40 45
 Ser Lys Thr Ile Ile His Val Ala Ser Gly Ala Ala Gly Ala Ala Gly
 50 55 60
 Leu Ile Pro Ile Pro Phe Ser Asp Ala Leu Ala Ile Ala Pro Ile Gln
 65 70 75 80
 Ala Gly Met Ile Tyr Lys Met Asn Asp Ala Phe Gly Met Asp Leu Asp
 85 90 95
 Lys Ser Val Ala Ala Ser Leu Ile Thr Gly Leu Leu Gly Val Thr Ala
 100 105 110
 Val Ala Gln Val Gly Arg Thr Leu Val Asn Gly Phe Leu Lys Phe Ile
 115 120 125
 Pro Val Val Gly Ser Val Ala Gly Gly Thr Thr Ala Val Ile Ile Thr
 130 135 140
 Glu Gly Ile Gly Phe Ala Tyr Leu Lys Val Leu Glu Lys Cys Phe Asn
 145 150 155 160
 Asp Glu Thr Gly Glu Val Asn Leu Pro Asp Glu Val Gly Met Ile Thr
 165 170 175
 Ser Leu Phe Lys Glu Asn Tyr Leu Asn Leu Asp Thr Ile Lys Lys Leu
 180 185 190
 Thr Gln

<210> 97
 <211> 900
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (6)...(821)

<400> 97
 agaag atg ggg aag ttt atg aat act ctt aaa aag cat tta gcc ttt atc 50
 Met Gly Lys Phe Met Asn Thr Leu Lys Lys His Leu Ala Phe Ile
 1 5 10 15

att ccc cta gta gcg tta ttg ttt agc ttg gag tgc gtg tta ttt atc 98
 Ile Pro Leu Val Ala Leu Leu Phe Ser Leu Glu Cys Val Leu Phe Ile
 20 25 30

aat caa gcg atc gaa cag aaa gaa aaa aaa ttg att gaa gat tat tcg 146

Asn	Gln	Ala	Ile	Glu	Gln	Lys	Glu	Lys	Lys	Leu	Ile	Glu	Asp	Tyr	Ser	
			35					40					45			
gtc	gtg	ttg	gcc	agc	acg	caa	aaa	tta	aac	ttg	gaa	ttg	ttg	cgt	caa	194
Val	Val	Leu	Ala	Ser	Thr	Gln	Lys	Leu	Asn	Leu	Glu	Leu	Leu	Arg	Gln	
		50					55					60				
aat	ttt	agc	gaa	atc	ata	gcg	tta	aaa	gaa	att	gat	cct	aat	tat	tct	242
Asn	Phe	Ser	Glu	Ile	Ile	Ala	Leu	Lys	Glu	Ile	Asp	Pro	Asn	Tyr	Ser	
	65					70					75					
tta	gaa	cct	ctt	caa	aaa	acc	tta	ggc	ata	gat	ggg	ctt	aag	gaa	tta	290
Leu	Glu	Pro	Leu	Gln	Lys	Thr	Leu	Gly	Ile	Asp	Gly	Leu	Lys	Glu	Leu	
80					85				90						95	
aga	aaa	aat	ttg	ccc	ttt	ttt	tat	tct	tta	caa	ctt	tcc	aca	ttc	ccc	338
Arg	Lys	Asn	Leu	Pro	Phe	Phe	Tyr	Ser	Leu	Gln	Leu	Ser	Thr	Phe	Pro	
				100					105					110		
act	caa	gag	cgt	tta	gaa	aac	att	aaa	gaa	aaa	ttg	ctc	aaa	atc	cct	386
Thr	Gln	Glu	Arg	Leu	Glu	Asn	Ile	Lys	Glu	Lys	Leu	Leu	Lys	Ile	Pro	
			115					120					125			
ggc	gtt	caa	aaa	gtt	gaa	gtc	ttt	gcc	aaa	act	tac	atg	caa	gtg	tat	434
Gly	Val	Gln	Lys	Val	Glu	Val	Phe	Ala	Lys	Thr	Tyr	Met	Gln	Val	Tyr	
		130					135					140				
gat	ctc	ttg	agt	ttt	att	aaa	aca	gcg	gtc	tat	atc	ttt	gcg	tta	gtg	482
Asp	Leu	Leu	Ser	Phe	Ile	Lys	Thr	Ala	Val	Tyr	Ile	Phe	Ala	Leu	Val	
	145					150					155					
gtc	ttt	gtt	tta	tcg	gtt	tta	ttg	atg	ttt	aaa	caa	gtc	cgc	atc	tgg	530
Val	Phe	Val	Leu	Ser	Val	Leu	Leu	Met	Phe	Lys	Gln	Val	Arg	Ile	Trp	
160					165					170					175	
atc	tat	caa	tac	cat	gag	aga	tta	gag	atc	atg	gat	tta	tta	ggg	gct	578
Ile	Tyr	Gln	Tyr	His	Glu	Arg	Leu	Glu	Ile	Met	Asp	Leu	Leu	Gly	Ala	
				180					185					190		
tcg	gtg	tct	ttt	aaa	aac	ggg	ttt	ttg	tat	aaa	ata	gct	tta	atg	gat	626
Ser	Val	Ser	Phe	Lys	Asn	Gly	Phe	Leu	Tyr	Lys	Ile	Ala	Leu	Met	Asp	
			195					200					205			
tct	gta	atc	gct	agt	ttt	tta	gcc	ccc	atg	ctc	atg	ctc	tat	acc	act	674
Ser	Val	Ile	Ala	Ser	Phe	Leu	Ala	Pro	Met	Leu	Met	Leu	Tyr	Thr	Thr	
		210					215					220				
tcg	caa	aaa	ggt	ttt	gaa	aaa	acg	atg	gat	act	ttg	ggt	att	ata	gga	722
Ser	Gln	Lys	Gly	Phe	Glu	Lys	Thr	Met	Asp	Thr	Leu	Gly	Ile	Ile	Gly	
	225					230					235					
ggc	gcg	ttt	gtt	tta	aac	cat	ttt	tta	tgg	gga	ctg	ctt	ttt	agc	ctt	770
Gly	Ala	Phe	Val	Leu	Asn	His	Phe	Leu	Trp	Gly	Leu	Leu	Phe	Ser	Leu	
240					245					250					255	
gtg	gtc	tca	ttt	gtt	tct	gtt	tta	ctt	gta	gct	tgg	agg	act	agg	cat	818
Val	Val	Ser	Phe	Val	Ser	Val	Leu	Leu	Val	Ala	Trp	Arg	Thr	Arg	His	
				260					265					270		

gta taaattaggg gtgtttttgt tagccacctt actatcagct aacacgcaaa 871
Val

aagtgagcga tattgctaaa gatattccaa 900

<210> 98
<211> 272
<212> PRT
<213> Helicobacter pylori

<400> 98
Met Gly Lys Phe Met Asn Thr Leu Lys Lys His Leu Ala Phe Ile Ile
1 5 10 15
Pro Leu Val Ala Leu Leu Phe Ser Leu Glu Cys Val Leu Phe Ile Asn
20 25 30
Gln Ala Ile Glu Gln Lys Glu Lys Leu Ile Glu Asp Tyr Ser Val
35 40 45
Val Leu Ala Ser Thr Gln Lys Leu Asn Leu Glu Leu Leu Arg Gln Asn
50 55 60
Phe Ser Glu Ile Ile Ala Leu Lys Glu Ile Asp Pro Asn Tyr Ser Leu
65 70 75 80
Glu Pro Leu Gln Lys Thr Leu Gly Ile Asp Gly Leu Lys Glu Leu Arg
85 90 95
Lys Asn Leu Pro Phe Phe Tyr Ser Leu Gln Leu Ser Thr Phe Pro Thr
100 105 110
Gln Glu Arg Leu Glu Asn Ile Lys Glu Lys Leu Leu Lys Ile Pro Gly
115 120 125
Val Gln Lys Val Glu Val Phe Ala Lys Thr Tyr Met Gln Val Tyr Asp
130 135 140
Leu Leu Ser Phe Ile Lys Thr Ala Val Tyr Ile Phe Ala Leu Val Val
145 150 155 160
Phe Val Leu Ser Val Leu Leu Met Phe Lys Gln Val Arg Ile Trp Ile
165 170 175
Tyr Gln Tyr His Glu Arg Leu Glu Ile Met Asp Leu Leu Gly Ala Ser
180 185 190
Val Ser Phe Lys Asn Gly Phe Leu Tyr Lys Ile Ala Leu Met Asp Ser
195 200 205
Val Ile Ala Ser Phe Leu Ala Pro Met Leu Met Leu Tyr Thr Thr Ser
210 215 220
Gln Lys Gly Phe Glu Lys Thr Met Asp Thr Leu Gly Ile Ile Gly Gly
225 230 235 240
Ala Phe Val Leu Asn His Phe Leu Trp Gly Leu Leu Phe Ser Leu Val
245 250 255
Val Ser Phe Val Ser Val Leu Leu Val Ala Trp Arg Thr Arg His Val
260 265 270

<210> 99
<211> 701
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (1)...(672)

<400> 99
agg ttg tct gaa ccc ata gat aga ttc acg cgc ata agg tgg ttg ttt 48

Arg	Leu	Ser	Glu	Pro	Ile	Asp	Arg	Phe	Thr	Arg	Ile	Arg	Trp	Leu	Phe																		
1				5					10					15																			
aaa	aac	gat	ttt	gaa	aaa	atc	cgc	caa	caa	agg	gtt	tta	atc	tgt	ggc	96																	
Lys	Asn	Asp	Phe	Glu	Lys	Ile	Arg	Gln	Gln	Arg	Val	Leu	Ile	Cys	Gly																		
			20					25					30																				
gtg	ggg	ggc	gtt	ggg	ggc	ttt	gcg	cta	gac	gct	ttg	tat	cgt	gtg	ggg	144																	
Val	Gly	Gly	Val	Gly	Gly	Phe	Ala	Leu	Asp	Ala	Leu	Tyr	Arg	Val	Gly																		
		35					40					45																					
ata	ggg	caa	atc	act	atc	att	gat	aaa	gac	gtg	ttt	gat	ggt	acc	aat	192																	
Ile	Gly	Gln	Ile	Thr	Ile	Ile	Asp	Lys	Asp	Val	Phe	Asp	Val	Thr	Asn																		
	50					55					60																						
caa	aac	cgc	cag	att	ggc	tca	gaa	agg	ata	gga	gaa	tct	aaa	gtg	ttg	240																	
Gln	Asn	Arg	Gln	Ile	Gly	Ser	Glu	Arg	Ile	Gly	Glu	Ser	Lys	Val	Leu																		
65					70					75					80																		
gtg	ttg	caa	gat	ctc	tat	aag	ggc	att	caa	gct	ttg	aac	ttg	cat	ata	288																	
Val	Leu	Gln	Asp	Leu	Tyr	Lys	Gly	Ile	Gln	Ala	Leu	Asn	Leu	His	Ile																		
				85					90					95																			
gat	gaa	gcg	ttt	tta	aat	tca	ttt	aat	ttt	aga	gat	tat	gat	tac	att	336																	
Asp	Glu	Ala	Phe	Leu	Asn	Ser	Phe	Asn	Phe	Arg	Asp	Tyr	Asp	Tyr	Ile																		
			100					105					110																				
tta	gat	tgc	atg	gac	gat	ttg	cct	att	aaa	aca	agc	tta	gcg	ata	aaa	384																	
Leu	Asp	Cys	Met	Asp	Asp	Leu	Pro	Ile	Lys	Thr	Ser	Leu	Ala	Ile	Lys																		
		115					120					125																					
tgc	cag	aat	ttc	gct	tac	gga	aaa	ttt	atc	agc	tct	atg	ggg	agt	gcg	432																	
Cys	Gln	Asn	Phe	Ala	Tyr	Gly	Lys	Phe	Ile	Ser	Ser	Met	Gly	Ser	Ala																		
	130					135					140																						
aaa	cgc	ttg	aac	cct	aaa	cac	atc	caa	gtg	ggg	agc	gtg	tgg	gaa	agc	480																	
Lys	Arg	Leu	Asn	Pro	Lys	His	Ile	Gln	Val	Gly	Ser	Val	Trp	Glu	Ser																		
145					150					155					160																		
tat	ggc	gat	aaa	ttc	ggg	cgt	aaa	ttt	agg	gat	ttt	tta	aaa	aaa	cgc	528																	
Tyr	Gly	Asp	Lys	Phe	Gly	Arg	Lys	Phe	Arg	Asp	Phe	Leu	Lys	Lys	Arg																		
				165					170					175																			
cgt	ttt	aaa	ggg	gat	ttt	aaa	gtg	gtt	ttt	agc	cct	gaa	att	ccg	cat	576																	
Arg	Phe	Lys	Gly	Asp	Phe	Lys	Val	Val	Phe	Ser	Pro	Glu	Ile	Pro	His																		
			180					185					190																				
tgc	ata	gag	ctt	ggg	agt	ttt	aat	gcg	gtt	acg	gcg	agt	ttt	ggt	ttg	624																	
Cys	Ile	Glu	Leu	Gly	Ser	Phe	Asn	Ala	Val	Thr	Ala	Ser	Phe	Gly	Leu																		
		195					200					205																					
caa	ata	gcg	agt	gaa	gtc	gtg	caa	gac	att	atc	aac	gat	aaa	agg	aag	672																	
Gln	Ile	Ala	Ser	Glu	Val	Val	Gln	Asp	Ile	Ile	Asn	Asp	Lys	Arg	Lys																		
	210					215					220																						
tgagatgaaa	gattacgaag acgaattgg																701																
<210> 100																																	
<211> 224																																	

<212> PRT

<213> Helicobacter pylori

<400> 100

```
Arg Leu Ser Glu Pro Ile Asp Arg Phe Thr Arg Ile Arg Trp Leu Phe
 1      5      10      15
Lys Asn Asp Phe Glu Lys Ile Arg Gln Arg Val Leu Ile Cys Gly
 20      25      30
Val Gly Gly Val Gly Gly Phe Ala Leu Asp Ala Leu Tyr Arg Val Gly
 35      40      45
Ile Gly Gln Ile Thr Ile Ile Asp Lys Asp Val Phe Asp Val Thr Asn
 50      55      60
Gln Asn Arg Gln Ile Gly Ser Glu Arg Ile Gly Glu Ser Lys Val Leu
 65      70      75      80
Val Leu Gln Asp Leu Tyr Lys Gly Ile Gln Ala Leu Asn Leu His Ile
 85      90      95
Asp Glu Ala Phe Leu Asn Ser Phe Asn Phe Arg Asp Tyr Asp Tyr Ile
100      105      110
Leu Asp Cys Met Asp Asp Leu Pro Ile Lys Thr Ser Leu Ala Ile Lys
115      120      125
Cys Gln Asn Phe Ala Tyr Gly Lys Phe Ile Ser Ser Met Gly Ser Ala
130      135      140
Lys Arg Leu Asn Pro Lys His Ile Gln Val Gly Ser Val Trp Glu Ser
145      150      155      160
Tyr Gly Asp Lys Phe Gly Arg Lys Phe Arg Asp Phe Leu Lys Lys Arg
165      170      175
Arg Phe Lys Gly Asp Phe Lys Val Val Phe Ser Pro Glu Ile Pro His
180      185      190
Cys Ile Glu Leu Gly Ser Phe Asn Ala Val Thr Ala Ser Phe Gly Leu
195      200      205
Gln Ile Ala Ser Glu Val Val Gln Asp Ile Ile Asn Asp Lys Arg Lys
210      215      220
```

<210> 101

<211> 1260

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (73)...(1236)

<400> 101

```
ctctcggttt tttttgtggg taagatttcg caccatcaca ttgtggcttt aggggtgggc 60
ttgcaatttt tg atg ctt ttt tat ggc atc aac acg att tta tac acc ggc 111
      Met Leu Phe Tyr Gly Ile Asn Thr Ile Leu Tyr Thr Gly
      1      5      10

act aac gcc att ctt tct agg ctt gtg ggg gct agg gat ttt act caa 159
Thr Asn Ala Ile Leu Ser Arg Leu Val Gly Ala Arg Asp Phe Thr Gln
      15      20      25

atc aac cac gct ttt tcc agt att ttc ata ggg gct ttt atg atc tgt 207
Ile Asn His Ala Phe Ser Ser Ile Phe Ile Gly Ala Phe Met Ile Cys
      30      35      40      45

ttg ggc gtg ctg ttt gtt tct tat ttt ttg att gag cct ttt tta aat 255
Leu Gly Val Leu Phe Val Ser Tyr Phe Leu Ile Glu Pro Phe Leu Asn
```

50					55					60						
tgg	atg	caa	tta	caa	gat	cct	tcg	cgc	caa	ttg	acg	caa	gat	tat	tta	303
Trp	Met	Gln	Leu	Gln	Asp	Pro	Ser	Arg	Gln	Leu	Thr	Gln	Asp	Tyr	Leu	
		65						70					75			
gaa	gtc	tta	gtt	gta	gcg	cta	ccg	agt	att	ttt	tta	aaa	aat	att	tta	351
Glu	Val	Leu	Val	Val	Ala	Leu	Pro	Ser	Ile	Phe	Leu	Lys	Asn	Ile	Leu	
		80					85					90				
gtt	tca	gcg	ctc	gct	agt	ttt	tca	gac	acc	cta	acc	ccc	ttt	att	gtc	399
Val	Ser	Ala	Leu	Ala	Ser	Phe	Ser	Asp	Thr	Leu	Thr	Pro	Phe	Ile	Val	
	95					100					105					
aaa	atc	atc	atg	gtc	att	gca	tgc	att	ttt	ttg	aat	caa	gcc	ttg	att	447
Lys	Ile	Ile	Met	Val	Ile	Ala	Cys	Ile	Phe	Leu	Asn	Gln	Ala	Leu	Ile	
110					115					120					125	
ttt	ggg	gat	ttt	ggt	ttt	aaa	gaa	atg	ggg	att	gta	ggc	tct	gct	tta	495
Phe	Gly	Asp	Phe	Gly	Phe	Lys	Glu	Met	Gly	Ile	Val	Gly	Ser	Ala	Leu	
			130						135					140		
gcg	aat	gtg	gtt	gtc	tct	tat	ttg	gaa	tta	ctc	gca	ctt	ggc	gtt	tgg	543
Ala	Asn	Val	Val	Val	Ser	Tyr	Leu	Glu	Leu	Leu	Ala	Leu	Gly	Val	Trp	
			145					150					155			
ata	caa	atc	aaa	aaa	atc	cct	tta	aaa	ttc	aaa	ata	acc	ttt	cat	ttt	591
Ile	Gln	Ile	Lys	Lys	Ile	Pro	Leu	Lys	Phe	Lys	Ile	Thr	Phe	His	Phe	
		160					165					170				
tct	ttt	tta	aaa	acc	atg	ttt	aga	gtg	ggt	tgg	cca	gcc	ggg	ttt	gag	639
Ser	Phe	Leu	Lys	Thr	Met	Phe	Arg	Val	Gly	Trp	Pro	Ala	Gly	Phe	Glu	
	175					180					185					
cgc	tta	ttg	agt	tta	ttt	tct	tta	atc	ctc	tta	tcc	aaa	ttt	gta	gcg	687
Arg	Leu	Leu	Ser	Leu	Phe	Ser	Leu	Ile	Leu	Leu	Ser	Lys	Phe	Val	Ala	
190					195					200					205	
agc	tat	ggg	gat	aaa	gtg	tta	gcg	ggc	atg	caa	ata	ggc	att	agg	gtt	735
Ser	Tyr	Gly	Asp	Lys	Val	Leu	Ala	Gly	Met	Gln	Ile	Gly	Ile	Arg	Val	
			210					215					220			
gaa	acc	ttt	tcg	ttc	atg	ccc	gga	ttt	ggg	ttt	atg	atc	gca	gcg	atg	783
Glu	Thr	Phe	Ser	Phe	Met	Pro	Gly	Phe	Gly	Phe	Met	Ile	Ala	Ala	Met	
			225				230						235			
gtt	tta	aca	ggg	caa	aat	tta	ggg	gca	aac	aag	cca	aag	atc	gcc	aca	831
Val	Leu	Thr	Gly	Gln	Asn	Leu	Gly	Ala	Asn	Lys	Pro	Lys	Ile	Ala	Thr	
		240					245					250				
gaa	tac	gcg	cat	ttg	att	tta	aaa	atc	tct	atg	ggt	tta	atg	ggg	gtt	879
Glu	Tyr	Ala	His	Leu	Ile	Leu	Lys	Ile	Ser	Met	Gly	Leu	Met	Gly	Val	
	255					260					265					
tta	ggg	att	gtt	tta	gtc	tta	ttc	gct	aaa	gaa	ttt	gcg	agc	ctt	ttt	927
Leu	Gly	Ile	Val	Leu	Val	Leu	Phe	Ala	Lys	Glu	Phe	Ala	Ser	Leu	Phe	
270					275					280					285	
tct	caa	gat	gaa	gaa	gtc	ttg	gaa	gtg	gcg	cga	tct	tat	ttg	atc	gct	975

Ser	Gln	Asp	Glu	Glu	Val	Leu	Glu	Val	Ala	Arg	Ser	Tyr	Leu	Ile	Ala		
				290					295					300			
gtg	ggc	ctc	tct	caa	gcc	ccc	tta	att	ggg	tat	ttt	gtg	cta	gat	gga	1023	
Val	Gly	Leu	Ser	Gln	Ala	Pro	Leu	Ile	Gly	Tyr	Phe	Val	Leu	Asp	Gly		
			305					310					315				
gtt	ttt	aga	ggg	gct	ggc	att	tct	aaa	gtc	tca	ctg	tat	att	aac	acc	1071	
Val	Phe	Arg	Gly	Ala	Gly	Ile	Ser	Lys	Val	Ser	Leu	Tyr	Ile	Asn	Thr		
		320					325					330					
cta	agc	tta	tgg	ggg	tta	agg	atc	atg	ccc	att	tac	ttg	ctt	tta	att	1119	
Leu	Ser	Leu	Trp	Gly	Leu	Arg	Ile	Met	Pro	Ile	Tyr	Leu	Leu	Leu	Ile		
	335					340					345						
cat	cat	ttt	aag	gtg	gaa	ttt	att	ttt	gta	gtg	atc	gca	tca	gaa	act	1167	
His	His	Phe	Lys	Val	Glu	Phe	Ile	Phe	Val	Val	Ile	Ala	Ser	Glu	Thr		
350					355				360						365		
ttt	ttg	cgc	tca	ttc	atc	tat	tat	aaa	ggt	ttt	tct	aaa	ggc	att	tgg	1215	
Phe	Leu	Arg	Ser	Phe	Ile	Tyr	Tyr	Lys	Val	Phe	Ser	Lys	Gly	Ile	Trp		
				370				375						380			
aaa	agg	tgc	ggg	aaa	aag	gct	tgattattgc	ttgagcgtag	cggt							1260	
Lys	Arg	Cys	Gly	Lys	Lys	Ala											
			385														

<210> 102

<211> 388

<212> PRT

<213> Helicobacter pylori

<400> 102

Met	Leu	Phe	Tyr	Gly	Ile	Asn	Thr	Ile	Leu	Tyr	Thr	Gly	Thr	Asn	Ala		
1				5					10					15			
Ile	Leu	Ser	Arg	Leu	Val	Gly	Ala	Arg	Asp	Phe	Thr	Gln	Ile	Asn	His		
			20					25				30					
Ala	Phe	Ser	Ser	Ile	Phe	Ile	Gly	Ala	Phe	Met	Ile	Cys	Leu	Gly	Val		
		35				40						45					
Leu	Phe	Val	Ser	Tyr	Phe	Leu	Ile	Glu	Pro	Phe	Leu	Asn	Trp	Met	Gln		
	50					55					60						
Leu	Gln	Asp	Pro	Ser	Arg	Gln	Leu	Thr	Gln	Asp	Tyr	Leu	Glu	Val	Leu		
65					70				75						80		
Val	Val	Ala	Leu	Pro	Ser	Ile	Phe	Leu	Lys	Asn	Ile	Leu	Val	Ser	Ala		
			85					90						95			
Leu	Ala	Ser	Phe	Ser	Asp	Thr	Leu	Thr	Pro	Phe	Ile	Val	Lys	Ile	Ile		
		100					105					110					
Met	Val	Ile	Ala	Cys	Ile	Phe	Leu	Asn	Gln	Ala	Leu	Ile	Phe	Gly	Asp		
		115					120					125					
Phe	Gly	Phe	Lys	Glu	Met	Gly	Ile	Val	Gly	Ser	Ala	Leu	Ala	Asn	Val		
	130					135				140							
Val	Val	Ser	Tyr	Leu	Glu	Leu	Leu	Ala	Leu	Gly	Val	Trp	Ile	Gln	Ile		
145					150				155						160		
Lys	Lys	Ile	Pro	Leu	Lys	Phe	Lys	Ile	Thr	Phe	His	Phe	Ser	Phe	Leu		
			165					170						175			
Lys	Thr	Met	Phe	Arg	Val	Gly	Trp	Pro	Ala	Gly	Phe	Glu	Arg	Leu	Leu		
		180					185						190				
Ser	Leu	Phe	Ser	Leu	Ile	Leu	Leu	Ser	Lys	Phe	Val	Ala	Ser	Tyr	Gly		

		195					200				205					
Asp	Lys	Val	Leu	Ala	Gly	Met	Gln	Ile	Gly	Ile	Arg	Val	Glu	Thr	Phe	
210						215					220					
Ser	Phe	Met	Pro	Gly	Phe	Gly	Phe	Met	Ile	Ala	Ala	Met	Val	Leu	Thr	
225					230					235					240	
Gly	Gln	Asn	Leu	Gly	Ala	Asn	Lys	Pro	Lys	Ile	Ala	Thr	Glu	Tyr	Ala	
				245					250					255		
His	Leu	Ile	Leu	Lys	Ile	Ser	Met	Gly	Leu	Met	Gly	Val	Leu	Gly	Ile	
			260					265					270			
Val	Leu	Val	Leu	Phe	Ala	Lys	Glu	Phe	Ala	Ser	Leu	Phe	Ser	Gln	Asp	
		275					280					285				
Glu	Glu	Val	Leu	Glu	Val	Ala	Arg	Ser	Tyr	Leu	Ile	Ala	Val	Gly	Leu	
290						295					300					
Ser	Gln	Ala	Pro	Leu	Ile	Gly	Tyr	Phe	Val	Leu	Asp	Gly	Val	Phe	Arg	
305					310					315					320	
Gly	Ala	Gly	Ile	Ser	Lys	Val	Ser	Leu	Tyr	Ile	Asn	Thr	Leu	Ser	Leu	
				325				330					335			
Trp	Gly	Leu	Arg	Ile	Met	Pro	Ile	Tyr	Leu	Leu	Leu	Ile	His	His	Phe	
		340					345						350			
Lys	Val	Glu	Phe	Ile	Phe	Val	Val	Ile	Ala	Ser	Glu	Thr	Phe	Leu	Arg	
		355					360					365				
Ser	Phe	Ile	Tyr	Tyr	Lys	Val	Phe	Ser	Lys	Gly	Ile	Trp	Lys	Arg	Cys	
370						375					380					
Gly	Lys	Lys	Ala													
385																

<210> 103
 <211> 1327
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (22)...(1305)

<221> misc_feature
 <222> 71
 <223> n = A,T,C or G

<400> 103																	
taaacatcta	aaggataaaa	c	atg	cca	ttg	cca	ttt	att	ata	gca	gct	gga				51	
			Met	Pro	Leu	Pro	Phe	Ile	Ile	Ala	Ala	Gly					
			1				5					10					
gtg gcc tta	gtg gcc gca	gna	tac	gga	ggt	aaa	aaa	aaa	ggt	gat	gca					99	
Val Ala Leu	Val Ala Ala	Xaa	Tyr	Gly	Val	Lys	Lys	Lys	Val	Asp	Ala						
			15				20				25						
gac att ctc	agt gaa gag	acc	aat	gaa	tat	att	aag	tat	atc	aat	gaa					147	
Asp Ile Leu	Ser Glu Glu	Thr	Asn	Glu	Tyr	Ile	Lys	Tyr	Ile	Asn	Glu						
			30				35				40						
ggc aat gac	ttg cta gag	gaa	gca	gaa	gaa	ggt	att	aaa	gct	gtg	gct					195	
Gly Asn Asp	Leu Leu Glu	Glu	Ala	Glu	Glu	Val	Ile	Lys	Ala	Val	Ala						
			45				50				55						
tct gat tgt	gag ttt gct	ctt	gcg	aga	ttt	gaa	gag	aaa	agg	tgc	tat					243	
Ser Asp Cys	Glu Phe Ala	Leu	Ala	Arg	Phe	Glu	Glu	Lys	Arg	Cys	Tyr						

60	65	70	
att aga aat cat gta att tca gaa ttt ttg cac cat ttt aat caa tta			291
Ile Arg Asn His Val Ile Ser Glu Phe Leu His His Phe Asn Gln Leu			
75	80	85	90
gaa gga ttc gag ctt acc aac aaa aaa gat agc atg gaa aat atc caa			339
Glu Gly Phe Glu Leu Thr Asn Lys Lys Asp Ser Met Glu Asn Ile Gln			
	95	100	105
ctc gat gta tca aat aca cta aaa att att gat aaa aat ctc aag atg			387
Leu Asp Val Ser Asn Thr Leu Lys Ile Ile Asp Lys Asn Leu Lys Met			
	110	115	120
agc tct ttt gac acc ctt ggt gcc gtt gga aat gtt gtg gga ggt ttt			435
Ser Ser Phe Asp Thr Leu Gly Ala Val Gly Asn Val Val Gly Gly Phe			
	125	130	135
tct atg gga ttt ggt ttg gct gct gga ggt ata gtt gga agt gta ggg			483
Ser Met Gly Phe Gly Leu Ala Ala Gly Gly Ile Val Gly Ser Val Gly			
	140	145	150
ctt tta gcc gga ccc aca ctc gct att ttt gga gct ttg aga gct gct			531
Leu Leu Ala Gly Pro Thr Leu Ala Ile Phe Gly Ala Leu Arg Ala Ala			
	155	160	170
gaa atg gaa aaa aaa tta gaa gat gct aag gct tat tgc tct caa gtt			579
Glu Met Glu Lys Lys Leu Glu Asp Ala Lys Ala Tyr Cys Ser Gln Val			
	175	180	185
gaa gca gcc gtc aaa aaa gcc gat gcg atg att gat aat ctt caa gcc			627
Glu Ala Ala Val Lys Lys Ala Asp Ala Met Ile Asp Asn Leu Gln Ala			
	190	195	200
gtt agg aaa atg gca gat ctt ttc act agg cag atc aca aaa ttt gac			675
Val Arg Lys Met Ala Asp Leu Phe Thr Arg Gln Ile Thr Lys Phe Asp			
	205	210	215
gca ctg ttt ttc tcg ctt gct caa gag gca atc gcc acg atg aaa aag			723
Ala Leu Phe Phe Ser Leu Ala Gln Glu Ala Ile Ala Thr Met Lys Lys			
	220	225	230
cac aac tac gat ttt tcg cat tac aat caa aaa gaa caa gat cag cta			771
His Asn Tyr Asp Phe Ser His Tyr Asn Gln Lys Glu Gln Asp Gln Leu			
	235	240	245
gct act gct tct tca acc ctt aaa act ttg ggt gct ttt ttg aaa gtg			819
Ala Thr Ala Ser Ser Thr Leu Lys Thr Leu Gly Ala Phe Leu Lys Val			
	255	260	265
cct atc atg gac aaa cac caa aag ctc aat gaa gct aca caa agt aag			867
Pro Ile Met Asp Lys His Gln Lys Leu Asn Glu Ala Thr Gln Ser Lys			
	270	275	280
cta gag ttt atg caa agg gag atg agt agc cta gaa gct aag cat tat			915
Leu Glu Phe Met Gln Arg Glu Met Ser Ser Leu Glu Ala Lys His Tyr			
	285	290	295
gat tca gtt aaa atc aaa ttt gga ttg gta cgc aga tta ttt gaa ttt			963

Asp	Ser	Val	Lys	Ile	Lys	Phe	Gly	Leu	Val	Arg	Arg	Leu	Phe	Glu	Phe		
300						305					310						
ttt	aga	tcg	ctt	tgg	gga	aaa	aat	gga	aga	atc	caa	aga	gcg	aaa	aca	1011	
Phe	Arg	Ser	Leu	Trp	Gly	Lys	Asn	Gly	Arg	Ile	Gln	Arg	Ala	Lys	Thr		
315					320					325					330		
act	cct	gat	cgc	ttc	cct	tgc	acc	tct	tgc	ggg	ctt	tgc	tgc	aag	aat	1059	
Thr	Pro	Asp	Arg	Phe	Pro	Cys	Thr	Ser	Cys	Gly	Leu	Cys	Cys	Lys	Asn		
				335					340					345			
atc	gcc	ggg	att	att	gag	ctt	att	ggg	ttt	gat	gct	ggc	aat	ggg	gtg	1107	
Ile	Ala	Gly	Ile	Ile	Glu	Leu	Ile	Gly	Phe	Asp	Ala	Gly	Asn	Gly	Val		
			350					355					360				
tgc	aaa	ttt	ttg	gat	tta	gaa	acc	aat	ctg	tgc	aag	att	tat	gaa	tcg	1155	
Cys	Lys	Phe	Leu	Asp	Leu	Glu	Thr	Asn	Leu	Cys	Lys	Ile	Tyr	Glu	Ser		
		365					370					375					
cgc	ccg	tta	att	tgc	agg	att	gat	gaa	gcg	cac	aaa	aag	ctt	tat	ccc	1203	
Arg	Pro	Leu	Ile	Cys	Arg	Ile	Asp	Glu	Ala	His	Lys	Lys	Leu	Tyr	Pro		
	380					385					390						
cac	atc	ccg	ctt	aag	gag	ttt	tat	gcc	aaa	aac	gca	gag	gtt	tgt	aac	1251	
His	Ile	Pro	Leu	Lys	Glu	Phe	Tyr	Ala	Lys	Asn	Ala	Glu	Val	Cys	Asn		
395				400					405					410			
gct	ttg	caa	gaa	gca	aac	cat	atg	gat	aag	agc	ttt	agg	gtt	att	ctt	1299	
Ala	Leu	Gln	Glu	Ala	Asn	His	Met	Asp	Lys	Ser	Phe	Arg	Val	Ile	Leu		
			415					420					425				
aag	aaa	taatttagaa	tttattgtcc	ca												1327	
Lys	Lys																

<210> 104
 <211> 428
 <212> PRT
 <213> Helicobacter pylori

<220>
 <221> VARIANT
 <222> 17
 <223> Xaa = Any Amino Acid

<400> 104																
Met	Pro	Leu	Pro	Phe	Ile	Ile	Ala	Ala	Gly	Val	Ala	Leu	Val	Ala	Ala	
1				5					10					15		
Xaa	Tyr	Gly	Val	Lys	Lys	Lys	Val	Asp	Ala	Asp	Ile	Leu	Ser	Glu	Glu	
			20					25				30				
Thr	Asn	Glu	Tyr	Ile	Lys	Tyr	Ile	Asn	Glu	Gly	Asn	Asp	Leu	Leu	Glu	
	35						40					45				
Glu	Ala	Glu	Glu	Val	Ile	Lys	Ala	Val	Ala	Ser	Asp	Cys	Glu	Phe	Ala	
	50					55				60						
Leu	Ala	Arg	Phe	Glu	Glu	Lys	Arg	Cys	Tyr	Ile	Arg	Asn	His	Val	Ile	
65				70					75					80		
Ser	Glu	Phe	Leu	His	His	Phe	Asn	Gln	Leu	Glu	Gly	Phe	Glu	Leu	Thr	
			85					90						95		

Asn	Lys	Lys	Asp	Ser	Met	Glu	Asn	Ile	Gln	Leu	Asp	Val	Ser	Asn	Thr	
			100					105					110			
Leu	Lys	Ile	Ile	Asp	Lys	Asn	Leu	Lys	Met	Ser	Ser	Phe	Asp	Thr	Leu	
		115					120					125				
Gly	Ala	Val	Gly	Asn	Val	Val	Gly	Gly	Phe	Ser	Met	Gly	Phe	Gly	Leu	
	130					135					140					
Ala	Ala	Gly	Gly	Ile	Val	Gly	Ser	Val	Gly	Leu	Leu	Ala	Gly	Pro	Thr	
145					150					155					160	
Leu	Ala	Ile	Phe	Gly	Ala	Leu	Arg	Ala	Ala	Glu	Met	Glu	Lys	Lys	Leu	
			165					170						175		
Glu	Asp	Ala	Lys	Ala	Tyr	Cys	Ser	Gln	Val	Glu	Ala	Ala	Val	Lys	Lys	
			180					185					190			
Ala	Asp	Ala	Met	Ile	Asp	Asn	Leu	Gln	Ala	Val	Arg	Lys	Met	Ala	Asp	
	195					200						205				
Leu	Phe	Thr	Arg	Gln	Ile	Thr	Lys	Phe	Asp	Ala	Leu	Phe	Phe	Ser	Leu	
	210				215						220					
Ala	Gln	Glu	Ala	Ile	Ala	Thr	Met	Lys	Lys	His	Asn	Tyr	Asp	Phe	Ser	
225					230					235					240	
His	Tyr	Asn	Gln	Lys	Glu	Gln	Asp	Gln	Leu	Ala	Thr	Ala	Ser	Ser	Thr	
			245					250						255		
Leu	Lys	Thr	Leu	Gly	Ala	Phe	Leu	Lys	Val	Pro	Ile	Met	Asp	Lys	His	
		260					265						270			
Gln	Lys	Leu	Asn	Glu	Ala	Thr	Gln	Ser	Lys	Leu	Glu	Phe	Met	Gln	Arg	
	275					280						285				
Glu	Met	Ser	Ser	Leu	Glu	Ala	Lys	His	Tyr	Asp	Ser	Val	Lys	Ile	Lys	
	290				295					300						
Phe	Gly	Leu	Val	Arg	Arg	Leu	Phe	Glu	Phe	Phe	Arg	Ser	Leu	Trp	Gly	
305				310					315						320	
Lys	Asn	Gly	Arg	Ile	Gln	Arg	Ala	Lys	Thr	Thr	Pro	Asp	Arg	Phe	Pro	
			325						330					335		
Cys	Thr	Ser	Cys	Gly	Leu	Cys	Cys	Lys	Asn	Ile	Ala	Gly	Ile	Ile	Glu	
		340					345						350			
Leu	Ile	Gly	Phe	Asp	Ala	Gly	Asn	Gly	Val	Cys	Lys	Phe	Leu	Asp	Leu	
	355					360						365				
Glu	Thr	Asn	Leu	Cys	Lys	Ile	Tyr	Glu	Ser	Arg	Pro	Leu	Ile	Cys	Arg	
	370				375						380					
Ile	Asp	Glu	Ala	His	Lys	Lys	Leu	Tyr	Pro	His	Ile	Pro	Leu	Lys	Glu	
385				390						395					400	
Phe	Tyr	Ala	Lys	Asn	Ala	Glu	Val	Cys	Asn	Ala	Leu	Gln	Glu	Ala	Asn	
			405					410						415		
His	Met	Asp	Lys	Ser	Phe	Arg	Val	Ile	Leu	Lys	Lys					
		420					425									

<210> 105

<211> 894

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (30)...(851)

<400> 105

tattaacacc	gttaaagagg	gggtaattc	atg	tta	gaa	aac	atg	caa	gat	att	53
			Met	Leu	Glu	Asn	Met	Gln	Asp	Ile	
			1				5				

tca	ttg	caa	agc	tct	cat	gaa	gta	gga	gtg	gat	att	aca	gag	agc	aaa	101
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Ser	Leu	Gln	Ser	Ser	His	Glu	Val	Gly	Val	Asp	Ile	Thr	Glu	Ser	Lys		
10						15					20						
atg	ctt	aca	aaa	ttt	gca	tcc	tcg	tta	tta	atg	aat	tta	tat	gaa	tat	149	
Met	Leu	Thr	Lys	Phe	Ala	Ser	Ser	Leu	Leu	Met	Asn	Leu	Tyr	Glu	Tyr	40	
25					30					35							
att	gga	aat	ggc	aag	gat	ccc	aaa	gaa	gcg	tcc	gat	cat	gcc	atg	agg	197	
Ile	Gly	Asn	Gly	Lys	Asp	Pro	Lys	Glu	Ala	Ser	Asp	His	Ala	Met	Arg	55	
				45				50									
gat	gca	aag	gat	gtg	gtg	ctt	agt	tgt	ggc	aga	gta	gcc	ttt	ctt	aaa	245	
Asp	Ala	Lys	Asp	Val	Val	Leu	Ser	Cys	Gly	Arg	Val	Ala	Phe	Leu	Lys	70	
			60					65									
gac	ata	gtt	tca	aat	agt	cca	aac	gaa	aca	atc	caa	agt	ttt	gat	gga	293	
Asp	Ile	Val	Ser	Asn	Ser	Pro	Asn	Glu	Thr	Ile	Gln	Ser	Phe	Asp	Gly	85	
		75					80										
gac	tta	gaa	gtt	gca	atg	cat	tta	gaa	aaa	att	ggc	ata	gaa	tgt	tat	341	
Asp	Leu	Glu	Val	Ala	Met	His	Leu	Glu	Lys	Ile	Gly	Ile	Glu	Cys	Tyr	100	
	90					95											
aag	ata	ttt	att	gac	tat	ggc	tct	caa	aag	atc	gat	gat	aat	gag	ctt	389	
Lys	Ile	Phe	Ile	Asp	Tyr	Gly	Ser	Gln	Lys	Ile	Asp	Asp	Asn	Glu	Leu	120	
105					110					115							
tct	tgt	cgt	ttg	tta	cac	act	ggc	acg	aaa	att	tta	ggc	aca	aaa	gct	437	
Ser	Cys	Arg	Leu	Leu	His	Thr	Gly	Thr	Lys	Ile	Leu	Gly	Thr	Lys	Ala	135	
				125					130								
atg	gca	gtt	gtt	ggc	caa	aca	ttc	atc	ccc	att	cct	gga	gtt	gga	gca	485	
Met	Ala	Val	Val	Gly	Gln	Thr	Phe	Ile	Pro	Ile	Pro	Gly	Val	Gly	Ala	150	
			140					145									
ata	att	gga	aat	ttt	gtg	ggc	gca	tta	ctg	agc	aaa	act	ctc	tgt	gaa	533	
Ile	Ile	Gly	Asn	Phe	Val	Gly	Ala	Leu	Leu	Ser	Lys	Thr	Leu	Cys	Glu	165	
		155					160										
aat	ttg	cga	gat	gtt	tta	aaa	gag	gct	aaa	ttg	gca	cgc	caa	agg	cgt	581	
Asn	Leu	Arg	Asp	Val	Leu	Lys	Glu	Ala	Lys	Leu	Ala	Arg	Gln	Arg	Arg	180	
	170					175											
ata	gag	att	gaa	aaa	gaa	tgc	cgt	gaa	agt	att	agg	ctg	tta	gag	atc	629	
Ile	Glu	Ile	Glu	Lys	Glu	Cys	Arg	Glu	Ser	Ile	Arg	Leu	Leu	Glu	Ile	200	
185					190					195							
tat	cgc	aat	caa	ttt	aag	gaa	gtg	ttt	gag	cgc	tat	ttt	cat	ggg	aat	677	
Tyr	Arg	Asn	Gln	Phe	Lys	Glu	Val	Phe	Glu	Arg	Tyr	Phe	His	Gly	Asn	215	
				205					210								
gta	aaa	ttc	ttt	aat	gag	aat	ttt	aat	aat	ctt	gag	agg	gca	ctt	tat	725	
Val	Lys	Phe	Phe	Asn	Glu	Asn	Phe	Asn	Asn	Leu	Glu	Arg	Ala	Leu	Tyr	230	
			220					225									
gca	gga	gat	gca	gat	ttg	gcc	ata	gga	gtc	aat	aat	gag	att	caa	gaa	773	
Ala	Gly	Asp	Ala	Asp	Leu	Ala	Ile	Gly	Val	Asn	Asn	Glu	Ile	Gln	Glu	245	
		235					240										

aga cta ggt caa aaa ccc ttg ttt aat aat acc caa gaa ttt ttg gaa 821
 Arg Leu Gly Gln Lys Pro Leu Phe Asn Asn Thr Gln Glu Phe Leu Glu
 250 255 260

ctc atg aat aat ggt gga aaa ata gaa att taaaggagaa atcatggaag 871
 Leu Met Asn Asn Gly Gly Lys Ile Glu Ile
 265 270

aacaaaagga tatgggtcaa agt 894

<210> 106
 <211> 274
 <212> PRT
 <213> Helicobacter pylori

<400> 106
 Met Leu Glu Asn Met Gln Asp Ile Ser Leu Gln Ser Ser His Glu Val
 1 5 10 15
 Gly Val Asp Ile Thr Glu Ser Lys Met Leu Thr Lys Phe Ala Ser Ser
 20 25 30
 Leu Leu Met Asn Leu Tyr Glu Tyr Ile Gly Asn Gly Lys Asp Pro Lys
 35 40 45
 Glu Ala Ser Asp His Ala Met Arg Asp Ala Lys Asp Val Val Leu Ser
 50 55 60
 Cys Gly Arg Val Ala Phe Leu Lys Asp Ile Val Ser Asn Ser Pro Asn
 65 70 75 80
 Glu Thr Ile Gln Ser Phe Asp Gly Asp Leu Glu Val Ala Met His Leu
 85 90 95
 Glu Lys Ile Gly Ile Glu Cys Tyr Lys Ile Phe Ile Asp Tyr Gly Ser
 100 105 110
 Gln Lys Ile Asp Asp Asn Glu Leu Ser Cys Arg Leu Leu His Thr Gly
 115 120 125
 Thr Lys Ile Leu Gly Thr Lys Ala Met Ala Val Val Gly Gln Thr Phe
 130 135 140
 Ile Pro Ile Pro Gly Val Gly Ala Ile Ile Gly Asn Phe Val Gly Ala
 145 150 155 160
 Leu Leu Ser Lys Thr Leu Cys Glu Asn Leu Arg Asp Val Leu Lys Glu
 165 170 175
 Ala Lys Leu Ala Arg Gln Arg Arg Ile Glu Ile Glu Lys Glu Cys Arg
 180 185 190
 Glu Ser Ile Arg Leu Leu Glu Ile Tyr Arg Asn Gln Phe Lys Glu Val
 195 200 205
 Phe Glu Arg Tyr Phe His Gly Asn Val Lys Phe Phe Asn Glu Asn Phe
 210 215 220
 Asn Asn Leu Glu Arg Ala Leu Tyr Ala Gly Asp Ala Asp Leu Ala Ile
 225 230 235 240
 Gly Val Asn Asn Glu Ile Gln Glu Arg Leu Gly Gln Lys Pro Leu Phe
 245 250 255
 Asn Asn Thr Gln Glu Phe Leu Glu Leu Met Asn Asn Gly Gly Lys Ile
 260 265 270
 Glu Ile

<210> 107
 <211> 1338
 <212> DNA
 <213> Helicobacter pylori

<220>

<221> CDS

<222> (70)...(1281)

<400> 107

cttcattacg cttacgctac aacccttaag atcaccaatg ttgtgccttt tggctctagc 60
agcgttaaa atg gtg ttc aat caa gag gtt aaa aaa ttc aaa gaa gtt tcg 111

Met Val Phe Asn Gln Glu Val Lys Lys Phe Lys Glu Val Ser
1 5 10

ctc aaa aat ttc aag agt tat ttg gaa tta gaa gcc att tta acc att 159
Leu Lys Asn Phe Lys Ser Tyr Leu Glu Leu Glu Ala Ile Leu Thr Ile
15 20 25 30

cct aaa aag cat tac caa ttc tcc aag caa tcg ttc atc acg atc gcg 207
Pro Lys Lys His Tyr Gln Phe Ser Lys Gln Ser Phe Ile Thr Ile Ala
35 40 45

caa ttc agc cct aag tta gtg cga gtg gtt atc ggc tat gct cct aag 255
Gln Phe Ser Pro Lys Leu Val Arg Val Val Ile Gly Tyr Ala Pro Lys
50 55 60

atg act tat gaa gtt aaa atc ctt aaa gac aag ctt tat gtt tct atc 303
Met Thr Tyr Glu Val Lys Ile Leu Lys Asp Lys Leu Tyr Val Ser Ile
65 70 75

gtg gag aaa aag ccc tta att agg cat caa atg gcg tta aaa cca ccc 351
Val Glu Lys Lys Pro Leu Ile Arg His Gln Met Ala Leu Lys Pro Pro
80 85 90

aaa cac cat gca ctc aaa cac aca acg cca aaa ccc gcc cat aag ccc 399
Lys His His Ala Leu Lys His Thr Thr Pro Lys Pro Ala His Lys Pro
95 100 105 110

att aaa aaa gag gct aaa aag gtt aaa gaa aaa acg cca act aaa cat 447
Ile Lys Lys Glu Ala Lys Lys Val Lys Glu Lys Thr Pro Thr Lys His
115 120 125

gcg cat tca aaa cac acg cat tcc cca ttg aac gaa agg agc act aaa 495
Ala His Ser Lys His Thr His Ser Pro Leu Asn Glu Arg Ser Thr Lys
130 135 140

aaa gaa att cct aaa aaa gaa att cct aaa aaa gaa gcg gaa aat gag 543
Lys Glu Ile Pro Lys Lys Glu Ile Pro Lys Lys Glu Ala Glu Asn Glu
145 150 155

agc aag aac caa gtc ttt ata gca gaa aaa aat gat act ttc atc aaa 591
Ser Lys Asn Gln Val Phe Ile Ala Glu Lys Asn Asp Thr Phe Ile Lys
160 165 170

acc aaa cgc aaa aaa cac aaa aag atc gtt tta gac gct ggg cat ggg 639
Thr Lys Arg Lys Lys His Lys Lys Ile Val Leu Asp Ala Gly His Gly
175 180 185 190

ggg aaa gat tgc ggg gcg atg agc gcg aat ttg gtg tgt gaa aaa gac 687
Gly Lys Asp Cys Gly Ala Met Ser Ala Asn Leu Val Cys Glu Lys Asp
195 200 205

att gtt tta gaa gtg gtg aag ttt tta cac aaa gag ctt aaa aaa aga 735

Ile Val Leu Glu Val Val Lys Phe Leu His Lys Glu Leu Lys Lys Arg	
210 215 220	
gat tat agc gtt tta ttg aca agg gat aag gat att tat att gat tta	783
Asp Tyr Ser Val Leu Leu Thr Arg Asp Lys Asp Ile Tyr Ile Asp Leu	
225 230 235	
gtg gct cgc acg gaa tta gcc aat aaa aaa agc gcg gat tta ttc atc	831
Val Ala Arg Thr Glu Leu Ala Asn Lys Lys Ser Ala Asp Leu Phe Ile	
240 245 250	
tca gtg cat gcc aat tcc atc ccc aaa cat tcc act tct aac gct cat	879
Ser Val His Ala Asn Ser Ile Pro Lys His Ser Thr Ser Asn Ala His	
255 260 265 270	
ggg ata gag act tat ttt tta tcc acc gca agg agc gaa agg gct agg	927
Gly Ile Glu Thr Tyr Phe Leu Ser Thr Ala Arg Ser Glu Arg Ala Arg	
275 280 285	
aaa gtg gct gag caa gaa aat aaa gac gat gtg aat tta atg gat tat	975
Lys Val Ala Glu Gln Glu Asn Lys Asp Asp Val Asn Leu Met Asp Tyr	
290 295 300	
ttt tct aaa agt ttg ttt tta aat tca ttg aac acg cag cga ttg atc	1023
Phe Ser Lys Ser Leu Phe Leu Asn Ser Leu Asn Thr Gln Arg Leu Ile	
305 310 315	
gtc tct aac aaa tta gcg att gat gtg caa tac ggc atg ctc caa agc	1071
Val Ser Asn Lys Leu Ala Ile Asp Val Gln Tyr Gly Met Leu Gln Ser	
320 325 330	
gtc cgc aaa aat tac cct gat gtg gtg gat gga ggc gtg aga gag ggg	1119
Val Arg Lys Asn Tyr Pro Asp Val Val Asp Gly Gly Val Arg Glu Gly	
335 340 345 350	
cct ttt tgg gtg ttg gcc ggg gct tta atg cct tca atc tta ata gaa	1167
Pro Phe Trp Val Leu Ala Gly Ala Leu Met Pro Ser Ile Leu Ile Glu	
355 360 365	
att ggt tat aat tcc cat gcg ata gaa tct aaa cgc atc caa agc aaa	1215
Ile Gly Tyr Asn Ser His Ala Ile Glu Ser Lys Arg Ile Gln Ser Lys	
370 375 380	
ccg tat caa aag atc ttg gct aag ggc att gct gat ggc att gat agt	1263
Pro Tyr Gln Lys Ile Leu Ala Lys Gly Ile Ala Asp Gly Ile Asp Ser	
385 390 395	
ttc ttc agc aag aat gat taggcaatga ttaggttgta gatgaatttt	1311
Phe Phe Ser Lys Asn Asp	
400	
tatcaaaaaa tatacactca taaagtc	1338
<210> 108	
<211> 404	
<212> PRT	
<213> Helicobacter pylori	
<400> 108	

```
<210> 109
<211> 1161
<212> DNA
<213> Helicobacter pylori
```

<220>

<221> CDS

<222> (37)...(1125)

<400> 109

tgaaattaa	tattaactaa	tattaaggaa	agagct	atg	gta	tca	aca	ctc	aaa	54
				Met	Val	Ser	Thr	Leu	Lys	
				1				5		
ccg	cta	aaa	atc	ggt	aag	cac	acc	ata	aaa	102
Pro	Leu	Lys	Ile	Gly	Lys	His	Thr	Ile	Lys	
			10					15		
gga	atg	ggt	gtg	ggg	att	agc	tgg	gat	gaa	150
Gly	Met	Gly	Val	Gly	Ile	Ser	Trp	Asp	Glu	
			25				30		35	
aaa	gaa	ggg	gct	tta	gga	gtg	att	tca	gcc	198
Lys	Glu	Gly	Ala	Leu	Gly	Val	Ile	Ser	Ala	
	40					45			50	
aaa	aac	atg	cgt	ttt	gta	gaa	agg	att	gtg	246
Lys	Asn	Met	Arg	Phe	Val	Glu	Arg	Ile	Val	
	55				60				65	
gcc	ttg	aat	ttt	tac	tcc	aaa	aaa	gcg	ttg	294
Ala	Leu	Asn	Phe	Tyr	Ser	Lys	Lys	Ala	Leu	
				75					80	
gct	agg	aag	att	tgc	ggg	aac	aac	cct	tta	342
Ala	Arg	Lys	Ile	Cys	Gly	Asn	Asn	Pro	Leu	
			90					95		
gct	atc	aat	gac	tat	ggc	cgt	gtt	tta	agg	390
Ala	Ile	Asn	Asp	Tyr	Gly	Arg	Val	Leu	Arg	
		105					110			
gcg	aat	atc	att	att	aca	ggg	gct	ggt	ttg	438
Ala	Asn	Ile	Ile	Ile	Thr	Gly	Ala	Gly	Leu	
	120					125			130	
ttc	gct	aag	gat	ttt	agc	gat	gtg	gcg	ctc	486
Phe	Ala	Lys	Asp	Phe	Ser	Asp	Val	Ala	Leu	
	135						140		145	
gcg	aag	gct	tta	aaa	atc	ctt	tgt	aaa	aga	534
Ala	Lys	Ala	Leu	Lys	Ile	Leu	Cys	Lys	Arg	
				155				160		
aga	atc	ccg	gac	gcg	ttc	att	gtg	gaa	ggg	582
Arg	Ile	Pro	Asp	Ala	Phe	Ile	Val	Glu	Gly	
			170					175		
cag	ggc	ttt	aaa	tac	gaa	gat	tgt	ttc	aaa	630
Gln	Gly	Phe	Lys	Tyr	Glu	Asp	Cys	Phe	Lys	
		185					190			
aac	tta	gtg	cct	aaa	gtc	gtg	gaa	gct	tct	678
Asn	Leu	Val	Pro	Lys	Val	Val	Glu	Ala	Ser	

200	205	210	
cct atc atc gcc gct ggg ggg att tgg gat agg aag gat ata gac acc			726
Pro Ile Ile Ala Ala Gly Gly Ile Trp Asp Arg Lys Asp Ile Asp Thr			
215	220	225	230
atg tta agt ctt gga gcg agt ggg gtg cag atg gcg act cgt ttt tta			774
Met Leu Ser Leu Gly Ala Ser Gly Val Gln Met Ala Thr Arg Phe Leu			
	235	240	245
ggc acg aaa gaa tgc gac gct aaa gtg tat gcc gat ctt ttg ccc acg			822
Gly Thr Lys Glu Cys Asp Ala Lys Val Tyr Ala Asp Leu Leu Pro Thr			
	250	255	260
ctc aaa aaa gaa gat att tta ctc att aaa tcg cct gta ggt tat ccg			870
Leu Lys Lys Glu Asp Ile Leu Ile Lys Ser Pro Val Gly Tyr Pro			
	265	270	275
gct agg gct att aat acg gga gtg atc aag cgc att gaa gag ggt aac			918
Ala Arg Ala Ile Asn Thr Gly Val Ile Lys Arg Ile Glu Glu Gly Asn			
	280	285	290
gcg ccc aaa atc gca tgc gtg agc aat tgt gta gcg cct tgc aac agg			966
Ala Pro Lys Ile Ala Cys Val Ser Asn Cys Val Ala Pro Cys Asn Arg			
	295	300	310
ggg gaa gag gct aaa aag gtg ggc tat tgt atc gct gat ggt ttg ggg			1014
Gly Glu Glu Ala Lys Lys Val Gly Tyr Cys Ile Ala Asp Gly Leu Gly			
	315	320	325
cgc agt tat tta ggg aac aga gaa gag ggg ctt tat ttt acc ggg gct			1062
Arg Ser Tyr Leu Gly Asn Arg Glu Glu Gly Leu Tyr Phe Thr Gly Ala			
	330	335	340
aat ggc tat aga gtg gat aag att atc agc gtg cat gaa ttg att aaa			1110
Asn Gly Tyr Arg Val Asp Lys Ile Ile Ser Val His Glu Leu Ile Lys			
	345	350	355
gag ctt aca gag ggt taatttgtag tgcttgtgag gttaggggtt gttgca			1161
Glu Leu Thr Glu Gly			
360			

<210> 110
 <211> 363
 <212> PRT
 <213> Helicobacter pylori

<400> 110
 Met Val Ser Thr Leu Lys Pro Leu Lys Ile Gly Lys His Thr Ile Lys
 1 5 10 15
 Phe Pro Ile Phe Gln Gly Gly Met Gly Val Gly Ile Ser Trp Asp Glu
 20 25 30
 Leu Ala Gly Asn Val Ala Lys Glu Gly Ala Leu Gly Val Ile Ser Ala
 35 40 45
 Val Gly Thr Gly Tyr Tyr Lys Asn Met Arg Phe Val Glu Arg Ile Val
 50 55 60
 Ala Lys Lys Pro Phe Glu Ala Leu Asn Phe Tyr Ser Lys Lys Ala Leu
 65 70 75 80

Asn	Glu	Ile	Phe	Ala	Asn	Ala	Arg	Lys	Ile	Cys	Gly	Asn	Asn	Pro	Leu	
				85					90					95		
Gly	Ala	Asn	Ile	Leu	Tyr	Ala	Ile	Asn	Asp	Tyr	Gly	Arg	Val	Leu	Arg	
			100					105					110			
Asp	Ser	Cys	Glu	Ala	Gly	Ala	Asn	Ile	Ile	Ile	Thr	Gly	Ala	Gly	Leu	
		115					120					125				
Pro	Thr	Asn	Met	Pro	Glu	Phe	Ala	Lys	Asp	Phe	Ser	Asp	Val	Ala	Leu	
		130				135					140					
Ile	Pro	Ile	Ile	Ser	Ser	Ala	Lys	Ala	Leu	Lys	Ile	Leu	Cys	Lys	Arg	
145				150						155					160	
Trp	Ser	Asp	Arg	Tyr	Lys	Arg	Ile	Pro	Asp	Ala	Phe	Ile	Val	Glu	Gly	
			165					170						175		
Pro	Leu	Ser	Gly	Gly	His	Gln	Gly	Phe	Lys	Tyr	Glu	Asp	Cys	Phe	Lys	
			180				185						190			
Glu	Glu	Phe	Arg	Leu	Glu	Asn	Leu	Val	Pro	Lys	Val	Val	Glu	Ala	Ser	
		195					200					205				
Lys	Glu	Trp	Gly	Asn	Ile	Pro	Ile	Ile	Ala	Ala	Gly	Gly	Ile	Trp	Asp	
		210				215					220					
Arg	Lys	Asp	Ile	Asp	Thr	Met	Leu	Ser	Leu	Gly	Ala	Ser	Gly	Val	Gln	
225				230						235					240	
Met	Ala	Thr	Arg	Phe	Leu	Gly	Thr	Lys	Glu	Cys	Asp	Ala	Lys	Val	Tyr	
			245						250					255		
Ala	Asp	Leu	Leu	Pro	Thr	Leu	Lys	Lys	Glu	Asp	Ile	Leu	Leu	Ile	Lys	
		260					265						270			
Ser	Pro	Val	Gly	Tyr	Pro	Ala	Arg	Ala	Ile	Asn	Thr	Gly	Val	Ile	Lys	
		275					280					285				
Arg	Ile	Glu	Glu	Gly	Asn	Ala	Pro	Lys	Ile	Ala	Cys	Val	Ser	Asn	Cys	
		290			295						300					
Val	Ala	Pro	Cys	Asn	Arg	Gly	Glu	Glu	Ala	Lys	Lys	Val	Gly	Tyr	Cys	
305				310						315					320	
Ile	Ala	Asp	Gly	Leu	Gly	Arg	Ser	Tyr	Leu	Gly	Asn	Arg	Glu	Glu	Gly	
			325					330					335			
Leu	Tyr	Phe	Thr	Gly	Ala	Asn	Gly	Tyr	Arg	Val	Asp	Lys	Ile	Ile	Ser	
			340				345						350			
Val	His	Glu	Leu	Ile	Lys	Glu	Leu	Thr	Glu	Gly						
		355					360									

<210> 111
 <211> 2373
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (13)...(2337)

<400> 111
 tagacaggat ag atg aac gaa att gat aaa tcc gtt gat atc gga ttc tta 51
 Met Asn Glu Ile Asp Lys Ser Val Asp Ile Gly Phe Leu
 1 5 10

cgg att ctt gat gtt att aaa aaa gtt acg acc cca aag ggt ggc att 99
 Arg Ile Leu Asp Val Ile Lys Lys Val Thr Thr Pro Lys Gly Gly Ile
 15 20 25

gaa atc tta agg act tta att gat ttt acg ccc aaa att gaa aac gcc 147
 Glu Ile Leu Arg Thr Leu Ile Asp Phe Thr Pro Lys Ile Glu Asn Ala
 30 35 40 45

ctg aat tta gcg gcc aaa agc cat aag ggg caa tac aga aaa agc ggc	195
Leu Asn Leu Ala Ala Lys Ser His Lys Gly Gln Tyr Arg Lys Ser Gly	
50 55 60	
gag cct tat att gtc cat cct att tgc gtg gca agc ttg gta gcg ttt	243
Glu Pro Tyr Ile Val His Pro Ile Cys Val Ala Ser Leu Val Ala Phe	
65 70 75	
tgt ggg ggc gat gag gcg atg gtg tgt gct gcg ctt ttg cat gat gtg	291
Cys Gly Gly Asp Glu Ala Met Val Cys Ala Ala Leu Leu His Asp Val	
80 85 90	
gtg gaa gac acg cct tgt aag att gaa acg att gag caa gaa ttt ggg	339
Val Glu Asp Thr Pro Cys Lys Ile Glu Thr Ile Glu Gln Glu Phe Gly	
95 100 105	
caa gat gtg gct aat tta gtg gat gcg ctc act aaa atc act gaa atc	387
Gln Asp Val Ala Asn Leu Val Asp Ala Leu Thr Lys Ile Thr Glu Ile	
110 115 120 125	
agg aaa gaa gaa tta ggc gtg agc tct caa gat ccc aga atg gtg gtt	435
Arg Lys Glu Glu Leu Gly Val Ser Ser Gln Asp Pro Arg Met Val Val	
130 135 140	
tca gcg ctc act ttc aga aag att tta att agc gcg ata caa gat cca	483
Ser Ala Leu Thr Phe Arg Lys Ile Leu Ile Ser Ala Ile Gln Asp Pro	
145 150 155	
aga gcc tta gtg gta aag att agc gac agg ttg cac aac atg ctc acc	531
Arg Ala Leu Val Val Lys Ile Ser Asp Arg Leu His Asn Met Leu Thr	
160 165 170	
tta gac gcc ttg cct cat gac aag caa gtg cgt att tct aaa gag act	579
Leu Asp Ala Leu Pro His Asp Lys Gln Val Arg Ile Ser Lys Glu Thr	
175 180 185	
cta gcg gtg tat gcc cct ata gcg agc cga ttg ggc atg tct tca atc	627
Leu Ala Val Tyr Ala Pro Ile Ala Ser Arg Leu Gly Met Ser Ser Ile	
190 195 200 205	
aaa aat gaa tta gaa gac aag agc ttt tat tat att tat cca gaa gag	675
Lys Asn Glu Leu Glu Asp Lys Ser Phe Tyr Tyr Ile Tyr Pro Glu Glu	
210 215 220	
tat aaa aat atc aag gaa tat ttg cac aaa aac aag cag tct tta ctc	723
Tyr Lys Asn Ile Lys Glu Tyr Leu His Lys Asn Lys Gln Ser Leu Leu	
225 230 235	
tta aag ctc aac gct ttt gcg agc aag tta gaa aaa aaa ctt ttt gat	771
Leu Lys Leu Asn Ala Phe Ala Ser Lys Leu Glu Lys Lys Leu Phe Asp	
240 245 250	
agt ggg ttt agc cat tcg gat ttt aaa ctc gtt aca agg gtg aaa cgc	819
Ser Gly Phe Ser His Ser Asp Phe Lys Leu Val Thr Arg Val Lys Arg	
255 260 265	
cct tat tct atc tat ctt aag atg caa cga aag ggc gcg gtt aat att	867
Pro Tyr Ser Ile Tyr Leu Lys Met Gln Arg Lys Gly Ala Val Asn Ile	

270	275	280	285	
gat gaa att ttg	gac ttg tta gcc	att agg att tta ttg	aaa aac ccg	915
Asp Glu Ile Leu	Asp Leu Leu Ala	Ile Arg Ile Leu	Lys Asn Pro	
	290	295	300	
att gat tgc tat	aaa gtt tta ggg	att atc cat ttg	aat ttc aaa ccc	963
Ile Asp Cys Tyr	Lys Val Leu Gly	Ile Ile His Leu	Asn Phe Lys Pro	
	305	310	315	
att gtc tct cgt	ttt aaa gat tac	atc gct ttg ccc	aaa gaa aat ggc	1011
Ile Val Ser Arg	Phe Lys Asp Tyr	Ile Ala Leu Pro	Lys Glu Asn Gly	
	320	325	330	
tat aag acg ata	cac acg acc att	ttt gat gaa tct	tct gtt tat gaa	1059
Tyr Lys Thr Ile	His Thr Thr Ile	Phe Asp Glu Ser	Ser Val Tyr Glu	
	335	340	345	
gtg cag atc cgc	acc ttt gat atg	cat atg ggg gcg	gag tat ggt aat	1107
Val Gln Ile Arg	Thr Phe Asp Met	His Met Gly Ala	Glu Tyr Gly Asn	
	350	355	360	365
tca gcc cac tgg	aag tat aaa gcc	ggg ggc gtg gat	cat gaa gat cat	1155
Ser Ala His Trp	Lys Tyr Lys Ala	Gly Gly Val Asp	His Glu Asp His	
	370	375	380	
cat gag ggc atg	aga tgg ttg caa	aat ttt aaa tac	cat gac agc gat	1203
His Glu Gly Met	Arg Trp Leu Gln	Asn Phe Lys Tyr	His Asp Ser Asp	
	385	390	395	
ttg aaa aac gac	cct aag gaa ttt	tac gaa ctc gct	aag aac gat ttg	1251
Leu Lys Asn Asp	Pro Lys Glu Phe	Tyr Glu Leu Ala	Lys Asn Asp Leu	
	400	405	410	
tat cgt gaa gat	att gtc gtt ttt	tcg cct cat ggg	gac act tac act	1299
Tyr Arg Glu Asp	Ile Val Val Phe	Ser Pro His Gly	Asp Thr Tyr Thr	
	415	420	425	
tta ccg gtg ggt	gcg atc gct tta	gat ttt gct tac	atg gtg cat agc	1347
Leu Pro Val Gly	Ala Ile Ala Leu	Asp Phe Ala Tyr	Met Val His Ser	
	430	435	440	445
gat ttg ggc gat	aaa gcc acg gac	gct tat atc aat	agt aaa aaa gcc	1395
Asp Leu Gly Asp	Lys Ala Thr Asp	Ala Tyr Ile Asn	Ser Lys Lys Ala	
	450	455	460	
tta ctc aat cag	gaa tta aga agt	ggg gat gtg gtt	aaa atc att aaa	1443
Leu Leu Asn Gln	Glu Leu Arg Ser	Gly Asp Val Val	Lys Ile Ile Lys	
	465	470	475	
ggc gat aaa ata	ata cct cgt ttc	att tgg atg gat	cag ctt aaa act	1491
Gly Asp Lys Ile	Ile Pro Arg Phe	Ile Trp Met Asp	Gln Leu Lys Thr	
	480	485	490	
tct aag gct aaa	aac cat ttg cgc	atc caa aga aga	aac cgc ttg aaa	1539
Ser Lys Ala Lys	Asn His Leu Arg	Ile Gln Arg Arg	Asn Arg Leu Lys	
	495	500	505	
gag gtt gac act	aag agc atg atc	aat atc tta gcg	act ttt ttt ggg	1587

Glu Val Asp Thr Lys Ser Met Ile Asn Ile Leu Ala Thr Phe Phe Gly	
510 515 520 525	
cgc tct gtt ttt gaa gac atg gat tta aag gat tat aaa aac ttt gaa	1635
Arg Ser Val Phe Glu Asp Met Asp Leu Lys Asp Tyr Lys Asn Phe Glu	
530 535 540	
gaa aga tta aca gat tgc ggg gtg gag acc acc tta aca gaa gcg atg	1683
Glu Arg Leu Thr Asp Cys Gly Val Glu Thr Thr Leu Thr Glu Ala Met	
545 550 555	
aaa agt ttt gaa aat tta gcc aaa ctc act gaa gaa att gaa aat aag	1731
Lys Ser Phe Glu Asn Leu Ala Lys Leu Thr Glu Glu Ile Glu Asn Lys	
560 565 570	
gtg ttt tct tta aaa gaa gat gcg att tta gaa tac caa gag atg agt	1779
Val Phe Ser Leu Lys Glu Asp Ala Ile Leu Glu Tyr Gln Glu Met Ser	
575 580 585	
tta tgg act cga ggt tta agg tat ttg ggc ttt aaa acc aat gtc ttg	1827
Leu Trp Thr Arg Gly Leu Arg Tyr Leu Gly Phe Lys Thr Asn Val Leu	
590 595 600 605	
aat ttt tta gcc ccc aat cgg cag tgg cag tgt aag gaa tta gaa cat	1875
Asn Phe Leu Ala Pro Asn Arg Gln Trp Gln Cys Lys Glu Leu Glu His	
610 615 620	
ttt agc gtt tgt tca agc aac gct tta gaa atc aaa cag gtg ttg ttg	1923
Phe Ser Val Cys Ser Ser Asn Ala Leu Glu Ile Lys Gln Val Leu Leu	
625 630 635	
aat gat tgt tgt tac cct aaa tat ggc gat gaa atc att gcg att gta	1971
Asn Asp Cys Cys Tyr Pro Lys Tyr Gly Asp Glu Ile Ile Ala Ile Val	
640 645 650	
acg gat tta aaa gat cca aaa gcg att gcg cac cat aaa ttt tgc aaa	2019
Thr Asp Leu Lys Asp Pro Lys Ala Ile Ala His His Lys Phe Cys Lys	
655 660 665	
aaa gcg atg gcg gaa gta gat gct aaa gtg cct atg gtt tat ata gaa	2067
Lys Ala Met Ala Glu Val Asp Ala Lys Val Pro Met Val Tyr Ile Glu	
670 675 680 685	
tgg cac aag cgg gat cga acg att tat aaa atg atg ttt tat ttg ggc	2115
Trp His Lys Arg Asp Arg Thr Ile Tyr Lys Met Met Phe Tyr Leu Gly	
690 695 700	
gaa aaa aag tcg gtt tta gcg ggt tta tta act ttt tta aac agg aat	2163
Glu Lys Lys Ser Val Leu Ala Gly Leu Leu Thr Phe Leu Asn Arg Asn	
705 710 715	
gaa tgc aac att gtg ggc gtg tct tat ttg ggc tat aaa gac aag tat	2211
Glu Cys Asn Ile Val Gly Val Ser Tyr Leu Gly Tyr Lys Asp Lys Tyr	
720 725 730	
tct agc cat tgt gaa gtg agt ttt gaa ata gcc aca gat aag gcg gat	2259
Ser Ser His Cys Glu Val Ser Phe Glu Ile Ala Thr Asp Lys Ala Asp	
735 740 745	

tgg atc aga gcc tta atc aat cgc aaa tat cag gat agg att gta gaa	2307
Trp Ile Arg Ala Leu Ile Asn Arg Lys Tyr Gln Asp Arg Ile Val Glu	
750 755 760 765	

tta tcc agt ctg gat gac gct tat gaa tca taataagccc taattaagga	2357
Leu Ser Ser Leu Asp Asp Ala Tyr Glu Ser	
770 775	

atgaacatgg aacaaa	2373
-------------------	------

<210> 112
 <211> 775
 <212> PRT
 <213> Helicobacter pylori

<400> 112

Met Asn Glu Ile Asp Lys Ser Val Asp Ile Gly Phe Leu Arg Ile Leu	
1 5 10 15	
Asp Val Ile Lys Lys Val Thr Thr Pro Lys Gly Gly Ile Glu Ile Leu	
20 25 30	
Arg Thr Leu Ile Asp Phe Thr Pro Lys Ile Glu Asn Ala Leu Asn Leu	
35 40 45	
Ala Ala Lys Ser His Lys Gly Gln Tyr Arg Lys Ser Gly Glu Pro Tyr	
50 55 60	
Ile Val His Pro Ile Cys Val Ala Ser Leu Val Ala Phe Cys Gly Gly	
65 70 75 80	
Asp Glu Ala Met Val Cys Ala Ala Leu Leu His Asp Val Val Glu Asp	
85 90 95	
Thr Pro Cys Lys Ile Glu Thr Ile Glu Gln Glu Phe Gly Gln Asp Val	
100 105 110	
Ala Asn Leu Val Asp Ala Leu Thr Lys Ile Thr Glu Ile Arg Lys Glu	
115 120 125	
Glu Leu Gly Val Ser Ser Gln Asp Pro Arg Met Val Val Ser Ala Leu	
130 135 140	
Thr Phe Arg Lys Ile Leu Ile Ser Ala Ile Gln Asp Pro Arg Ala Leu	
145 150 155 160	
Val Val Lys Ile Ser Asp Arg Leu His Asn Met Leu Thr Leu Asp Ala	
165 170 175	
Leu Pro His Asp Lys Gln Val Arg Ile Ser Lys Glu Thr Leu Ala Val	
180 185 190	
Tyr Ala Pro Ile Ala Ser Arg Leu Gly Met Ser Ser Ile Lys Asn Glu	
195 200 205	
Leu Glu Asp Lys Ser Phe Tyr Tyr Ile Tyr Pro Glu Glu Tyr Lys Asn	
210 215 220	
Ile Lys Glu Tyr Leu His Lys Asn Lys Gln Ser Leu Leu Leu Lys Leu	
225 230 235 240	
Asn Ala Phe Ala Ser Lys Leu Glu Lys Lys Leu Phe Asp Ser Gly Phe	
245 250 255	
Ser His Ser Asp Phe Lys Leu Val Thr Arg Val Lys Arg Pro Tyr Ser	
260 265 270	
Ile Tyr Leu Lys Met Gln Arg Lys Gly Ala Val Asn Ile Asp Glu Ile	
275 280 285	
Leu Asp Leu Leu Ala Ile Arg Ile Leu Leu Lys Asn Pro Ile Asp Cys	
290 295 300	
Tyr Lys Val Leu Gly Ile Ile His Leu Asn Phe Lys Pro Ile Val Ser	
305 310 315 320	
Arg Phe Lys Asp Tyr Ile Ala Leu Pro Lys Glu Asn Gly Tyr Lys Thr	
325 330 335	
Ile His Thr Thr Ile Phe Asp Glu Ser Ser Val Tyr Glu Val Gln Ile	

$$\begin{array}{ll} \langle 210 \rangle & 113 \\ \langle 211 \rangle & 310 \end{array}$$

<212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (10)...(279)

<400> 113
 aaaaggaga gtg gcg gtg aaa aaa atc gtt gtg agt tgg tgt gtg gcg ttg 51
 Val Ala Val Lys Lys Ile Val Val Ser Trp Cys Val Ala Leu
 1 5 10

gct ttt tta agc gcg gat tca gca caa gcc aat aaa gcg atc agt aat 99
 Ala Phe Leu Ser Ala Asp Ser Ala Gln Ala Asn Lys Ala Ile Ser Asn
 15 20 25 30

gcg gat ttg att aaa gag ata agg gat tta aaa aaa atc atc agc gcg 147
 Ala Asp Leu Ile Lys Glu Ile Arg Asp Leu Lys Lys Ile Ile Ser Ala
 35 40 45

caa aac act gag att aac aac tta aga aaa gtg caa gaa gtg ttg tct 195
 Gln Asn Thr Glu Ile Asn Asn Leu Arg Lys Val Gln Glu Val Leu Ser
 50 55 60

ggg caa tta ggg gac atg cgt aag gat ata tta agc act aga gat tat 243
 Gly Gln Leu Gly Asp Met Arg Lys Asp Ile Leu Ser Thr Arg Asp Tyr
 65 70 75

tgc att agc tta agg cct tat atc tat aat tgg cgc taggggataa 289
 Cys Ile Ser Leu Arg Pro Tyr Ile Tyr Asn Trp Arg
 80 85 90

tccaaaaaaat gaaagcatgc g 310

<210> 114
 <211> 90
 <212> PRT
 <213> Helicobacter pylori

<400> 114
 Val Ala Val Lys Lys Ile Val Val Ser Trp Cys Val Ala Leu Ala Phe
 1 5 10 15
 Leu Ser Ala Asp Ser Ala Gln Ala Asn Lys Ala Ile Ser Asn Ala Asp
 20 25 30
 Leu Ile Lys Glu Ile Arg Asp Leu Lys Lys Ile Ile Ser Ala Gln Asn
 35 40 45
 Thr Glu Ile Asn Asn Leu Arg Lys Val Gln Glu Val Leu Ser Gly Gln
 50 55 60
 Leu Gly Asp Met Arg Lys Asp Ile Leu Ser Thr Arg Asp Tyr Cys Ile
 65 70 75 80
 Ser Leu Arg Pro Tyr Ile Tyr Asn Trp Arg
 85 90

<210> 115
 <211> 1631
 <212> DNA
 <213> Helicobacter pylori

<220>

<221> CDS

<222> (52)...(1569)

<400> 115

```
tgaaaaagaa ctcaaagagc tgcaaaaaaa acaaaaacac gagtaacaac c atg att 57
                                     Met Ile
                                     1

aac acg atg ttt tgc gcg acc atg caa agg gga gtg gcg gaa atc gtg 105
Asn Thr Met Phe Cys Ala Thr Met Gln Arg Gly Val Ala Glu Ile Val
      5              10              15

gct gtg gaa gcg act ttc aca agg gct ttg ccg gcg ttt gtg att tca 153
Ala Val Glu Ala Thr Phe Thr Arg Ala Leu Pro Ala Phe Val Ile Ser
      20              25              30

ggg tta gct aat agc tct atc caa gaa gcc aaa cag cgg gtt caa tcg 201
Gly Leu Ala Asn Ser Ser Ile Gln Glu Ala Lys Gln Arg Val Gln Ser
      35              40              45              50

gct tta caa aat aac gat ttc act ttc ccg cct tta aaa atc acc atc 249
Ala Leu Gln Asn Asn Asp Phe Thr Phe Pro Pro Leu Lys Ile Thr Ile
              55              60              65

aac ctt tcc ccc tca gat ttg cct aaa tcc ggg agt cat ttt gat ttg 297
Asn Leu Ser Pro Ser Asp Leu Pro Lys Ser Gly Ser His Phe Asp Leu
              70              75              80

cct atc gct ctt tta atc gct ttg caa aaa caa gag ttg gct ttt aaa 345
Pro Ile Ala Leu Leu Ile Ala Leu Gln Lys Gln Glu Leu Ala Phe Lys
              85              90              95

gag tgg ttt gct ttt ggg gag tta ggg ctt gat ggc aag atc aaa ccc 393
Glu Trp Phe Ala Phe Gly Glu Leu Gly Leu Asp Gly Lys Ile Lys Pro
      100              105              110

aat cct aac att ttc ccc atg ctt tta gac att gcc att aaa cac ccc 441
Asn Pro Asn Ile Phe Pro Met Leu Leu Asp Ile Ala Ile Lys His Pro
      115              120              125              130

cat gct aag atc att gcg cct aag gcc aat gaa gag ctt ttt tcg ctt 489
His Ala Lys Ile Ile Ala Pro Lys Ala Asn Glu Glu Leu Phe Ser Leu
              135              140              145

atc cct aat ttg caa tgc ttt ttt gtg ggg cat ttt aaa gaa gcg tta 537
Ile Pro Asn Leu Gln Cys Phe Phe Val Gly His Phe Lys Glu Ala Leu
              150              155              160

gaa atc ttg caa aac cct gaa acc aaa gca gac acc cac acg aaa aaa 585
Glu Ile Leu Gln Asn Pro Glu Thr Lys Ala Asp Thr His Thr Lys Lys
      165              170              175

cta ccc ttt aaa acg ata gaa ttg aac gat aaa gag tat tat ttt tca 633
Leu Pro Phe Lys Thr Ile Glu Leu Asn Asp Lys Glu Tyr Tyr Phe Ser
      180              185              190

gac gcc tat gcc tta gat ttt aaa gaa gtt aag ggg caa gct gtc gct 681
Asp Ala Tyr Ala Leu Asp Phe Lys Glu Val Lys Gly Gln Ala Val Ala
```


195	200	205	210	
aaa gag gcc gct ttg atc gct agc gct ggg ttt cat aac ttg att tta	729			
Lys Glu Ala Ala Leu Ile Ala Ser Ala Gly Phe His Asn Leu Ile Leu				
215 220 225				
gag gga agt cca ggg tgt ggg aaa agc atg atc att aat cgc atg cgt	777			
Glu Gly Ser Pro Gly Cys Gly Lys Ser Met Ile Ile Asn Arg Met Arg				
230 235 240				
tat atc ttg cct cca tta agc ctg aat gaa atc cta gaa gcg aca aaa	825			
Tyr Ile Leu Pro Pro Leu Ser Leu Asn Glu Ile Leu Glu Ala Thr Lys				
245 250 255				
tta cgc att tta agc gag caa gac agt gcc tat tac ccc tta agg agt	873			
Leu Arg Ile Leu Ser Glu Gln Asp Ser Ala Tyr Tyr Pro Leu Arg Ser				
260 265 270				
ttt aga aac cct cac caa agc gct tca aaa tcc agt att tta ggc tca	921			
Phe Arg Asn Pro His Gln Ser Ala Ser Lys Ser Ser Ile Leu Gly Ser				
275 280 285 290				
agc tct cta aga gag cca aaa cct ggc gaa atc gcg cta gcg cat aac	969			
Ser Ser Leu Arg Glu Pro Lys Pro Gly Glu Ile Ala Leu Ala His Asn				
295 300 305				
ggc atg ctt ttt ttt gat gaa ttg cct cat ttt aaa aag gat att ttg	1017			
Gly Met Leu Phe Phe Asp Glu Leu Pro His Phe Lys Lys Asp Ile Leu				
310 315 320				
gaa gct tta aga gag cct tta gaa aac aat aaa ttg gtg gtt tca aga	1065			
Glu Ala Leu Arg Glu Pro Leu Glu Asn Asn Lys Leu Val Val Ser Arg				
325 330 335				
gtg cat agc aaa att gaa tac gaa acc tct ttt tta ttt gta ggg gct	1113			
Val His Ser Lys Ile Glu Tyr Glu Thr Ser Phe Leu Phe Val Gly Ala				
340 345 350				
caa aac cct tgc ttg tgc ggg aat tta ctc agc gcg acc aaa gca tgc	1161			
Gln Asn Pro Cys Leu Cys Gly Asn Leu Leu Ser Ala Thr Lys Ala Cys				
355 360 365 370				
cgt tgc caa gac aga gaa atc acg cag tat aaa aac cgc ttg agc gag	1209			
Arg Cys Gln Asp Arg Glu Ile Thr Gln Tyr Lys Asn Arg Leu Ser Glu				
375 380 385				
cct ttt ttg gat agg att gat ttg ttt gtg caa atg gaa gag ggg aat	1257			
Pro Phe Leu Asp Arg Ile Asp Leu Phe Val Gln Met Glu Glu Gly Asn				
390 395 400				
tat aaa gac acg ccg tcg cat tct tgg act tca aaa gag atg cat gaa	1305			
Tyr Lys Asp Thr Pro Ser His Ser Trp Thr Ser Lys Glu Met His Glu				
405 410 415				
ttg gtg tta tta gct ttc aag cag caa aag tta agg aaa cag agc gtt	1353			
Leu Val Leu Leu Ala Phe Lys Gln Gln Lys Leu Arg Lys Gln Ser Val				
420 425 430				
ttt aat ggt aag ctt aat gaa gag cag ata gaa cga ttt tgc ccc tta	1401			

Phe	Asn	Gly	Lys	Leu	Asn	Glu	Glu	Gln	Ile	Glu	Arg	Phe	Cys	Pro	Leu	
435					440					445					450	
aac	gct	gaa	gca	aaa	aag	ttg	ttg	gag	cag	gcg	gtt	gaa	agg	ttt	aat	1449
Asn	Ala	Glu	Ala	Lys	Lys	Leu	Leu	Glu	Gln	Ala	Val	Glu	Arg	Phe	Asn	
				455					460					465		
ctc	tcc	atg	cgc	tct	att	aat	aag	gtc	aaa	aaa	gtc	gct	agg	acg	att	1497
Leu	Ser	Met	Arg	Ser	Ile	Asn	Lys	Val	Lys	Lys	Val	Ala	Arg	Thr	Ile	
			470					475					480			
gcg	gat	tta	aac	gct	tgc	gag	gat	ata	gaa	aaa	tct	cac	atg	ctt	aaa	1545
Ala	Asp	Leu	Asn	Ala	Cys	Glu	Asp	Ile	Glu	Lys	Ser	His	Met	Leu	Lys	
		485				490						495				
gcg	ctg	agt	ttt	aga	aag	att	tct	taaaaggatt	tttataaggg	agaaaaaatg						1599
Ala	Leu	Ser	Phe	Arg	Lys	Ile	Ser									
	500					505										
caagaatacc	acattcataa	tttgattgc	cc													1631
<210> 116																
<211> 506																
<212> PRT																
<213> Helicobacter pylori																
<400> 116																
Met	Ile	Asn	Thr	Met	Phe	Cys	Ala	Thr	Met	Gln	Arg	Gly	Val	Ala	Glu	
1				5					10					15		
Ile	Val	Ala	Val	Glu	Ala	Thr	Phe	Thr	Arg	Ala	Leu	Pro	Ala	Phe	Val	
			20					25					30			
Ile	Ser	Gly	Leu	Ala	Asn	Ser	Ser	Ile	Gln	Glu	Ala	Lys	Gln	Arg	Val	
		35					40					45				
Gln	Ser	Ala	Leu	Gln	Asn	Asn	Asp	Phe	Thr	Phe	Pro	Pro	Leu	Lys	Ile	
	50				55						60					
Thr	Ile	Asn	Leu	Ser	Pro	Ser	Asp	Leu	Pro	Lys	Ser	Gly	Ser	His	Phe	
65				70						75				80		
Asp	Leu	Pro	Ile	Ala	Leu	Leu	Ile	Ala	Leu	Gln	Lys	Gln	Glu	Leu	Ala	
			85					90					95			
Phe	Lys	Glu	Trp	Phe	Ala	Phe	Gly	Glu	Leu	Gly	Leu	Asp	Gly	Lys	Ile	
		100					105						110			
Lys	Pro	Asn	Pro	Asn	Ile	Phe	Pro	Met	Leu	Leu	Asp	Ile	Ala	Ile	Lys	
		115				120						125				
His	Pro	His	Ala	Lys	Ile	Ile	Ala	Pro	Lys	Ala	Asn	Glu	Glu	Leu	Phe	
	130				135						140					
Ser	Leu	Ile	Pro	Asn	Leu	Gln	Cys	Phe	Phe	Val	Gly	His	Phe	Lys	Glu	
145				150						155				160		
Ala	Leu	Glu	Ile	Leu	Gln	Asn	Pro	Glu	Thr	Lys	Ala	Asp	Thr	His	Thr	
			165					170						175		
Lys	Lys	Leu	Pro	Phe	Lys	Thr	Ile	Glu	Leu	Asn	Asp	Lys	Glu	Tyr	Tyr	
		180						185					190			
Phe	Ser	Asp	Ala	Tyr	Ala	Leu	Asp	Phe	Lys	Glu	Val	Lys	Gly	Gln	Ala	
		195					200					205				
Val	Ala	Lys	Glu	Ala	Ala	Leu	Ile	Ala	Ser	Ala	Gly	Phe	His	Asn	Leu	
	210					215					220					
Ile	Leu	Glu	Gly	Ser	Pro	Gly	Cys	Gly	Lys	Ser	Met	Ile	Ile	Asn	Arg	
225				230						235				240		
Met	Arg	Tyr	Ile	Leu	Pro	Pro	Leu	Ser	Leu	Asn	Glu	Ile	Leu	Glu	Ala	
			245						250					255		

Thr	Lys	Leu	Arg	Ile	Leu	Ser	Glu	Gln	Asp	Ser	Ala	Tyr	Tyr	Pro	Leu
			260					265					270		
Arg	Ser	Phe	Arg	Asn	Pro	His	Gln	Ser	Ala	Ser	Lys	Ser	Ser	Ile	Leu
		275					280					285			
Gly	Ser	Ser	Ser	Leu	Arg	Glu	Pro	Lys	Pro	Gly	Glu	Ile	Ala	Leu	Ala
	290					295					300				
His	Asn	Gly	Met	Leu	Phe	Asp	Glu	Leu	Pro	His	Phe	Lys	Lys	Asp	
305					310					315				320	
Ile	Leu	Glu	Ala	Leu	Arg	Glu	Pro	Leu	Glu	Asn	Asn	Lys	Leu	Val	Val
				325					330					335	
Ser	Arg	Val	His	Ser	Lys	Ile	Glu	Tyr	Glu	Thr	Ser	Phe	Leu	Phe	Val
			340					345					350		
Gly	Ala	Gln	Asn	Pro	Cys	Leu	Cys	Gly	Asn	Leu	Leu	Ser	Ala	Thr	Lys
		355					360					365			
Ala	Cys	Arg	Cys	Gln	Asp	Arg	Glu	Ile	Thr	Gln	Tyr	Lys	Asn	Arg	Leu
	370					375						380			
Ser	Glu	Pro	Phe	Leu	Asp	Arg	Ile	Asp	Leu	Phe	Val	Gln	Met	Glu	Glu
385					390					395					400
Gly	Asn	Tyr	Lys	Asp	Thr	Pro	Ser	His	Ser	Trp	Thr	Ser	Lys	Glu	Met
			405						410					415	
His	Glu	Leu	Val	Leu	Leu	Ala	Phe	Lys	Gln	Gln	Lys	Leu	Arg	Lys	Gln
			420					425					430		
Ser	Val	Phe	Asn	Gly	Lys	Leu	Asn	Glu	Glu	Gln	Ile	Glu	Arg	Phe	Cys
		435					440					445			
Pro	Leu	Asn	Ala	Glu	Ala	Lys	Lys	Leu	Leu	Glu	Gln	Ala	Val	Glu	Arg
	450					455					460				
Phe	Asn	Leu	Ser	Met	Arg	Ser	Ile	Asn	Lys	Val	Lys	Lys	Val	Ala	Arg
465					470					475					480
Thr	Ile	Ala	Asp	Leu	Asn	Ala	Cys	Glu	Asp	Ile	Glu	Lys	Ser	His	Met
			485						490					495	
Leu	Lys	Ala	Leu	Ser	Phe	Arg	Lys	Ile	Ser						
			500					505							

<210> 117
 <211> 605
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (26)...(547)

<400> 117																
ttacagaaaa	acgtgaagtg	attgca	atg	gcg	tta	tta	gag	att	atc	cat	tac				52	
			Met	Ala	Leu	Leu	Glu	Ile	Ile	His	Tyr					
			1				5									
cct	tct	aaa	atc	tta	aga	acg	att	tct	aaa	gag	gtc	gtt	tct	ttt	gat	100
Pro	Ser	Lys	Ile	Leu	Arg	Thr	Ile	Ser	Lys	Glu	Val	Val	Ser	Phe	Asp	
10					15					20					25	
tca	aaa	ctc	cac	caa	cag	cta	gat	gac	atg	cat	gag	act	atg	atc	gct	148
Ser	Lys	Leu	His	Gln	Gln	Leu	Asp	Asp	Met	His	Glu	Thr	Met	Ile	Ala	
				30					35					40		
agt	gag	ggg	ata	ggg	tta	gcc	gct	att	caa	gtg	ggg	ttg	cct	tta	aga	196
Ser	Glu	Gly	Ile	Gly	Leu	Ala	Ala	Ile	Gln	Val	Gly	Leu	Pro	Leu	Arg	
			45					50					55			

atg ctc atc atc aac ctc ccg caa gaa gac ggc gtg caa cac aaa gaa	244
Met Leu Ile Ile Asn Leu Pro Gln Glu Asp Gly Val Gln His Lys Glu	
60 65 70	
gac tgc ttg gaa atc att aac cct aag ttt ata gaa act ggg gga tca	292
Asp Cys Leu Glu Ile Ile Asn Pro Lys Phe Ile Glu Thr Gly Gly Ser	
75 80 85	
atg atg tat aga gaa ggg tgc ttg tct gtg ccg gga ttt tac gaa gaa	340
Met Met Tyr Arg Glu Gly Cys Leu Ser Val Pro Gly Phe Tyr Glu Glu	
90 95 100 105	
gtg gag cgt ttt gaa aag gtt aag ata gag tat caa aac cgc ttc gct	388
Val Glu Arg Phe Glu Lys Val Lys Ile Glu Tyr Gln Asn Arg Phe Ala	
110 115 120	
gaa gtg aaa gtt tta gaa gcg agc gag ctt tta gcg gta gcc att cag	436
Glu Val Lys Val Leu Glu Ala Ser Glu Leu Leu Ala Val Ala Ile Gln	
125 130 135	
cat gag atc gat cac ctc aat ggc gtg tta ttc gtg gat aaa tta tcc	484
His Glu Ile Asp His Leu Asn Gly Val Leu Phe Val Asp Lys Leu Ser	
140 145 150	
att ttg aag cgt aag aaa ttt gaa aaa gaa ctc aaa gag ctg caa aaa	532
Ile Leu Lys Arg Lys Lys Phe Glu Lys Glu Leu Lys Glu Leu Gln Lys	
155 160 165	
aaa caa aaa cac gag taacaacat gattaacacg atgttttgcg cgaccatgca	587
Lys Gln Lys His Glu	
170	
aaggggagtg gcggaaat	605

<210> 118

<211> 174

<212> PRT

<213> Helicobacter pylori

<400> 118

Met Ala Leu Leu Glu Ile Ile His Tyr Pro Ser Lys Ile Leu Arg Thr	
1 5 10 15	
Ile Ser Lys Glu Val Val Ser Phe Asp Ser Lys Leu His Gln Gln Leu	
20 25 30	
Asp Asp Met His Glu Thr Met Ile Ala Ser Glu Gly Ile Gly Leu Ala	
35 40 45	
Ala Ile Gln Val Gly Leu Pro Leu Arg Met Leu Ile Ile Asn Leu Pro	
50 55 60	
Gln Glu Asp Gly Val Gln His Lys Glu Asp Cys Leu Glu Ile Ile Asn	
65 70 75 80	
Pro Lys Phe Ile Glu Thr Gly Gly Ser Met Met Tyr Arg Glu Gly Cys	
85 90 95	
Leu Ser Val Pro Gly Phe Tyr Glu Glu Val Glu Arg Phe Glu Lys Val	
100 105 110	
Lys Ile Glu Tyr Gln Asn Arg Phe Ala Glu Val Lys Val Leu Glu Ala	
115 120 125	
Ser Glu Leu Leu Ala Val Ala Ile Gln His Glu Ile Asp His Leu Asn	
130 135 140	

acattttgac aacaaaagcg tggttggtg

564

<210> 120
 <211> 158
 <212> PRT
 <213> Helicobacter pylori

<400> 120
 Met Pro Leu Thr His Leu Asn Glu Glu Asn Gln Pro Lys Met Val Asp
 1 5 10 15
 Ile Gly Asp Lys Glu Thr Thr Glu Arg Ile Ala Leu Ala Ser Gly Arg
 20 25 30
 Ile Ser Met Asn Lys Glu Ala Tyr Asp Ala Ile Ile Asn His Cys Val
 35 40 45
 Lys Lys Gly Pro Val Leu Gln Thr Ala Ile Ile Ala Gly Ile Met Gly
 50 55 60
 Ala Lys Lys Thr Ser Glu Leu Ile Pro Met Cys His Pro Ile Met Leu
 65 70 75 80
 Asn Gly Val Asp Ile Asp Ile Leu Glu Glu Lys Glu Thr Cys Ser Phe
 85 90 95
 Lys Leu Tyr Ala Arg Val Lys Thr Gln Ala Lys Thr Gly Val Glu Met
 100 105 110
 Glu Ala Leu Met Ser Val Ser Ile Gly Leu Leu Thr Ile Tyr Asp Met
 115 120 125
 Val Lys Ala Ile Asp Lys Ser Met Thr Ile Ser Gly Val Met Leu Glu
 130 135 140
 His Lys Ser Gly Gly Lys Ser Gly Asp Tyr Asn Ala Lys Lys -
 145 150 155

<210> 121
 <211> 605
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (25)...(552)

<400> 121
 ctttttagctt aaaaaggagt tcaa atg caa acg att cat ata ggc gtt ttg 51
 Met Gln Thr Ile His Ile Gly Val Leu
 1 5
 agc gcg agc gat aga gcg tca aaa ggg att tat gaa gat tta agc ggt 99
 Ser Ala Ser Asp Arg Ala Ser Lys Gly Ile Tyr Glu Asp Leu Ser Gly
 10 15 20 25
 aag gcg ata caa gaa gtg ttg agc gaa tac ttg ctc aat cct tta gaa 147
 Lys Ala Ile Gln Glu Val Leu Ser Glu Tyr Leu Leu Asn Pro Leu Glu
 30 35 40
 ttt tat tac gaa att gtc gct gat gaa agg gat tta att gaa aaa tca 195
 Phe Tyr Tyr Glu Ile Val Ala Asp Glu Arg Asp Leu Ile Glu Lys Ser
 45 50 55
 ctg att aaa atg tgc gat gaa tac caa tgc gat cta gtc gtt act aca 243
 Leu Ile Lys Met Cys Asp Glu Tyr Gln Cys Asp Leu Val Val Thr Thr

60	65	70	
gga ggc aca ggc cct gct tta aga gat ata acc cca gaa gcc aca gaa			291
Gly Gly Thr Gly Pro Ala Leu Arg Asp Ile Thr Pro Glu Ala Thr Glu			
75	80	85	
aaa gtg tgc caa aaa atg ctt cct ggt ttt gga gag ctt atg cga atg			339
Lys Val Cys Gln Lys Met Leu Pro Gly Phe Gly Glu Leu Met Arg Met			
90	95	100	105
act agt tta aaa tat gtg cct aca gcg atc ctg tcg cgc cag agc gct			387
Thr Ser Leu Lys Tyr Val Pro Thr Ala Ile Leu Ser Arg Gln Ser Ala			
110	115	120	
ggt att agg aat aag agt ttg att att aat ctc cct ggt aag cca aaa			435
Gly Ile Arg Asn Lys Ser Leu Ile Ile Asn Leu Pro Gly Lys Pro Lys			
125	130	135	
agt att aga gaa tgc tta gag gcg gtt ttt cca gcg att cct tat tgc			483
Ser Ile Arg Glu Cys Leu Glu Ala Val Phe Pro Ala Ile Pro Tyr Cys			
140	145	150	
gtg gat ttg att tta ggg aat tat atg caa gtg aat gaa aaa aac att			531
Val Asp Leu Ile Leu Gly Asn Tyr Met Gln Val Asn Glu Lys Asn Ile			
155	160	165	
caa gcg ttt cgc ccc aaa caa taggataaaaa aatgccgctc actcatttga			582
Gln Ala Phe Arg Pro Lys Gln			
170	175		
atgaagaaaa tcagcctaaa atg			605
<210> 122			
<211> 176			
<212> PRT			
<213> Helicobacter pylori			
<400> 122			
Met Gln Thr Ile His Ile Gly Val Leu Ser Ala Ser Asp Arg Ala Ser			
1	5	10	15
Lys Gly Ile Tyr Glu Asp Leu Ser Gly Lys Ala Ile Gln Glu Val Leu			
20	25	30	
Ser Glu Tyr Leu Leu Asn Pro Leu Glu Phe Tyr Tyr Glu Ile Val Ala			
35	40	45	
Asp Glu Arg Asp Leu Ile Glu Lys Ser Leu Ile Lys Met Cys Asp Glu			
50	55	60	
Tyr Gln Cys Asp Leu Val Val Thr Thr Gly Gly Thr Gly Pro Ala Leu			
65	70	75	80
Arg Asp Ile Thr Pro Glu Ala Thr Glu Lys Val Cys Gln Lys Met Leu			
85	90	95	
Pro Gly Phe Gly Glu Leu Met Arg Met Thr Ser Leu Lys Tyr Val Pro			
100	105	110	
Thr Ala Ile Leu Ser Arg Gln Ser Ala Gly Ile Arg Asn Lys Ser Leu			
115	120	125	
Ile Ile Asn Leu Pro Gly Lys Pro Lys Ser Ile Arg Glu Cys Leu Glu			
130	135	140	
Ala Val Phe Pro Ala Ile Pro Tyr Cys Val Asp Leu Ile Leu Gly Asn			
145	150	155	160
Tyr Met Gln Val Asn Glu Lys Asn Ile Gln Ala Phe Arg Pro Lys Gln			

165

170

175

<210> 123
 <211> 659
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (31)...(630)

<400> 123

```

gcaattacta gaagaatata cccacaaatt atg cca aat cat cag cca gta aaa 54
                        Met Pro Asn His Gln Pro Val Lys
                          1                      5

aaa ttt aag att att ggg ggg gct tgt aag gga tta ggc ttg aat ttg 102
Lys Phe Lys Ile Ile Gly Gly Ala Cys Lys Gly Leu Gly Leu Asn Leu
      10                      15                      20

cct aac att tct agc acg cgc ccc acc aaa gcg atc gta aga gag tcg 150
Pro Asn Ile Ser Ser Thr Arg Pro Thr Lys Ala Ile Val Arg Glu Ser
      25                      30                      35                      40

ttt ttt aac acc ttg caa gca gaa att aat gga gcg cat ttt ata gaa 198
Phe Phe Asn Thr Leu Gln Ala Glu Ile Asn Gly Ala His Phe Ile Glu
                        45                      50                      55

gtg ttt tca ggc agc gct tct atg ggt tta gag gct ttg agt agg ggg 246
Val Phe Ser Gly Ser Ala Ser Met Gly Leu Glu Ala Leu Ser Arg Gly
                        60                      65                      70

gct aaa agt gcg gtg ttt ttt gaa caa aac aaa agc gct tat aag acg 294
Ala Lys Ser Ala Val Phe Phe Glu Gln Asn Lys Ser Ala Tyr Lys Thr
      75                      80                      85

ctt tta gaa aat att tcc ctt ttt aaa aac cgc ttg aaa aaa gaa atg 342
Leu Leu Glu Asn Ile Ser Leu Phe Lys Asn Arg Leu Lys Lys Glu Met
      90                      95                      100

gaa att caa acc ttt tta gat gac gct ttc aag ctt ttg ccc acg ctg 390
Glu Ile Gln Thr Phe Leu Asp Asp Ala Phe Lys Leu Leu Pro Thr Leu
    105                      110                      115                      120

tgt tta aaa aat ggc gtt ttg aat att att tat ttg gat cct cct ttt 438
Cys Leu Lys Asn Gly Val Leu Asn Ile Ile Tyr Leu Asp Pro Pro Phe
                        125                      130                      135

gaa aca agt ggg ttt tta ggg att tat gaa aag tgt ttt caa gct tta 486
Glu Thr Ser Gly Phe Leu Gly Ile Tyr Glu Lys Cys Phe Gln Ala Leu
      140                      145                      150

gaa agg tta ttg aaa cgc ttt aat cca aaa aat ctt tta gtg gtt ttt 534
Glu Arg Leu Leu Lys Arg Phe Asn Pro Lys Asn Leu Leu Val Val Phe
      155                      160                      165

gag cat gaa agc atg cat gaa atg cct aaa agt ctt gta act tta gct 582
Glu His Glu Ser Met His Glu Met Pro Lys Ser Leu Val Thr Leu Ala

```


170	175	180	
ata atc aaa caa aaa aaa ttt gga aaa acc act tta act tat ttt caa			630
Ile Ile Lys Gln Lys Lys Phe Gly Lys Thr Thr Leu Thr Tyr Phe Gln			
185	190	195	200

taggaatagg catggcagaa gaacaagaa 659

<210> 124
 <211> 200
 <212> PRT
 <213> Helicobacter pylori

<400> 124

Met	Pro	Asn	His	Gln	Pro	Val	Lys	Lys	Phe	Lys	Ile	Ile	Gly	Gly	Ala
1				5					10					15	
Cys	Lys	Gly	Leu	Gly	Leu	Asn	Leu	Pro	Asn	Ile	Ser	Ser	Thr	Arg	Pro
			20					25					30		
Thr	Lys	Ala	Ile	Val	Arg	Glu	Ser	Phe	Phe	Asn	Thr	Leu	Gln	Ala	Glu
		35				40						45			
Ile	Asn	Gly	Ala	His	Phe	Ile	Glu	Val	Phe	Ser	Gly	Ser	Ala	Ser	Met
	50					55					60				
Gly	Leu	Glu	Ala	Leu	Ser	Arg	Gly	Ala	Lys	Ser	Ala	Val	Phe	Phe	Glu
65					70				75						80
Gln	Asn	Lys	Ser	Ala	Tyr	Lys	Thr	Leu	Leu	Glu	Asn	Ile	Ser	Leu	Phe
				85					90					95	
Lys	Asn	Arg	Leu	Lys	Lys	Glu	Met	Glu	Ile	Gln	Thr	Phe	Leu	Asp	Asp
			100					105					110		
Ala	Phe	Lys	Leu	Leu	Pro	Thr	Leu	Cys	Leu	Lys	Asn	Gly	Val	Leu	Asn
			115				120					125			
Ile	Ile	Tyr	Leu	Asp	Pro	Pro	Phe	Glu	Thr	Ser	Gly	Phe	Leu	Gly	Ile
	130				135						140				
Tyr	Glu	Lys	Cys	Phe	Gln	Ala	Leu	Glu	Arg	Leu	Leu	Lys	Arg	Phe	Asn
145					150					155					160
Pro	Lys	Asn	Leu	Leu	Val	Val	Phe	Glu	His	Glu	Ser	Met	His	Glu	Met
				165					170					175	
Pro	Lys	Ser	Leu	Val	Thr	Leu	Ala	Ile	Ile	Lys	Gln	Lys	Lys	Phe	Gly
			180					185					190		
Lys	Thr	Thr	Leu	Thr	Tyr	Phe	Gln								
			195				200								

<210> 125
 <211> 695
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (26)...(655)

<400> 125

cgtgcctact	tcgctttttg	ccgcc	atg	aca	ggc	aca	cat	gcg	cgt	tac	gtg	52
			Met	Thr	Gly	Thr	His	Ala	Arg	Tyr	Val	
			1				5					

aaa	gcc	gct	tac	aaa	gag	ata	aaa	att	gtt	ttt	tta	aac	cct	aaa	atc	100
Lys	Ala	Ala	Tyr	Lys	Glu	Ile	Lys	Ile	Val	Phe	Leu	Asn	Pro	Lys	Ile	
10					15					20					25	

aat tta aac gaa acc atc aaa aat tta gtg gaa tta gcc act ctg gct	148
Asn Leu Asn Glu Thr Ile Lys Asn Leu Val Glu Leu Ala Thr Leu Ala	
30 35 40	
aga aaa gat ggg gtg ttg agt tta gag ggg cga gtg gcg caa att gaa	196
Arg Lys Asp Gly Val Leu Ser Leu Glu Gly Arg Val Ala Gln Ile Glu	
45 50 55	
gac gat ttc acc cgt aat ggc ttg tct atg atc ata gat ggc aag gat	244
Asp Asp Phe Thr Arg Asn Gly Leu Ser Met Ile Ile Asp Gly Lys Asp	
60 65 70	
tta aaa tcc gtt aag gaa agc tta gaa atc agc att gaa gaa atg gaa	292
Leu Lys Ser Val Lys Glu Ser Leu Glu Ile Ser Ile Glu Glu Met Glu	
75 80 85	
gag tat tac cac ggc gcc gct cat tat tgg gag acg gcc ggt gag acc	340
Glu Tyr Tyr His Gly Ala Ala His Tyr Trp Glu Thr Ala Gly Glu Thr	
90 95 100 105	
gct cct act atg ggg tta gtg ggg gcg gtt atg ggg ctt atg tta gcc	388
Ala Pro Thr Met Gly Leu Val Gly Ala Val Met Gly Leu Met Leu Ala	
110 115 120	
ttg caa aaa cta gac aac ccg gct gaa atg gca gca ggg atc gct ggg	436
Leu Gln Lys Leu Asp Asn Pro Ala Glu Met Ala Ala Gly Ile Ala Gly	
125 130 135	
gct ttt acg gct act gtt aca ggg att atg tgt tct tat gcg att ttt	484
Ala Phe Thr Ala Thr Val Thr Gly Ile Met Cys Ser Tyr Ala Ile Phe	
140 145 150	
ggc cct ttt ggg cat aag ctc aaa gct aag tct aaa gac att atc aaa	532
Gly Pro Phe Gly His Lys Leu Lys Ala Lys Ser Lys Asp Ile Ile Lys	
155 160 165	
gaa aaa acc gtt ctt tta gag ggg att tta ggc atc gct aat ggg gaa	580
Glu Lys Thr Val Leu Leu Glu Gly Ile Leu Gly Ile Ala Asn Gly Glu	
170 175 180 185	
aac cca agg gat tta gaa aac aaa ctc tta aac tac atc gct ccc ggt	628
Asn Pro Arg Asp Leu Glu Asn Lys Leu Leu Asn Tyr Ile Ala Pro Gly	
190 195 200	
gaa cct aaa aaa tct caa ttt gag ggc taaagatggc taagaaaaac	675
Glu Pro Lys Lys Ser Gln Phe Glu Gly	
205 210	
amaccaccg aatgccccgc	695
<210> 126	
<211> 210	
<212> PRT	
<213> Helicobacter pylori	
<400> 126	
Met Thr Gly Thr His Ala Arg Tyr Val Lys Ala Ala Tyr Lys Glu Ile	
1 5 10 15	

Lys	Ile	Val	Phe	Leu	Asn	Pro	Lys	Ile	Asn	Leu	Asn	Glu	Thr	Ile	Lys
			20					25					30		
Asn	Leu	Val	Glu	Leu	Ala	Thr	Leu	Ala	Arg	Lys	Asp	Gly	Val	Leu	Ser
		35					40					45			
Leu	Glu	Gly	Arg	Val	Ala	Gln	Ile	Glu	Asp	Asp	Phe	Thr	Arg	Asn	Gly
	50					55					60				
Leu	Ser	Met	Ile	Ile	Asp	Gly	Lys	Asp	Leu	Lys	Ser	Val	Lys	Glu	Ser
65					70					75				80	
Leu	Glu	Ile	Ser	Ile	Glu	Glu	Met	Glu	Glu	Tyr	Tyr	His	Gly	Ala	Ala
			85						90					95	
His	Tyr	Trp	Glu	Thr	Ala	Gly	Glu	Thr	Ala	Pro	Thr	Met	Gly	Leu	Val
			100					105					110		
Gly	Ala	Val	Met	Gly	Leu	Met	Leu	Ala	Leu	Gln	Lys	Leu	Asp	Asn	Pro
		115					120					125			
Ala	Glu	Met	Ala	Ala	Gly	Ile	Ala	Gly	Ala	Phe	Thr	Ala	Thr	Val	Thr
		130					135					140			
Gly	Ile	Met	Cys	Ser	Tyr	Ala	Ile	Phe	Gly	Pro	Phe	Gly	His	Lys	Leu
145					150					155					160
Lys	Ala	Lys	Ser	Lys	Asp	Ile	Ile	Lys	Glu	Lys	Thr	Val	Leu	Leu	Glu
				165					170					175	
Gly	Ile	Leu	Gly	Ile	Ala	Asn	Gly	Glu	Asn	Pro	Arg	Asp	Leu	Glu	Asn
			180					185					190		
Lys	Leu	Leu	Asn	Tyr	Ile	Ala	Pro	Gly	Glu	Pro	Lys	Lys	Ser	Gln	Phe
		195					200					205			
Glu	Gly														
	210														

<210> 127
 <211> 810
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (13)...(783)

<400> 127
 tgaggggctaa ag atg gct aag aaa aac ama ccc acc gaa tgc ccc gcc ggt 51
 Met Ala Lys Lys Asn Xaa Pro Thr Glu Cys Pro Ala Gly
 1 5 10

gaa aaa tgg gcg gtt cct tat gcg gac ttt ttg tcg ttg ttg ctc gcg 99
 Glu Lys Trp Ala Val Pro Tyr Ala Asp Phe Leu Ser Leu Leu Leu Ala
 15 20 25

ctt ttt atc gct ctt tat gcc att tca gcg gtc aac aaa tcc aaa gtg 147
 Leu Phe Ile Ala Leu Tyr Ala Ile Ser Ala Val Asn Lys Ser Lys Val
 30 35 40 45

gaa gcc tta aaa acc gaa ttt att aag att ttt aat tac gct ccc aag 195
 Glu Ala Leu Lys Thr Glu Phe Ile Lys Ile Phe Asn Tyr Ala Pro Lys
 50 55 60

cca gag gcg atg cag ccg gtt gta gtg atc ccg cct gat tca ggg aaa 243
 Pro Glu Ala Met Gln Pro Val Val Val Ile Pro Pro Asp Ser Gly Lys
 65 70 75

gaa gaa gaa caa atg gcg agc gaa agc tcc aaa ccg gct tcg caa aat 291

Glu	Glu	Glu	Gln	Met	Ala	Ser	Glu	Ser	Ser	Lys	Pro	Ala	Ser	Gln	Asn	
		80					85					90				
acc	gaa	aca	aaa	gcc	act	atc	gct	cgc	aaa	ggc	gaa	ggc	agt	gtt	tta	339
Thr	Glu	Thr	Lys	Ala	Thr	Ile	Ala	Arg	Lys	Gly	Glu	Gly	Ser	Val	Leu	
	95					100					105					
gag	caa	att	gat	caa	ggc	tct	atc	tta	aag	ctc	ccc	tct	aat	ttg	ctg	387
Glu	Gln	Ile	Asp	Gln	Gly	Ser	Ile	Leu	Lys	Leu	Pro	Ser	Asn	Leu	Leu	
110					115					120					125	
ttt	gaa	aac	gct	act	tca	gac	gct	atc	aat	caa	gac	atg	atg	ctt	tat	435
Phe	Glu	Asn	Ala	Thr	Ser	Asp	Ala	Ile	Asn	Gln	Asp	Met	Met	Leu	Tyr	
				130					135					140		
att	gaa	cgg	atc	gct	aaa	atc	att	caa	aaa	ctc	cct	aaa	agg	gtg	cat	483
Ile	Glu	Arg	Ile	Ala	Lys	Ile	Ile	Gln	Lys	Leu	Pro	Lys	Arg	Val	His	
				145				150					155			
att	aat	gtg	aga	ggc	ttt	acg	gat	gat	acg	cct	tta	gtt	aaa	acc	cgt	531
Ile	Asn	Val	Arg	Gly	Phe	Thr	Asp	Asp	Thr	Pro	Leu	Val	Lys	Thr	Arg	
	160						165					170				
ttt	aaa	agc	cat	tat	gaa	tta	gcc	gcc	aat	cgc	gct	tat	agg	gtg	atg	579
Phe	Lys	Ser	His	Tyr	Glu	Leu	Ala	Ala	Asn	Arg	Ala	Tyr	Arg	Val	Met	
	175					180					185					
aaa	gtc	ctt	ata	caa	tac	ggc	gta	aat	cct	aac	caa	ttg	tct	ttt	tct	627
Lys	Val	Leu	Ile	Gln	Tyr	Gly	Val	Asn	Pro	Asn	Gln	Leu	Ser	Phe	Ser	
190					195					200					205	
tct	tac	ggc	tct	acc	aac	cct	atc	gcg	cct	aac	gac	tcc	cta	gag	aac	675
Ser	Tyr	Gly	Ser	Thr	Asn	Pro	Ile	Ala	Pro	Asn	Asp	Ser	Leu	Glu	Asn	
				210					215					220		
aga	atg	aaa	aac	aat	cgt	gtg	gaa	atc	ttt	ttt	tca	acc	gat	gcg	aac	723
Arg	Met	Lys	Asn	Asn	Arg	Val	Glu	Ile	Phe	Phe	Ser	Thr	Asp	Ala	Asn	
			225					230					235			
gat	ttg	agt	aaa	att	cat	tct	att	tta	gat	aat	gag	ttc	aat	ccc	cac	771
Asp	Leu	Ser	Lys	Ile	His	Ser	Ile	Leu	Asp	Asn	Glu	Phe	Asn	Pro	His	
	240						245					250				
aaa	cag	caa	gaa	tgaatcgc	at	gaataaaaa	t	tatcttt								810
Lys	Gln	Gln	Glu													
	255															

<210> 128
 <211> 257
 <212> PRT
 <213> Helicobacter pylori

 <220>
 <221> VARIANT
 <222> 6
 <223> Xaa = Any Amino Acid

 <400> 128

Met	Ala	Lys	Lys	Asn	Xaa	Pro	Thr	Glu	Cys	Pro	Ala	Gly	Glu	Lys	Trp
1				5					10					15	
Ala	Val	Pro	Tyr	Ala	Asp	Phe	Leu	Ser	Leu	Leu	Leu	Ala	Leu	Phe	Ile
			20					25					30		
Ala	Leu	Tyr	Ala	Ile	Ser	Ala	Val	Asn	Lys	Ser	Lys	Val	Glu	Ala	Leu
		35				40						45			
Lys	Thr	Glu	Phe	Ile	Lys	Ile	Phe	Asn	Tyr	Ala	Pro	Lys	Pro	Glu	Ala
	50				55						60				
Met	Gln	Pro	Val	Val	Val	Ile	Pro	Pro	Asp	Ser	Gly	Lys	Glu	Glu	Glu
65				70					75						80
Gln	Met	Ala	Ser	Glu	Ser	Ser	Lys	Pro	Ala	Ser	Gln	Asn	Thr	Glu	Thr
			85						90					95	
Lys	Ala	Thr	Ile	Ala	Arg	Lys	Gly	Glu	Gly	Ser	Val	Leu	Glu	Gln	Ile
			100					105					110		
Asp	Gln	Gly	Ser	Ile	Leu	Lys	Leu	Pro	Ser	Asn	Leu	Leu	Phe	Glu	Asn
		115					120					125			
Ala	Thr	Ser	Asp	Ala	Ile	Asn	Gln	Asp	Met	Met	Leu	Tyr	Ile	Glu	Arg
		130				135					140				
Ile	Ala	Lys	Ile	Ile	Gln	Lys	Leu	Pro	Lys	Arg	Val	His	Ile	Asn	Val
145					150					155					160
Arg	Gly	Phe	Thr	Asp	Asp	Thr	Pro	Leu	Val	Lys	Thr	Arg	Phe	Lys	Ser
			165						170					175	
His	Tyr	Glu	Leu	Ala	Ala	Asn	Arg	Ala	Tyr	Arg	Val	Met	Lys	Val	Leu
			180				185						190		
Ile	Gln	Tyr	Gly	Val	Asn	Pro	Asn	Gln	Leu	Ser	Phe	Ser	Ser	Tyr	Gly
		195					200					205			
Ser	Thr	Asn	Pro	Ile	Ala	Pro	Asn	Asp	Ser	Leu	Glu	Asn	Arg	Met	Lys
	210					215					220				
Asn	Asn	Arg	Val	Glu	Ile	Phe	Phe	Ser	Thr	Asp	Ala	Asn	Asp	Leu	Ser
225					230					235					240
Lys	Ile	His	Ser	Ile	Leu	Asp	Asn	Glu	Phe	Asn	Pro	His	Lys	Gln	Gln
				245					250					255	

Glu

<210> 129
 <211> 549
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (16)...(474)

<400> 129
 tgttaagatc agttt atg gaa caa aat att ttc tcc tta ctc att caa aaa 51
 Met Glu Gln Asn Ile Phe Ser Leu Leu Ile Gln Lys
 1 5 10

aag tct tat aaa aag ctt gaa acc ctt ttg aaa ctc aaa aag ctt aag 99
 Lys Ser Tyr Lys Lys Leu Glu Thr Leu Leu Lys Leu Lys Lys Leu Lys
 15 20 25

gtt ttt atg cct tta agt tta caa gaa aat ttg ctt ttt atc ttc ata 147
 Val Phe Met Pro Leu Ser Leu Gln Glu Asn Leu Leu Phe Ile Phe Ile
 30 35 40

aaa gac tct aaa ttg ctt ttt gcg ttt aaa gac att tgg gct tct aaa 195

Lys Asp Ser Lys Leu Leu Phe Ala Phe Lys Asp Ile Trp Ala Ser Lys
 45 50 55 60
 gaa ttt aac caa cga ttc gct aaa gaa atc agc cat ttt tta aac acg 243
 Glu Phe Asn Gln Arg Phe Ala Lys Glu Ile Ser His Phe Leu Asn Thr
 65 70 75
 caa ggg cat gct tat ggg ttt gac ggg ttg aat ggg tta gaa att tta 291
 Gln Gly His Ala Tyr Gly Phe Asp Gly Leu Asn Gly Leu Glu Ile Leu
 80 85 90
 ggt tat gtg cct aaa gac gcg cta aaa aaa tcc aat ttt tat gcc ccc 339
 Gly Tyr Val Pro Lys Asp Ala Leu Lys Lys Ser Asn Phe Tyr Ala Pro
 95 100 105
 att aaa aaa caa gcc cgt ttt ttt cgc cct agt gct tta ggg ttg ttc 387
 Ile Lys Lys Gln Ala Arg Phe Phe Arg Pro Ser Ala Leu Gly Leu Phe
 110 115 120
 cat aac ccc att aaa gac gct cgt ttg cat gaa tgt ttt gaa aaa gcg 435
 His Asn Pro Ile Lys Asp Ala Arg Leu His Glu Cys Phe Glu Lys Ala
 125 130 135 140
 cgc gct ttg atc cac tac caa cga agt ttt ttt gag gaa tgaatggctg 484
 Arg Ala Leu Ile His Tyr Gln Arg Ser Phe Phe Glu Glu
 145 150
 atttattgtc cagtttaaaa aaccttccta acagcagtgg cgtgtatcaa tattttgata 544
 aaaac 549

<210> 130
 <211> 153
 <212> PRT
 <213> *Helicobacter pylori*

<400> 130
 Met Glu Gln Asn Ile Phe Ser Leu Leu Ile Gln Lys Lys Ser Tyr Lys
 1 5 10 15
 Lys Leu Glu Thr Leu Leu Lys Leu Lys Lys Leu Lys Val Phe Met Pro
 20 25 30
 Leu Ser Leu Gln Glu Asn Leu Leu Phe Ile Phe Ile Lys Asp Ser Lys
 35 40 45
 Leu Leu Phe Ala Phe Lys Asp Ile Trp Ala Ser Lys Glu Phe Asn Gln
 50 55 60
 Arg Phe Ala Lys Glu Ile Ser His Phe Leu Asn Thr Gln Gly His Ala
 65 70 75 80
 Tyr Gly Phe Asp Gly Leu Asn Gly Leu Glu Ile Leu Gly Tyr Val Pro
 85 90 95
 Lys Asp Ala Leu Lys Lys Ser Asn Phe Tyr Ala Pro Ile Lys Lys Gln
 100 105 110
 Ala Arg Phe Phe Arg Pro Ser Ala Leu Gly Leu Phe His Asn Pro Ile
 115 120 125
 Lys Asp Ala Arg Leu His Glu Cys Phe Glu Lys Ala Arg Ala Leu Ile
 130 135 140
 His Tyr Gln Arg Ser Phe Phe Glu Glu
 145 150

<210> 131

<211> 352
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (1)...(318)

<400> 131
 aag tgt tac ttt ttt ata act ttt tca tat tct tat ggg tat gtt gtc 48
 Lys Cys Tyr Phe Phe Ile Thr Phe Ser Tyr Ser Tyr Gly Tyr Val Val
 1 5 10 15
 att ttt tta ccg gag aat ttt atc ttg aga aac att tat gta ggg aat 96
 Ile Phe Leu Pro Glu Asn Phe Ile Leu Arg Asn Ile Tyr Val Gly Asn
 20 25 30
 ttg gtt tat agc gct acc agt gag caa gtc aag gag ctt ttc agt caa 144
 Leu Val Tyr Ser Ala Thr Ser Glu Gln Val Lys Glu Leu Phe Ser Gln
 35 40 45
 ttt ggc aaa gtt ttt aat gtc aag ctg att tat gac aga gaa acg aag 192
 Phe Gly Lys Val Phe Asn Val Lys Leu Ile Tyr Asp Arg Glu Thr Lys
 50 55 60
 aaa cct aaa ggt ttt ggc ttt gta gaa atg caa gaa gag agc gtt agt 240
 Lys Pro Lys Gly Phe Gly Phe Val Glu Met Gln Glu Glu Ser Val Ser
 65 70 75 80
 gaa gcg atc gct aaa tta gac aat acg gat ttt atg ggc aga acg att 288
 Glu Ala Ile Ala Lys Leu Asp Asn Thr Asp Phe Met Gly Arg Thr Ile
 85 90 95
 agg gta acc gaa gct aat cct aaa aag tct tagtaacatt agaaaataat 338
 Arg Val Thr Glu Ala Asn Pro Lys Lys Ser
 100 105
 tttctaattgc gctt 352

<210> 132
 <211> 106
 <212> PRT
 <213> Helicobacter pylori

<400> 132
 Lys Cys Tyr Phe Phe Ile Thr Phe Ser Tyr Ser Tyr Gly Tyr Val Val
 1 5 10 15
 Ile Phe Leu Pro Glu Asn Phe Ile Leu Arg Asn Ile Tyr Val Gly Asn
 20 25 30
 Leu Val Tyr Ser Ala Thr Ser Glu Gln Val Lys Glu Leu Phe Ser Gln
 35 40 45
 Phe Gly Lys Val Phe Asn Val Lys Leu Ile Tyr Asp Arg Glu Thr Lys
 50 55 60
 Lys Pro Lys Gly Phe Gly Phe Val Glu Met Gln Glu Glu Ser Val Ser
 65 70 75 80
 Glu Ala Ile Ala Lys Leu Asp Asn Thr Asp Phe Met Gly Arg Thr Ile
 85 90 95
 Arg Val Thr Glu Ala Asn Pro Lys Lys Ser
 100 105

```
<210> 133
<211> 1558
<212> DNA
<213> Helicobacter pylori
```

<400> 133

act ttt gaa gat gtg ttg atg gtg cct aga aag tct agc gtt tta cct 102
Thr Phe Glu Asp Val Leu Met Val Pro Arg Lys Ser Ser Val Leu Pro
10 15 20

atc ccc ttt atc agt gcg gct atg gat acg gtt aca gag cat aaa acc 198
Ile Pro Phe Ile Ser Ala Ala Met Asp Thr Val Thr Glu His Lys Thr
45 50 55

atg gat att caa acg caa gtt aaa gaa atc act aag gtt aaa aaa agc 294
Met Asp Ile Gln Thr Gln Val Lys Glu Ile Thr Lys Val Lys Lys Ser
75 80 85

cta gcg gac gct aaa gtc ata acg gat aat tac aag att tca ggc gtg 390
Leu Ala Asp Ala Lys Val Ile Thr Asp Asn Tyr Lys Ile Ser Gly Val
105 110 115 120

gat gtg cgc ttt gaa acc gat ttg agt aaa aaa gtg ggc gat gtg atg 486
Asp Val Arg Phe Glu Thr Asp Leu Ser Lys Lys Val Gly Asp Val Met
140 145 150

gcg agc gat ttg atg cac aag cat aag att gaa aaa ttg ccc att gtg 582
Ala Ser Asp Leu Met His Lys His Lys Ile Glu Lys Leu Pro Ile Val
170 175 180

gat	aaa	gat	aat	gtc	tta	aaa	ggc	ttg	atc	acg	atc	aaa	gat	att	caa	630
Asp	Lys	Asp	Asn	Val	Leu	Lys	Gly	Leu	Ile	Thr	Ile	Lys	Asp	Ile	Gln	
185					190					195					200	
aaa	cgc	att	gaa	tac	cct	gag	gcc	aat	aaa	gat	gat	ttt	ggg	agg	ttg	678
Lys	Arg	Ile	Glu	Tyr	Pro	Glu	Ala	Asn	Lys	Asp	Asp	Phe	Gly	Arg	Leu	
				205					210					215		
aga	gtg	ggg	gcg	gct	att	gga	gtg	ggg	cag	ttg	gat	agg	gct	gag	atg	726
Arg	Val	Gly	Ala	Ala	Ile	Gly	Val	Gly	Gln	Leu	Asp	Arg	Ala	Glu	Met	
			220					225					230			
tta	gtt	aaa	gcg	ggg	gtg	gat	gca	ctg	gtg	cta	gac	agc	gca	cat	ggg	774
Leu	Val	Lys	Ala	Gly	Val	Asp	Ala	Leu	Val	Leu	Asp	Ser	Ala	His	Gly	
		235					240					245				
cat	tca	gcc	aat	atc	tta	cac	act	tta	gaa	gag	att	aaa	aaa	agc	ttg	822
His	Ser	Ala	Asn	Ile	Leu	His	Thr	Leu	Glu	Glu	Ile	Lys	Lys	Ser	Leu	
	250					255					260					
gta	gtg	gat	gtg	att	gtg	ggg	aat	gtg	gtt	act	aaa	gaa	gcc	aca	agc	870
Val	Val	Asp	Val	Ile	Val	Gly	Asn	Val	Val	Thr	Lys	Glu	Ala	Thr	Ser	
265					270					275					280	
gat	ttg	att	agc	gcg	gga	gca	gac	gct	att	aaa	gtg	ggt	att	ggg	cca	918
Asp	Leu	Ile	Ser	Ala	Gly	Ala	Asp	Ala	Ile	Lys	Val	Gly	Ile	Gly	Pro	
				285					290					295		
gga	agc	att	tgc	acc	act	agg	att	gtg	gct	ggg	gtg	gga	atg	ccc	caa	966
Gly	Ser	Ile	Cys	Thr	Thr	Arg	Ile	Val	Ala	Gly	Val	Gly	Met	Pro	Gln	
			300					305					310			
gtg	agc	gcg	att	gat	aat	tgc	gta	gaa	gtg	gcg	tct	aaa	ttt	gat	att	1014
Val	Ser	Ala	Ile	Asp	Asn	Cys	Val	Glu	Val	Ala	Ser	Lys	Phe	Asp	Ile	
		315					320					325				
cct	gtg	att	gca	gat	gga	ggg	atc	cgc	tat	tca	ggc	gat	gtg	gct	aag	1062
Pro	Val	Ile	Ala	Asp	Gly	Gly	Ile	Arg	Tyr	Ser	Gly	Asp	Val	Ala	Lys	
	330					335					340					
gct	ttg	gct	ttg	ggg	gca	tca	agc	gtg	atg	ata	ggc	tct	tta	ctc	gct	1110
Ala	Leu	Ala	Leu	Gly	Ala	Ser	Ser	Val	Met	Ile	Gly	Ser	Leu	Leu	Ala	
345					350					355					360	
ggc	aca	gaa	gaa	tct	cct	ggg	gat	ttt	atg	atc	tat	caa	ggg	agg	caa	1158
Gly	Thr	Glu	Glu	Ser	Pro	Gly	Asp	Phe	Met	Ile	Tyr	Gln	Gly	Arg	Gln	
				365					370					375		
tat	aaa	agc	tat	agg	ggc	atg	ggc	agc	att	ggg	gct	atg	act	aaa	ggg	1206
Tyr	Lys	Ser	Tyr	Arg	Gly	Met	Gly	Ser	Ile	Gly	Ala	Met	Thr	Lys	Gly	
			380					385					390			
agc	tct	gat	agg	tat	ttt	caa	gag	ggc	gta	gcg	agt	gaa	aag	tta	gtc	1254
Ser	Ser	Asp	Arg	Tyr	Phe	Gln	Glu	Gly	Val	Ala	Ser	Glu	Lys	Leu	Val	
		395					400					405				
cca	gaa	ggc	att	gaa	ggg	cgt	gtg	cct	tat	cgt	ggt	aag	ggt	tcg	gat	1302
Pro	Glu	Gly	Ile	Glu	Gly	Arg	Val	Pro	Tyr	Arg	Gly	Lys	Val	Ser	Asp	
	410					415					420					

atg att ttc caa tta gta ggg ggc gtg cgc tct tct atg ggg tat cag	1350
Met Ile Phe Gln Leu Val Gly Gly Val Arg Ser Ser Met Gly Tyr Gln	
425 430 435 440	

ggg gcg aaa aat att ttg gaa ttg tat caa aac gct gaa ttt gta gaa	1398
Gly Ala Lys Asn Ile Leu Glu Leu Tyr Gln Asn Ala Glu Phe Val Glu	
445 450 455	

atc act agc gcg ggg tta aaa gaa agc cat gtg cat ggc gtg gat att	1446
Ile Thr Ser Ala Gly Leu Lys Glu Ser His Val His Gly Val Asp Ile	
460 465 470	

act aaa gaa gcc cct aat tat tat ggg tgaattgtaa aagaaaacaa	1493
Thr Lys Glu Ala Pro Asn Tyr Tyr Gly	
475 480	

gacaaatcgt taaaaaactc gttaaaaagc ttgggttaat gagtttttaa aacttaattg	1553
ctaca	1558

<210> 134
 <211> 481
 <212> PRT
 <213> Helicobacter pylori

<400> 134	
Met Arg Ile Leu Gln Arg Ala Leu Thr Phe Glu Asp Val Leu Met Val	
1 5 10 15	
Pro Arg Lys Ser Ser Val Leu Pro Lys Asp Val Ser Leu Lys Ser Arg	
20 25 30	
Leu Thr Lys Asn Ile Arg Leu Asn Ile Pro Phe Ile Ser Ala Ala Met	
35 40 45	
Asp Thr Val Thr Glu His Lys Thr Ala Ile Ala Met Ala Arg Leu Gly	
50 55 60	
Gly Ile Gly Ile Val His Lys Asn Met Asp Ile Gln Thr Gln Val Lys	
65 70 75 80	
Glu Ile Thr Lys Val Lys Lys Ser Glu Ser Gly Val Ile Asn Asp Pro	
85 90 95	
Ile Phe Ile His Ala His Arg Thr Leu Ala Asp Ala Lys Val Ile Thr	
100 105 110	
Asp Asn Tyr Lys Ile Ser Gly Val Pro Val Val Asp Asp Lys Gly Leu	
115 120 125	
Leu Ile Gly Ile Leu Thr Asn Arg Asp Val Arg Phe Glu Thr Asp Leu	
130 135 140	
Ser Lys Lys Val Gly Asp Val Met Thr Lys Met Pro Leu Val Thr Ala	
145 150 155 160	
His Val Gly Ile Ser Leu Asp Glu Ala Ser Asp Leu Met His Lys His	
165 170 175	
Lys Ile Glu Lys Leu Pro Ile Val Asp Lys Asp Asn Val Leu Lys Gly	
180 185 190	
Leu Ile Thr Ile Lys Asp Ile Gln Lys Arg Ile Glu Tyr Pro Glu Ala	
195 200 205	
Asn Lys Asp Asp Phe Gly Arg Leu Arg Val Gly Ala Ala Ile Gly Val	
210 215 220	
Gly Gln Leu Asp Arg Ala Glu Met Leu Val Lys Ala Gly Val Asp Ala	
225 230 235 240	
Leu Val Leu Asp Ser Ala His Gly His Ser Ala Asn Ile Leu His Thr	
245 250 255	
Leu Glu Glu Ile Lys Lys Ser Leu Val Val Asp Val Ile Val Gly Asn	

50		55		60		65	
gac gcg ctc gct atc aat att ggc acc ctt aat gat cgc gct att tta							300
Asp Ala Leu Ala Ile Asn Ile Gly Thr Leu Asn Asp Arg Ala Ile Leu							
		70		75		80	
tgc gct aaa gag gct atc aag cat tac aag gct ttg aac aaa ccc att							348
Cys Ala Lys Glu Ala Ile Lys His Tyr Lys Ala Leu Asn Lys Pro Ile							
		85		90		95	
gtg tta gat cct gtg ggg tgt tca gcg agc gct ttg cgt cat gac acc							396
Val Leu Asp Pro Val Gly Cys Ser Ala Ser Ala Leu Arg His Asp Thr							
		100		105		110	
agt tta gag ctt ttg aaa agt ggt ggg att agc gcg ctt agg ggt aat							444
Ser Leu Glu Leu Leu Lys Ser Gly Gly Ile Ser Ala Leu Arg Gly Asn							
		115		120		125	
gct gca gaa tta ggc tct tta gtg ggg att tct tgc gaa agt aag ggg							492
Ala Ala Glu Leu Gly Ser Leu Val Gly Ile Ser Cys Glu Ser Lys Gly							
		130		135		140	145
cta gac tct aat gat gcc gcc acg cct gta gaa ata atc aaa tta gcg							540
Leu Asp Ser Asn Asp Ala Ala Thr Pro Val Glu Ile Ile Lys Leu Ala							
		150		155		160	
gct caa aaa tat tct gtg ata gcg gta atg acg ggt aaa aca gat tac							588
Ala Gln Lys Tyr Ser Val Ile Ala Val Met Thr Gly Lys Thr Asp Tyr							
		165		170		175	
gtg agc gat ggg aaa aag gtt ttg agt att act ggg ggg agc gag tat							636
Val Ser Asp Gly Lys Lys Val Leu Ser Ile Thr Gly Gly Ser Glu Tyr							
		180		185		190	
tta gcg ctc att act ggg gct ggg tgt ttg cat gcc gca gca tgc gcg							684
Leu Ala Leu Ile Thr Gly Ala Gly Cys Leu His Ala Ala Ala Cys Ala							
		195		200		205	
agc ttt tta agt ttg aaa aaa gac ccc tta gat tct atg gcg caa ctt							732
Ser Phe Leu Ser Leu Lys Lys Asp Pro Leu Asp Ser Met Ala Gln Leu							
		210		215		220	225
tgc gcg ctc tat aaa caa gcc gct ttt aac gcg caa aaa aag gtg ttg							780
Cys Ala Leu Tyr Lys Gln Ala Ala Phe Asn Ala Gln Lys Lys Val Leu							
		230		235		240	
gaa aat aac ggc tct aat ggt tcg ttc ttg ttt tat ttt tta gat gct							828
Glu Asn Asn Gly Ser Asn Gly Ser Phe Leu Phe Tyr Phe Leu Asp Ala							
		245		250		255	
cta agc ttg ccc ata gag tta gaa aac agc ctt att aag gaa gag tgg							876
Leu Ser Leu Pro Ile Glu Leu Glu Asn Ser Leu Ile Lys Glu Glu Trp							
		260		265		270	
tgaaaattta cccgcaagtt ttaagcattg ctggcagcga tag							919

<210> 136
 <211> 273
 <212> PRT

<213> Helicobacter pylori

<400> 136

```
Met Asp Phe Cys Lys Ile Lys Glu Ile Leu Arg Arg Leu Val Val Leu
 1      5      10
Lys Glu Leu Arg Gln Lys Arg Pro Leu Val His Asn Ile Thr Asn Tyr
 20      25      30
Val Ala Ala Gln Phe Val Ala Asn Gly Leu Leu Ala Leu Gly Ala Ser
 35      40      45
Pro Leu Met Ser Asp Ala Ile Asp Glu Met Arg Asp Leu Ala Lys Ile
 50      55      60
Ser Asp Ala Leu Ala Ile Asn Ile Gly Thr Leu Asn Asp Arg Ala Ile
 65      70      75      80
Leu Cys Ala Lys Glu Ala Ile Lys His Tyr Lys Ala Leu Asn Lys Pro
 85      90      95
Ile Val Leu Asp Pro Val Gly Cys Ser Ala Ser Ala Leu Arg His Asp
100      105      110
Thr Ser Leu Glu Leu Leu Lys Ser Gly Gly Ile Ser Ala Leu Arg Gly
115      120      125
Asn Ala Ala Glu Leu Gly Ser Leu Val Gly Ile Ser Cys Glu Ser Lys
130      135      140
Gly Leu Asp Ser Asn Asp Ala Ala Thr Pro Val Glu Ile Ile Lys Leu
145      150      155      160
Ala Ala Gln Lys Tyr Ser Val Ile Ala Val Met Thr Gly Lys Thr Asp
165      170      175
Tyr Val Ser Asp Gly Lys Lys Val Leu Ser Ile Thr Gly Gly Ser Glu
180      185      190
Tyr Leu Ala Leu Ile Thr Gly Ala Gly Cys Leu His Ala Ala Ala Cys
195      200      205
Ala Ser Phe Leu Ser Leu Lys Lys Asp Pro Leu Asp Ser Met Ala Gln
210      215      220
Leu Cys Ala Leu Tyr Lys Gln Ala Ala Phe Asn Ala Gln Lys Lys Val
225      230      235      240
Leu Glu Asn Asn Gly Ser Asn Gly Ser Phe Leu Phe Tyr Phe Leu Asp
245      250      255
Ala Leu Ser Leu Pro Ile Glu Leu Glu Asn Ser Leu Ile Lys Glu Glu
260      265      270
Trp
```

<210> 137

<211> 1010

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (78)...(971)

<400> 137

```
atccaaataa ttgggcgatt aaagagggaa tttattcaat caaaccaaata aaaaaaatag 60
tattttccaag atttttta atg ttt tgc ttt gaa aat ttg aat att caa aat 110
      Met Phe Cys Phe Glu Asn Leu Asn Ile Gln Asn
      1      5      10

gmt ata aaa agt aaa agt ttt gga gga ata gtt aaa agt ata tca atg 158
Xaa Ile Lys Ser Lys Ser Phe Gly Gly Ile Val Lys Ser Ile Ser Met
      15      20      25
```

aac gat tta caa caa ata acc atc ccc atc cca ccc cta gag atc caa	206
Asn Asp Leu Gln Gln Ile Thr Ile Pro Ile Pro Pro Leu Glu Ile Gln	
30 35 40	
caa gag atc gtt aag att ttg gac gct ttc aca gaa tta aac aca gaa	254
Gln Glu Ile Val Lys Ile Leu Asp Ala Phe Thr Glu Leu Asn Thr Glu	
45 50 55	
tta aac aca gaa tta aaa gcg cgc aaa aag caa tat gag tat tac caa	302
Leu Asn Thr Glu Leu Lys Ala Arg Lys Lys Gln Tyr Glu Tyr Tyr Gln	
60 65 70 75	
aac atg ctt tta gac ttt aac gat att aat caa aac cac aaa gac gcc	350
Asn Met Leu Leu Asp Phe Asn Asp Ile Asn Gln Asn His Lys Asp Ala	
80 85 90	
aaa ata aaa acc tac cct aaa cgc ttg aaa acc tta ctc cac act tta	398
Lys Ile Lys Thr Tyr Pro Lys Arg Leu Lys Thr Leu Leu His Thr Leu	
95 100 105	
gcg cct aag ggg gtg gag ttt agg aaa ttg ggg gag gtg tgt gaa agc	446
Ala Pro Lys Gly Val Glu Phe Arg Lys Leu Gly Glu Val Cys Glu Ser	
110 115 120	
aca aat aaa aaa aca ctc aaa ata agc gaa gta agt gaa gta aaa aat	494
Thr Asn Lys Lys Thr Leu Lys Ile Ser Glu Val Ser Glu Val Lys Asn	
125 130 135	
aag gga atg tat cca gtg ata aat tca ggg agg gat ttg tat ggt tat	542
Lys Gly Met Tyr Pro Val Ile Asn Ser Gly Arg Asp Leu Tyr Gly Tyr	
140 145 150 155	
tac cat gat ttt aac aat gat gga gaa aat ata act att gca tct agg	590
Tyr His Asp Phe Asn Asn Asp Gly Glu Asn Ile Thr Ile Ala Ser Arg	
160 165 170	
gga gaa tat gca gga ttt ata aac tat ttc aat gaa aaa ttt ttt gca	638
Gly Glu Tyr Ala Gly Phe Ile Asn Tyr Phe Asn Glu Lys Phe Phe Ala	
175 180 185	
ggg ggt cta tgt tat ccc tat aaa gtt aaa gac act aac gag ctt tta	686
Gly Gly Leu Cys Tyr Pro Tyr Lys Val Lys Asp Thr Asn Glu Leu Leu	
190 195 200	
aca aaa ttt tta tac ttt tat ctc aaa act aat gaa atc caa att atg	734
Thr Lys Phe Leu Tyr Phe Tyr Leu Lys Thr Asn Glu Ile Gln Ile Met	
205 210 215	
gag aac ctt gtt ttt cgt ggc agt atc ccc gca ctc aat aaa gca gat	782
Glu Asn Leu Val Phe Arg Gly Ser Ile Pro Ala Leu Asn Lys Ala Asp	
220 225 230 235	
att gaa act tta aca atc ccc atc cca cct cta gag atc caa caa gag	830
Ile Glu Thr Leu Thr Ile Pro Ile Pro Pro Leu Glu Ile Gln Gln Glu	
240 245 250	
atc gtt aag att ttg gat caa ttt tca gcc cta acc acc gat tta tta	878
Ile Val Lys Ile Leu Asp Gln Phe Ser Ala Leu Thr Thr Asp Leu Leu	

255	260	265	
gcc ggt atc ccc gct gaa ata aaa gcc cga aaa aag caa tac gaa tat			926
Ala Gly Ile Pro Ala Glu Ile Lys Ala Arg Lys Lys Gln Tyr Glu Tyr			
270	275	280	
tac cga gaa aaa cta ctg acc ttc aaa cct ctc caa aac aag gaa			971
Tyr Arg Glu Lys Leu Leu Thr Phe Lys Pro Leu Gln Asn Lys Glu			
285	290	295	
taacatgagt tacgaaacga tcgcagaaag caatgaaag			1010
 <210> 138			
<211> 298			
<212> PRT			
<213> Helicobacter pylori			
 <220>			
<221> VARIANT			
<222> 12			
<223> Xaa = Any Amino Acid			
 <400> 138			
Met Phe Cys Phe Glu Asn Leu Asn Ile Gln Asn Xaa Ile Lys Ser Lys			
1 5 10 15			
Ser Phe Gly Gly Ile Val Lys Ser Ile Ser Met Asn Asp Leu Gln Gln			
20 25 30			
Ile Thr Ile Pro Ile Pro Pro Leu Glu Ile Gln Gln Glu Ile Val Lys			
35 40 45			
Ile Leu Asp Ala Phe Thr Glu Leu Asn Thr Glu Leu Asn Thr Glu Leu			
50 55 60			
Lys Ala Arg Lys Lys Gln Tyr Glu Tyr Tyr Gln Asn Met Leu Leu Asp			
65 70 75 80			
Phe Asn Asp Ile Asn Gln Asn His Lys Asp Ala Lys Ile Lys Thr Tyr			
85 90 95			
Pro Lys Arg Leu Lys Thr Leu Leu His Thr Leu Ala Pro Lys Gly Val			
100 105 110			
Glu Phe Arg Lys Leu Gly Glu Val Cys Glu Ser Thr Asn Lys Lys Thr			
115 120 125			
Leu Lys Ile Ser Glu Val Ser Glu Val Lys Asn Lys Gly Met Tyr Pro			
130 135 140			
Val Ile Asn Ser Gly Arg Asp Leu Tyr Gly Tyr Tyr His Asp Phe Asn			
145 150 155 160			
Asn Asp Gly Glu Asn Ile Thr Ile Ala Ser Arg Gly Glu Tyr Ala Gly			
165 170 175			
Phe Ile Asn Tyr Phe Asn Glu Lys Phe Phe Ala Gly Gly Leu Cys Tyr			
180 185 190			
Pro Tyr Lys Val Lys Asp Thr Asn Glu Leu Leu Thr Lys Phe Leu Tyr			
195 200 205			
Phe Tyr Leu Lys Thr Asn Glu Ile Gln Ile Met Glu Asn Leu Val Phe			
210 215 220			
Arg Gly Ser Ile Pro Ala Leu Asn Lys Ala Asp Ile Glu Thr Leu Thr			
225 230 235 240			
Ile Pro Ile Pro Pro Leu Glu Ile Gln Gln Glu Ile Val Lys Ile Leu			
245 250 255			
Asp Gln Phe Ser Ala Leu Thr Thr Asp Leu Leu Ala Gly Ile Pro Ala			
260 265 270			
Glu Ile Lys Ala Arg Lys Lys Gln Tyr Glu Tyr Tyr Arg Glu Lys Leu			
275 280 285			

<400> 139																
gattaggggga gttagaaacc atttgcgtgg aagaagatcc c atg tat gaa tgc gaa																56
Met Tyr Glu Cys Glu																
1 5																
gtg gcg att gaa aaa atc cta gaa gat tta ggc att cct agc tct aaa																104
Val Ala Ile Glu Lys Ile Leu Glu Asp Leu Gly Ile Pro Ser Ser Lys																
10 15 20																
cac aac gat ttg atg aaa acc ctg cca agc agc gat aaa ttt aaa atc																152
His Asn Asp Leu Met Lys Thr Leu Pro Ser Ser Asp Lys Phe Lys Ile																
25 30 35																
ctt ctc gct caa gtc ttg ttc cct aaa ccg gat att ttg ctt tta gat																200
Leu Leu Ala Gln Val Leu Phe Pro Lys Pro Asp Ile Leu Leu Leu Asp																
40 45 50																
gag ccg acc aac aac ctg gat tta aac gcc att gaa tgg cta gaa aac																248
Glu Pro Thr Asn Asn Leu Asp Leu Asn Ala Ile Glu Trp Leu Glu Asn																
55 60 65																
aac ctc aaa cgc cat gaa ggc acg atg gtc gtc att agc cat gac agg																296
Asn Leu Lys Arg His Glu Gly Thr Met Val Val Ile Ser His Asp Arg																
70 75 80 85																
cat ttt tta aat gcg gta tgc acg cat att ttg gat ttg gat ttc cac																344
His Phe Leu Asn Ala Val Cys Thr His Ile Leu Asp Leu Asp Phe His																
90 95 100																
agc gtg cgc gaa ttt agc ggg aat tat gac gat tgg tat atc gct tcc																392
Ser Val Arg Glu Phe Ser Gly Asn Tyr Asp Asp Trp Tyr Ile Ala Ser																
105 110 115																
act ctg atc gct aaa cag caa gag gcc gaa cgc aat aaa aaa ctc aaa																440
Thr Leu Ile Ala Lys Gln Gln Glu Ala Glu Arg Asn Lys Lys Leu Lys																
120 125 130																
gaa aaa gaa gag cta gaa aaa ttc atc gcg cgc ttt arn nnn nac gct																488
Glu Lys Glu Glu Leu Glu Lys Phe Ile Ala Arg Phe Xaa Xaa Xaa Ala																
135 140 145																
tct aaa gcc aag caa gcc acc agc cgc caa aaa caa ctg gat aaa tta																536

Ser 150	Lys	Ala	Lys	Gln	Ala 155	Thr	Ser	Arg	Gln	Lys 160	Gln	Leu	Asp	Lys	Leu 165	
gac Asp	att Ile	caa Gln	agt Ser	tta Leu 170	gcg Ala	gta Val	tct Ser	agc Ser	agg Arg 175	agg Arg	gat Asp	cct Pro	agc Ser	att Ile 180	att Ile	584
ttt Phe	aaa Lys	ccc Pro	aaa Lys 185	cgc Arg	acc Thr	att Ile	ggg Gly	aat Asn 190	gaa Glu	gcc Ala	tta Leu	gag Glu	tgc Cys 195	gaa Glu	aac Asn	632
atc Ile	tct Ser	aaa Lys 200	agt Ser	tat Tyr	gac Asp	gac Asp	caa Gln 205	atc Ile	ggt Val	tta Leu	aat Asn	caa Gln 210	gtg Val	agc Ser	ttg Leu	680
aaa Lys	gtg Val 215	atg Met	cct Pro	aaa Lys	gac Asp	aag Lys 220	atc Ile	gcc Ala	ctc Leu	ata Ile	ggg Gly 225	cca Pro	aac Asn	ggc Gly	gtg Val	728
ggg Gly 230	aaa Lys	tcc Ser	acg Thr	ctt Leu	tgt Cys 235	aaa Lys	att Ile	cta Leu	gta Val	gaa Glu 240	gaa Glu	tta Leu	aag Lys	ccg Pro	gat Asp 245	776
aag Lys	ggc Gly	gtg Val	gtg Val	aaa Lys 250	tgg Trp	ggg Gly	gcg Ala	acg Thr	ggt Val 255	tca Ser	aaa Lys	ggc Gly	tat Tyr	ttc Phe 260	cct Pro	824
caa Gln	aac Asn	gtg Val	agc Ser	gaa Glu 265	gaa Glu	att Ile	agc Ser	ggg Gly 270	gaa Glu	gag Glu	acc Thr	ttg Leu	tat Tyr 275	caa Gln	tgg Trp	872
ctc Leu	ttt Phe 280	aac Asn	ttc Phe	aat Asn	aaa Lys	aag Lys	att Ile 285	gaa Glu	agc Ser	gct Ala	gag Glu	ggt Val 290	agg Arg	aac Asn	gct Ala	920
tta Leu 295	ggg Gly	agg Arg	atg Met	ctg Leu	ttt Phe	aat Asn 300	ggc Gly	gaa Glu	gag Glu	caa Gln	gaa Glu 305	aaa Lys	tgc Cys	gtg Val	aac Asn	968
gct Ala 310	tta Leu	agt Ser	ggg Gly	ggc Gly	gaa Glu 315	aaa Lys	cac His	cga Arg	atg Met	ggt Val 320	tta Leu	tcc Ser	aag Lys	ctc Leu	atg Met 325	1016
cta Leu	gag Glu	ggg Gly	ggg Gly	aat Asn 330	ttt Phe	tta Leu	gtc Val	tta Leu	gat Asp 335	gag Glu	cca Pro	acc Thr	aac Asn	cat His 340	ttg Leu	1064
gat Asp	tta Leu	gaa Glu	gcg Ala 345	att Ile	atc Ile	gct Ala	tta Leu	ggc Gly 350	gaa Glu	gcg Ala	ctc Leu	ttt Phe	aaa Lys 355	ttt Phe	gat Asp	1112
ggg Gly	gag Ala	ctg Leu 360	att Ile	tgc Cys	gta Val	agc Ser	cat His 365	gac Asp	aga Arg	gag Glu	ctc Leu	att Ile 370	gat Asp	gag Ala	tat Tyr	1160
gct Ala 375	aat Asn	agg Arg	atc Ile	att Ile	gaa Glu	tta Leu 380	gtc Val	cca Pro	agc Ser	cct Pro	aaa Lys 385	ggc Gly	gct Ala	tca Ser	atc Ile	1208

att gat ttt aaa ggc agt tat gaa gag tat ttg gcg agc aaa aaa 1253
 Ile Asp Phe Lys Gly Ser Tyr Glu Glu Tyr Leu Ala Ser Lys Lys
 390 395 400

tgaaaccgca agacattgaa atcgttcaaaa gcgttttaga gattacagga cc 1305

<210> 140
 <211> 404
 <212> PRT
 <213> Helicobacter pylori

<220>
 <221> VARIANT
 <222> 146, 147, 148
 <223> Xaa = Any Amino Acid

<400> 140
 Met Tyr Glu Cys Glu Val Ala Ile Glu Lys Ile Leu Glu Asp Leu Gly
 1 5 10 15
 Ile Pro Ser Ser Lys His Asn Asp Leu Met Lys Thr Leu Pro Ser Ser
 20 25 30
 Asp Lys Phe Lys Ile Leu Leu Ala Gln Val Leu Phe Pro Lys Pro Asp
 35 40 45
 Ile Leu Leu Leu Asp Glu Pro Thr Asn Asn Leu Asp Leu Asn Ala Ile
 50 55 60
 Glu Trp Leu Glu Asn Asn Leu Lys Arg His Glu Gly Thr Met Val Val
 65 70 75 80
 Ile Ser His Asp Arg His Phe Leu Asn Ala Val Cys Thr His Ile Leu
 85 90 95
 Asp Leu Asp Phe His Ser Val Arg Glu Phe Ser Gly Asn Tyr Asp Asp
 100 105 110
 Trp Tyr Ile Ala Ser Thr Leu Ile Ala Lys Gln Gln Glu Ala Glu Arg
 115 120 125
 Asn Lys Lys Leu Lys Glu Lys Glu Glu Leu Glu Lys Phe Ile Ala Arg
 130 135 140
 Phe Xaa Xaa Xaa Ala Ser Lys Ala Lys Gln Ala Thr Ser Arg Gln Lys
 145 150 155 160
 Gln Leu Asp Lys Leu Asp Ile Gln Ser Leu Ala Val Ser Ser Arg Arg
 165 170 175
 Asp Pro Ser Ile Ile Phe Lys Pro Lys Arg Thr Ile Gly Asn Glu Ala
 180 185 190
 Leu Glu Cys Glu Asn Ile Ser Lys Ser Tyr Asp Asp Gln Ile Val Leu
 195 200 205
 Asn Gln Val Ser Leu Lys Val Met Pro Lys Asp Lys Ile Ala Leu Ile
 210 215 220
 Gly Pro Asn Gly Val Gly Lys Ser Thr Leu Cys Lys Ile Leu Val Glu
 225 230 235 240
 Glu Leu Lys Pro Asp Lys Gly Val Val Lys Trp Gly Ala Thr Val Ser
 245 250 255
 Lys Gly Tyr Phe Pro Gln Asn Val Ser Glu Glu Ile Ser Gly Glu Glu
 260 265 270
 Thr Leu Tyr Gln Trp Leu Phe Asn Phe Asn Lys Lys Ile Glu Ser Ala
 275 280 285
 Glu Val Arg Asn Ala Leu Gly Arg Met Leu Phe Asn Gly Glu Glu Gln
 290 295 300
 Glu Lys Cys Val Asn Ala Leu Ser Gly Gly Glu Lys His Arg Met Val
 305 310 315 320
 Leu Ser Lys Leu Met Leu Glu Gly Gly Asn Phe Leu Val Leu Asp Glu
 325 330 335

Gly	Phe	Leu	Pro	Cys	Met	Met	Val	Tyr	Ser	Phe	Leu	Ala	Ser	Val	Ile	
140					145					150					155	
ctc	agt	cat	agc	gcg	ttt	atg	gga	gcg	atg	cta	ggc	ctt	tct	ttt	ggg	531
Leu	Ser	His	Ser	Ala	Phe	Met	Gly	Ala	Met	Leu	Gly	Leu	Ser	Phe	Gly	
				160					165					170		
ctt	ggc	acc	agc	atg	ccg	ttg	ttt	tta	atg	ggg	att	ttt	tta	agc	aaa	579
Leu	Gly	Thr	Ser	Met	Pro	Leu	Phe	Leu	Met	Gly	Ile	Phe	Leu	Ser	Lys	
			175					180					185			
att	tcc	ggt	tct	tac	agg	aaa	ttt	ttc	aat	ctt	ttg	tct	aaa	att	tta	627
Ile	Ser	Val	Ser	Tyr	Arg	Lys	Phe	Phe	Asn	Leu	Leu	Ser	Lys	Ile	Leu	
		190					195					200				
atg	ggg	ggt	ttt	ggg	ctt	tat	atc	ctt	tat	atg	ggg	atc	atg	ctc	att	675
Met	Gly	Val	Phe	Gly	Leu	Tyr	Ile	Leu	Tyr	Met	Gly	Ile	Met	Leu	Ile	
	205					210					215					
aac	cac	aaa	atg	cct	cat	gcc	atg	cat	cat	caa	aac	aac	acc	act	cag	723
Asn	His	Lys	Met	Pro	His	Ala	Met	His	His	Gln	Asn	Asn	Thr	Thr	Gln	
220					225					230					235	
cat	gat	cat	aaa	gga	gtg	cat	tcg	cat	gaa	cac	taacaaaagcc	cttttttttgg				776
His	Asp	His	Lys	Gly	Val	His	Ser	His	Glu	His						
				240					245							
acagagacgg	cattatcaat	attga														801

<210> 142

<211> 246

<212> PRT

<213> Helicobacter pylori

<400> 142

Met	Gln	Met	Met	His	Asn	Leu	Ser	Phe	Leu	Gly	Met	Phe	Leu	Ala	Ala	
1				5					10					15		
Leu	Ser	Met	Ser	Leu	Gly	His	Cys	Val	Gly	Met	Cys	Gly	Gly	Ile	Val	
			20					25					30			
Ser	Ala	Phe	Ser	Gln	Ile	Arg	Phe	Ser	Lys	Val	Thr	Ser	Phe	Ser	Tyr	
		35					40					45				
Gln	Leu	Thr	Cys	His	Ala	Leu	Tyr	Asn	Val	Gly	Arg	Ile	Ser	Thr	Tyr	
	50					55				60						
Met	Leu	Leu	Gly	Ala	Ile	Ala	Ala	Ser	Leu	Gly	His	Ser	Leu	Ser	Val	
65				70						75					80	
Ser	Met	Gly	Phe	Arg	Gly	Val	Leu	Phe	Ile	Ser	Met	Gly	Ile	Ile	Leu	
				85					90					95		
Ile	Cys	Leu	Ala	Leu	Leu	Gly	Ala	Arg	Met	Glu	Lys	Leu	Ser	Phe	Gln	
			100					105					110			
Ile	Pro	Phe	Ile	Ser	Phe	Leu	Met	Lys	Lys	Thr	Leu	Gln	Ser	Gln	Asn	
		115					120					125				
Ile	Leu	Gly	Leu	Tyr	Phe	Leu	Gly	Val	Leu	Asn	Gly	Phe	Leu	Pro	Cys	
	130					135					140					
Met	Met	Val	Tyr	Ser	Phe	Leu	Ala	Ser	Val	Ile	Leu	Ser	His	Ser	Ala	
145					150					155					160	
Phe	Met	Gly	Ala	Met	Leu	Gly	Leu	Ser	Phe	Gly	Leu	Gly	Thr	Ser	Met	
				165					170					175		
Pro	Leu	Phe	Leu	Met	Gly	Ile	Phe	Leu	Ser	Lys	Ile	Ser	Val	Ser	Tyr	
			180					185						190		

Arg	Lys	Phe	Phe	Asn	Leu	Leu	Ser	Lys	Ile	Leu	Met	Gly	Val	Phe	Gly
		195					200					205			
Leu	Tyr	Ile	Leu	Tyr	Met	Gly	Ile	Met	Leu	Ile	Asn	His	Lys	Met	Pro
	210					215					220				
His	Ala	Met	His	His	Gln	Asn	Asn	Thr	Thr	Gln	His	Asp	His	Lys	Gly
225					230					235					240
Val	His	Ser	His	Glu	His										
				245											

<210> 143
 <211> 735
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (1)...(693)

<221> misc_feature
 <222> 9, 12
 <223> n = A,T,C or G

aac	tgc	ctn	tcn	tcg	ctc	aac	acg	att	gta	tta	aac	cat	aat	aaa	ttg	48
Asn	Cys	Leu	Ser	Ser	Leu	Asn	Thr	Ile	Val	Leu	Asn	His	Asn	Lys	Leu	
1				5					10					15		
tat	tct	tta	gaa	aaa	cga	ggg	tat	gtg	ata	gag	gtg	gat	tta	aat	gat	96
Tyr	Ser	Leu	Glu	Lys	Arg	Gly	Tyr	Val	Ile	Glu	Val	Asp	Leu	Asn	Asp	
			20					25					30			
ttt	gat	tcg	tat	aat	gtc	tat	aaa	acg	cca	act	ata	ggc	agt	ttt	aag	144
Phe	Asp	Ser	Tyr	Asn	Val	Tyr	Lys	Thr	Pro	Thr	Ile	Gly	Ser	Phe	Lys	
			35				40					45				
ttt	ttt	tca	tct	aat	cgt	ttg	gat	aaa	ggg	gtg	ttt	tat	gat	aaa	aat	192
Phe	Phe	Ser	Ser	Asn	Arg	Leu	Asp	Lys	Gly	Val	Phe	Tyr	Asp	Lys	Asn	
		50				55					60					
cgg	gtg	tat	tac	gat	cgc	tac	tat	tta	gat	tat	aac	gat	ttt	aaa	cca	240
Arg	Val	Tyr	Tyr	Asp	Arg	Tyr	Tyr	Leu	Asp	Tyr	Asn	Asp	Phe	Lys	Pro	
65					70				75						80	
aaa	ctt	tat	ccc	ggt	gtg	gaa	aaa	tcg	gca	tct	aaa	aaa	tct	caa	aaa	288
Lys	Leu	Tyr	Pro	Val	Val	Glu	Lys	Ser	Ala	Ser	Lys	Lys	Ser	Gln	Lys	
				85					90					95		
ggc	gaa	aaa	ggg	aac	gct	cct	att	tat	ttg	caa	gaa	agg	cat	aaa	gct	336
Gly	Glu	Lys	Gly	Asn	Ala	Pro	Ile	Tyr	Leu	Gln	Glu	Arg	His	Lys	Ala	
			100				105						110			
aaa	gaa	aat	aaa	cag	cct	tta	gaa	gaa	aac	aaa	gtt	aaa	cca	aga	aat	384
Lys	Glu	Asn	Lys	Gln	Pro	Leu	Glu	Glu	Asn	Lys	Val	Lys	Pro	Arg	Asn	
		115				120						125				
agc	ggg	ttt	gaa	gaa	gaa	gag	gtt	aaa	acc	aga	agg	cct	gag	cct	att	432
Ser	Gly	Phe	Glu	Glu	Glu	Glu	Val	Lys	Thr	Arg	Arg	Pro	Glu	Pro	Ile	
	130					135					140					

agg gat caa aat aac gcc acc caa caa ggc gaa aca aaa aac aat gaa 480
 Arg Asp Gln Asn Asn Ala Thr Gln Gln Gly Glu Thr Lys Asn Asn Glu
 145 150 155 160

agt aaa aac gct cct gtc tta aaa gaa aac gcc gct aaa aaa gaa gtg 528
 Ser Lys Asn Ala Pro Val Leu Lys Glu Asn Ala Ala Lys Lys Glu Val
 165 170 175

cca aaa cca aat tct aaa gaa gaa aaa cgc cgc ttg aaa gaa gaa aag 576
 Pro Lys Pro Asn Ser Lys Glu Glu Lys Arg Arg Leu Lys Glu Glu Lys
 180 185 190

aaa aaa gcc aaa gcc gaa caa aga gcg aga gaa ttt gaa caa aga gcg 624
 Lys Lys Ala Lys Ala Glu Gln Arg Ala Arg Glu Phe Glu Gln Arg Ala
 195 200 205

aga gag cat caa gaa aga gat gaa aaa gag ctt gaa gaa aga aga aaa 672
 Arg Glu His Gln Glu Arg Asp Glu Lys Glu Leu Glu Glu Arg Arg Lys
 210 215 220

gct tta gaa atg aat aag aag taggcctatg ccagctaggc aatcttttac 723
 Ala Leu Glu Met Asn Lys Lys
 225 230

agatttgaaa aa 735

<210> 144

<211> 231

<212> PRT

<213> Helicobacter pylori

<220>

<221> VARIANT

<222> 3, 4

<223> Xaa = Any Amino Acid

<400> 144

Asn Cys Xaa Xaa Ser Leu Asn Thr Ile Val Leu Asn His Asn Lys Leu
 1 5 10 15
 Tyr Ser Leu Glu Lys Arg Gly Tyr Val Ile Glu Val Asp Leu Asn Asp
 20 25 30
 Phe Asp Ser Tyr Asn Val Tyr Lys Thr Pro Thr Ile Gly Ser Phe Lys
 35 40 45
 Phe Phe Ser Ser Asn Arg Leu Asp Lys Gly Val Phe Tyr Asp Lys Asn
 50 55 60
 Arg Val Tyr Tyr Asp Arg Tyr Tyr Leu Asp Tyr Asn Asp Phe Lys Pro
 65 70 75 80
 Lys Leu Tyr Pro Val Val Glu Lys Ser Ala Ser Lys Lys Ser Gln Lys
 85 90 95
 Gly Glu Lys Gly Asn Ala Pro Ile Tyr Leu Gln Glu Arg His Lys Ala
 100 105 110
 Lys Glu Asn Lys Gln Pro Leu Glu Glu Asn Lys Val Lys Pro Arg Asn
 115 120 125
 Ser Gly Phe Glu Glu Glu Glu Val Lys Thr Arg Arg Pro Glu Pro Ile
 130 135 140
 Arg Asp Gln Asn Asn Ala Thr Gln Gln Gly Glu Thr Lys Asn Asn Glu
 145 150 155 160
 Ser Lys Asn Ala Pro Val Leu Lys Glu Asn Ala Ala Lys Lys Glu Val

120	125	130	135	
att agc aat aac cct aac gcc agc caa caa tct atc gtt att cct ttg				486
Ile Ser Asn Asn Pro Asn Ala Ser Gln Gln Ser Ile Val Ile Pro Leu	140	145	150	
gag act ttt gcc ttg agc gca agc gtt aaa ggg aat ctt tta gcg gtg				534
Glu Thr Phe Ala Leu Ser Ala Ser Val Lys Gly Asn Leu Leu Ala Val	155	160	165	
gtg tta gcg gac aat tca gcg aac tta tac gac atc act tct caa aaa				582
Val Leu Ala Asp Asn Ser Ala Asn Leu Tyr Asp Ile Thr Ser Gln Lys	170	175	180	
ttg ctt ttt agt gag aaa ggt tcc cca agc acc acg atc aat tct tta				630
Leu Leu Phe Ser Glu Lys Gly Ser Pro Ser Thr Thr Ile Asn Ser Leu	185	190	195	
atg gcg atg cct att ttt atg gat acg gtc gtg gtg ttc ccc atg cta				678
Met Ala Met Pro Ile Phe Met Asp Thr Val Val Val Phe Pro Met Leu	200	205	210	215
gat ggg cgc ttg ttg gtc gtg gat tat gtg cac gga aac cct acg cct				726
Asp Gly Arg Leu Leu Val Val Asp Tyr Val His Gly Asn Pro Thr Pro	220	225	230	
att aga aac att gtt atc agc agc gat aag ttt ttt aac aat atc acc				774
Ile Arg Asn Ile Val Ile Ser Ser Asp Lys Phe Phe Asn Asn Ile Thr	235	240	245	
tac ctt atc gta gat ggc aat aac atg atc gct tct aca ggg aaa agg				822
Tyr Leu Ile Val Asp Gly Asn Asn Met Ile Ala Ser Thr Gly Lys Arg	250	255	260	
ata ctc tca gta gtg agc ggt caa gag ttc aac tat gat ggg gat att				870
Ile Leu Ser Val Val Ser Gly Gln Glu Phe Asn Tyr Asp Gly Asp Ile	265	270	275	
gtg gat ttg ctt tat gat aag ggg act tta tat gtg ctc acg cta gac				918
Val Asp Leu Leu Tyr Asp Lys Gly Thr Leu Tyr Val Leu Thr Leu Asp	280	285	290	295
ggg cag att ttg caa atg gat aag agt ttg agg gaa tta aac agc gtg				966
Gly Gln Ile Leu Gln Met Asp Lys Ser Leu Arg Glu Leu Asn Ser Val	300	305	310	
aaa ctg cct ntc ntc gct caa cac gat tgt att aaa cca taataaattg				1015
Lys Leu Pro Xaa Xaa Ala Gln His Asp Cys Ile Lys Pro	315	320		
tattcttttag aaaaacgagg gtatgtgata ga				1047
<210> 146				
<211> 324				
<212> PRT				
<213> Helicobacter pylori				
<220>				
<221> VARIANT				

<222> 315, 316
 <223> Xaa = Any Amino Acid

<400> 146

Met	Asn	Lys	Pro	Phe	Leu	Ile	Leu	Leu	Ile	Ala	Leu	Ile	Val	Phe	Ser
1				5				10						15	
Gly	Cys	Asn	Met	Arg	Lys	Tyr	Phe	Lys	Pro	Ala	Lys	His	Gln	Ile	Lys
		20						25					30		
Gly	Glu	Ala	Tyr	Phe	Pro	Asn	His	Leu	Gln	Glu	Ser	Ile	Val	Ser	Ser
		35					40					45			
Asn	Arg	Tyr	Gly	Ala	Ile	Leu	Lys	Asn	Gly	Ala	Val	Ile	Gly	Asp	Lys
	50					55					60				
Gly	Leu	Thr	Gln	Leu	Arg	Ile	Gly	Lys	Asn	Phe	Asn	Tyr	Glu	Ser	Ser
65				70						75					80
Phe	Leu	Asn	Glu	Ser	Gln	Gly	Phe	Phe	Ile	Leu	Ala	Gln	Asp	Cys	Leu
				85					90					95	
Asn	Lys	Ile	Asp	Lys	Lys	Thr	Asn	Lys	Ser	Lys	Val	Ala	Lys	Thr	Glu
			100					105					110		
Glu	Thr	Glu	Leu	Lys	Leu	Lys	Gly	Val	Glu	Ala	Glu	Val	Gln	Asp	Lys
		115					120					125			
Val	Cys	His	Gln	Val	Glu	Leu	Ile	Ser	Asn	Asn	Pro	Asn	Ala	Ser	Gln
	130					135					140				
Gln	Ser	Ile	Val	Ile	Pro	Leu	Glu	Thr	Phe	Ala	Leu	Ser	Ala	Ser	Val
145					150					155					160
Lys	Gly	Asn	Leu	Leu	Ala	Val	Val	Leu	Ala	Asp	Asn	Ser	Ala	Asn	Leu
				165					170					175	
Tyr	Asp	Ile	Thr	Ser	Gln	Lys	Leu	Leu	Phe	Ser	Glu	Lys	Gly	Ser	Pro
			180					185					190		
Ser	Thr	Thr	Ile	Asn	Ser	Leu	Met	Ala	Met	Pro	Ile	Phe	Met	Asp	Thr
		195					200					205			
Val	Val	Val	Phe	Pro	Met	Leu	Asp	Gly	Arg	Leu	Leu	Val	Val	Asp	Tyr
	210					215					220				
Val	His	Gly	Asn	Pro	Thr	Pro	Ile	Arg	Asn	Ile	Val	Ile	Ser	Ser	Asp
225					230					235					240
Lys	Phe	Phe	Asn	Asn	Ile	Thr	Tyr	Leu	Ile	Val	Asp	Gly	Asn	Asn	Met
				245						250				255	
Ile	Ala	Ser	Thr	Gly	Lys	Arg	Ile	Leu	Ser	Val	Val	Ser	Gly	Gln	Glu
			260					265					270		
Phe	Asn	Tyr	Asp	Gly	Asp	Ile	Val	Asp	Leu	Leu	Tyr	Asp	Lys	Gly	Thr
		275					280					285			
Leu	Tyr	Val	Leu	Thr	Leu	Asp	Gly	Gln	Ile	Leu	Gln	Met	Asp	Lys	Ser
	290					295					300				
Leu	Arg	Glu	Leu	Asn	Ser	Val	Lys	Leu	Pro	Xaa	Xaa	Ala	Gln	His	Asp
305					310					315					320
Cys	Ile	Lys	Pro												

<210> 147
 <211> 410
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (16)...(366)

<400> 147
 agattaaggt ttagt atg cat gaa tac tcg gtc gtt tct tct tta atc gct 51

Met	His	Glu	Tyr	Ser	Val	Val	Ser	Ser	Leu	Ile	Ala	
1				5					10			
ctt tgc gaa gag cat gcg aag aaa aat caa gcc cat aag att gaa aga	99											
Leu Cys Glu Glu His Ala Lys Lys Asn Gln Ala His Lys Ile Glu Arg												
15 20 25												
gtc gtg gtc ggt att ggt gaa aga agt gct atg gat aag agc ttg ttt	147											
Val Val Val Gly Ile Gly Glu Arg Ser Ala Met Asp Lys Ser Leu Phe												
30 35 40												
gtg agt gcg ttt gag act ttt aga gaa gaa tct ttg gtg tgt aaa gac	195											
Val Ser Ala Phe Glu Thr Phe Arg Glu Glu Ser Leu Val Cys Lys Asp												
45 50 55 60												
gct att tta gac att gta gat gaa aag gtt gaa tta gaa tgc aag gat	243											
Ala Ile Leu Asp Ile Val Asp Glu Lys Val Glu Leu Glu Cys Lys Asp												
65 70 75												
tgt tcg cat gtt ttt aag cct aac gcg cta gat tat ggg gtg tgt gag	291											
Cys Ser His Val Phe Lys Pro Asn Ala Leu Asp Tyr Gly Val Cys Glu												
80 85 90												
aaa tgc cac agc aag aat gtt att atc act caa ggc aat gaa atg cgt	339											
Lys Cys His Ser Lys Asn Val Ile Ile Thr Gln Gly Asn Glu Met Arg												
95 100 105												
ttg ttg tct tta gaa atg tta gcg gaa taaccgatgc aagaagaatt	386											
Leu Leu Ser Leu Glu Met Leu Ala Glu												
110 115												
gaacgcttac cagcaagaaa ttga	410											
<210> 148												
<211> 117												
<212> PRT												
<213> Helicobacter pylori												
<400> 148												
Met His Glu Tyr Ser Val Val Ser Ser Leu Ile Ala Leu Cys Glu Glu												
1 5 10 15												
His Ala Lys Lys Asn Gln Ala His Lys Ile Glu Arg Val Val Val Gly												
20 25 30												
Ile Gly Glu Arg Ser Ala Met Asp Lys Ser Leu Phe Val Ser Ala Phe												
35 40 45												
Glu Thr Phe Arg Glu Glu Ser Leu Val Cys Lys Asp Ala Ile Leu Asp												
50 55 60												
Ile Val Asp Glu Lys Val Glu Leu Glu Cys Lys Asp Cys Ser His Val												
65 70 75 80												
Phe Lys Pro Asn Ala Leu Asp Tyr Gly Val Cys Glu Lys Cys His Ser												
85 90 95												
Lys Asn Val Ile Ile Thr Gln Gly Asn Glu Met Arg Leu Leu Ser Leu												
100 105 110												
Glu Met Leu Ala Glu												
115												
<210> 149												
<211> 840												

<212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (38)...(769)

```

<400> 149
ttgcaaaaac tctcattaaa aacaaggagc aaaaaag atg aaa aag gcg ggc ttt 55
                                   Met Lys Lys Ala Gly Phe
                                   1           5

ctt ttt tta gcg gta atg gct atc gtt gtt atg agt tta aac gct aaa 103
Leu Phe Leu Ala Val Met Ala Ile Val Val Met Ser Leu Asn Ala Lys
              10              15              20

gat ccg aat gtg ttg cgt aag att gtt ttt gag aaa tgt ctg cct aat 151
Asp Pro Asn Val Leu Arg Lys Ile Val Phe Glu Lys Cys Leu Pro Asn
              25              30              35

tat gag aaa aat cag aat cct tcg cca tgc ata gaa gtc aaa ccc gat 199
Tyr Glu Lys Asn Gln Asn Pro Ser Pro Cys Ile Glu Val Lys Pro Asp
              40              45              50

gcc ggc tat gtg gtt tta aaa gat att aac ggc ccg ttg caa tat ttg 247
Ala Gly Tyr Val Val Leu Lys Asp Ile Asn Gly Pro Leu Gln Tyr Leu
              55              60              65

ttg atg cca aca act cac att agc ggt att gaa agc cct ttg tta ctt 295
Leu Met Pro Thr Thr His Ile Ser Gly Ile Glu Ser Pro Leu Leu Leu
              75              80              85

gat cct tct acg cct aac ttt ttt tat tta tcc tgg caa gcg cgt gat 343
Asp Pro Ser Thr Pro Asn Phe Phe Tyr Leu Ser Trp Gln Ala Arg Asp
              90              95              100

ttt atg agt aaa aaa tac ggc caa ccc att cct gat tat gcg att tct 391
Phe Met Ser Lys Lys Tyr Gly Gln Pro Ile Pro Asp Tyr Ala Ile Ser
              105              110              115

ttg acg att aac tct agc aaa ggg cga tcg caa aac cat ttt cat atc 439
Leu Thr Ile Asn Ser Ser Lys Gly Arg Ser Gln Asn His Phe His Ile
              120              125              130

cat atc tct tgc att agt ctt gaa gca cgc aaa cag ctg gat aat aac 487
His Ile Ser Cys Ile Ser Leu Glu Ala Arg Lys Gln Leu Asp Asn Asn
              135              140              145              150

cta aaa aaa atc aac agc cgt tgg tcg cca tta ccg ggc ggt ttg aat 535
Leu Lys Lys Ile Asn Ser Arg Trp Ser Pro Leu Pro Gly Gly Leu Asn
              155              160              165

ggg cat aaa tac ttg gcg cgt cgg gta aca gag agc gag tta gtg caa 583
Gly His Lys Tyr Leu Ala Arg Arg Val Thr Glu Ser Glu Leu Val Gln
              170              175              180

aaa agc ccg ttt gtc atg ctt aat aaa gaa gtg cct aat gcg tac aaa 631
Lys Ser Pro Phe Val Met Leu Asn Lys Glu Val Pro Asn Ala Tyr Lys
              185              190              195

```

cgc atg ggg gac tat ggc tta gcg gtg gtg caa caa agc gat aac tcc 679
 Arg Met Gly Asp Tyr Gly Leu Ala Val Val Gln Gln Ser Asp Asn Ser
 200 205 210

ttt gtc tta tta gcg aca caa ttt aac cca ttg act tta aat cgc gct 727
 Phe Val Leu Leu Ala Thr Gln Phe Asn Pro Leu Thr Leu Asn Arg Ala
 215 220 225 230

tca gcc gaa gag att caa gat cat gaa tgc gcg att ttg cac 769
 Ser Ala Glu Glu Ile Gln Asp His Glu Cys Ala Ile Leu His
 235 240

taaagcgagt tagattctta agcttgagcg ataaccttta aaaagcgta tgggggtggtg 829
 ttgcaaaacc c 840

<210> 150
 <211> 244
 <212> PRT
 <213> Helicobacter pylori

<400> 150
 Met Lys Lys Ala Gly Phe Leu Phe Leu Ala Val Met Ala Ile Val Val
 1 5 10 15
 Met Ser Leu Asn Ala Lys Asp Pro Asn Val Leu Arg Lys Ile Val Phe
 20 25 30
 Glu Lys Cys Leu Pro Asn Tyr Glu Lys Asn Gln Asn Pro Ser Pro Cys
 35 40 45
 Ile Glu Val Lys Pro Asp Ala Gly Tyr Val Val Leu Lys Asp Ile Asn
 50 55 60
 Gly Pro Leu Gln Tyr Leu Leu Met Pro Thr Thr His Ile Ser Gly Ile
 65 70 75 80
 Glu Ser Pro Leu Leu Leu Asp Pro Ser Thr Pro Asn Phe Phe Tyr Leu
 85 90 95
 Ser Trp Gln Ala Arg Asp Phe Met Ser Lys Lys Tyr Gly Gln Pro Ile
 100 105 110
 Pro Asp Tyr Ala Ile Ser Leu Thr Ile Asn Ser Ser Lys Gly Arg Ser
 115 120 125
 Gln Asn His Phe His Ile His Ile Ser Cys Ile Ser Leu Glu Ala Arg
 130 135 140
 Lys Gln Leu Asp Asn Asn Leu Lys Lys Ile Asn Ser Arg Trp Ser Pro
 145 150 155 160
 Leu Pro Gly Gly Leu Asn Gly His Lys Tyr Leu Ala Arg Arg Val Thr
 165 170 175
 Glu Ser Glu Leu Val Gln Lys Ser Pro Phe Val Met Leu Asn Lys Glu
 180 185 190
 Val Pro Asn Ala Tyr Lys Arg Met Gly Asp Tyr Gly Leu Ala Val Val
 195 200 205
 Gln Gln Ser Asp Asn Ser Phe Val Leu Leu Ala Thr Gln Phe Asn Pro
 210 215 220
 Leu Thr Leu Asn Arg Ala Ser Ala Glu Glu Ile Gln Asp His Glu Cys
 225 230 235 240
 Ala Ile Leu His

<210> 151
 <211> 481
 <212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (22)...(441)

<400> 151

```
atattgaaag ataatcaaaa a atg aag aca agc gct aaa gta tta ttg act 51
                        Met Lys Thr Ser Ala Lys Val Leu Leu Thr 10
                        1                    5

tta ttg att gta ata tca tta ggt aag gga tta aat agt ctc ata tca 99
Leu Leu Ile Val Ile Ser Leu Gly Lys Gly Leu Asn Ser Leu Ile Ser 25
                        15                    20

gct tgg cgt ggc aaa gat gat gcg atc ccc att gaa aca aga ctc cat 147
Ala Trp Arg Gly Lys Asp Asp Ala Ile Pro Ile Glu Thr Arg Leu His 40
                        30                    35

aaa aac aaa ctg aca atc att tct aaa aca gac agc ata gaa atc caa 195
Lys Asn Lys Leu Thr Ile Ile Ser Lys Thr Asp Ser Ile Glu Ile Gln 55
                        45                    50

gac att cag ttt aat aga gag aat tgt tct cac act tat act agt aag 243
Asp Ile Gln Phe Asn Arg Glu Asn Cys Ser His Thr Tyr Thr Ser Lys 70
                        60                    65

gat ttg gaa aaa att caa aaa gat tta gaa gag ctt gaa gaa gga gtg 291
Asp Leu Glu Lys Ile Gln Lys Asp Leu Glu Glu Leu Glu Glu Gly Val 90
                        75                    80

cct gaa ttg ttc gag gag ctt gag cgt gat gaa gag tcc atc gct aaa 339
Pro Glu Leu Phe Glu Glu Leu Glu Arg Asp Glu Glu Ser Ile Ala Lys 105
                        95                    100

aat aaa aaa acg atc caa gag tat caa aat aaa att gct aat ttt caa 387
Asn Lys Lys Thr Ile Gln Glu Tyr Gln Asn Lys Ile Ala Asn Phe Gln 120
                        110                    115

aaa tac tat aaa gat ata aaa gat att gac gat tat tcg gcg tta atg 435
Lys Tyr Tyr Lys Asp Ile Lys Asp Ile Asp Asp Tyr Ser Ala Leu Met 135
                        125                    130

gct caa tgaacataaa gattcttata cttgggataa tgatcttgat 481
Ala Gln
140
```

<210> 152

<211> 140

<212> PRT

<213> Helicobacter pylori

<400> 152

```
Met Lys Thr Ser Ala Lys Val Leu Leu Thr Leu Leu Ile Val Ile Ser
1                    5                    10                    15
Leu Gly Lys Gly Leu Asn Ser Leu Ile Ser Ala Trp Arg Gly Lys Asp
20                    25                    30
Asp Ala Ile Pro Ile Glu Thr Arg Leu His Lys Asn Lys Leu Thr Ile
```

		35					40				45						
Ile	Ser	Lys	Thr	Asp	Ser	Ile	Glu	Ile	Gln	Asp	Ile	Gln	Phe	Asn	Arg		
	50					55					60						
Glu	Asn	Cys	Ser	His	Thr	Tyr	Thr	Ser	Lys	Asp	Leu	Glu	Lys	Ile	Gln		
65					70					75					80		
Lys	Asp	Leu	Glu	Glu	Leu	Glu	Glu	Gly	Val	Pro	Glu	Leu	Phe	Glu	Glu		
			85						90					95			
Leu	Glu	Arg	Asp	Glu	Glu	Ser	Ile	Ala	Lys	Asn	Lys	Lys	Thr	Ile	Gln		
			100					105						110			
Glu	Tyr	Gln	Asn	Lys	Ile	Ala	Asn	Phe	Gln	Lys	Tyr	Tyr	Lys	Asp	Ile		
		115					120						125				
Lys	Asp	Ile	Asp	Asp	Tyr	Ser	Ala	Leu	Met	Ala	Gln						
	130					135					140						

<210> 153
 <211> 540
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (28)...(486)
 <221> misc_feature
 <222> 409, 457
 <223> n = A,T,C or G

<400> 153
 gaaaattagg taataaatat aaccagt atg cta aaa aaa ata ttt tta acc aac 54
 Met Leu Lys Lys Ile Phe Leu Thr Asn
 1 5

agc tta ggg att tta tgc tct agg att ttt ggc ttt tta cgg gat ttg 102
 Ser Leu Gly Ile Leu Cys Ser Arg Ile Phe Gly Phe Leu Arg Asp Leu
 10 15 20 25

atg atg gct aat att cta ggg gct ggg gtg tat agc gat att ttc ttt 150
 Met Met Ala Asn Ile Leu Gly Ala Gly Val Tyr Ser Asp Ile Phe Phe
 30 35 40

gtg gct ttc aaa ttg cct aat tta ttc agg cgt att ttt gcg gag ggc 198
 Val Ala Phe Lys Leu Pro Asn Leu Phe Arg Arg Ile Phe Ala Glu Gly
 45 50 55

tct ttt tca caa agc ttt tta ccg agc ttc ata cga agt tct att aaa 246
 Ser Phe Ser Gln Ser Phe Leu Pro Ser Phe Ile Arg Ser Ser Ile Lys
 60 65 70

ggg agc ttt gcg agt ttg gta ggg ctt att ttt tgt atc gtt tta ttc 294
 Gly Ser Phe Ala Ser Leu Val Gly Leu Ile Phe Cys Ile Val Leu Phe
 75 80 85

atg tgg tgc tta ttg gtg gcg tta aat ccc tta tgg cta gct aaa ctc 342
 Met Trp Cys Leu Leu Val Ala Leu Asn Pro Leu Trp Leu Ala Lys Leu
 90 95 100 105

cta gct tac ggc ttt gat gaa gaa acg ctc aaa tta tgc gcc cct att 390
 Leu Ala Tyr Gly Phe Asp Glu Glu Thr Leu Lys Leu Cys Ala Pro Ile

	110								115				120				
gta gcg atc aat ttt tgg nat ctt tta ttg gtg ttt atc acc acc ttt																	438
Val Ala Ile Asn Phe Trp Xaa Leu Leu Leu Val Phe Ile Thr Thr Phe																	
	125								130				135				
tta ggc gcg ctt tta caa nta caa aca cag ctt ttt tgc cag cgc tta																	486
Leu Gly Ala Leu Leu Gln Xaa Gln Thr Gln Leu Phe Cys Gln Arg Leu																	
	140								145				150				
tagcgcaagc ttactcaatg tatgcatgat ttagccctt ttgatttcta aaga																	540

atc gcc tta gct tgc gtg att tta gcg gtg gtg gtg ctg ttg ttt gga	104
Ile Ala Leu Ala Cys Val Ile Leu Ala Val Val Val Leu Leu Phe Gly	
10 15 20	
ggg gag tcc ttg agc ttg gaa gaa tgg caa gaa gtg tgc ctt aat gtg	152
Gly Glu Ser Leu Ser Leu Glu Glu Trp Gln Glu Val Cys Leu Asn Val	
25 30 35	
aaa aac cac ttt ttg cac aat gaa gaa ctg agc tct tta agt att att	200
Lys Asn His Phe Leu His Asn Glu Glu Leu Ser Ser Leu Ser Ile Ile	
40 45 50	
att tta gaa ata cga cta cca cga gtg att tta gcg ctc ctg gtg gga	248
Ile Leu Glu Ile Arg Leu Pro Arg Val Ile Leu Ala Leu Leu Val Gly	
55 60 65 70	
gcg agt ttg tct ggg agt ggg gtg gtg atg caa acg att ttt aga aac	296
Ala Ser Leu Ser Gly Ser Gly Val Val Met Gln Thr Ile Phe Arg Asn	
75 80 85	
ccc tta gtg gat ccc ttt tta cta ggg att tct agc ggg gcg atg cta	344
Pro Leu Val Asp Pro Phe Leu Leu Gly Ile Ser Ser Gly Ala Met Leu	
90 95 100	
ggc gtg gcg atg gcg ata gcg gta gtg gag tct aac att gcg att ttg	392
Gly Val Ala Met Ala Ile Ala Val Val Glu Ser Asn Ile Ala Ile Leu	
105 110 115	
gcg ttt ttt ggg gcg att tta gct agc ctt gct gtt ttg gcg atg aat	440
Ala Phe Phe Gly Ala Ile Leu Ala Ser Leu Ala Val Leu Ala Met Asn	
120 125 130	
agg gtt ttg ggt aat tcc gtc ctt tcg ttg gtg ctt tca ggg gtg gtg	488
Arg Val Leu Gly Asn Ser Val Leu Ser Leu Val Leu Ser Gly Val Val	
135 140 145 150	
ttg agc gcg ttt tta agc gcc tta gcc gga gcg ata aaa ttc ttt gtg	536
Leu Ser Ala Phe Leu Ser Ala Leu Ala Gly Ala Ile Lys Phe Phe Val	
155 160 165	
atc ccc caa aaa gcg caa gcg att gtc gtg tgg ctt tta ggg agc ttg	584
Ile Pro Gln Lys Ala Gln Ala Ile Val Val Trp Leu Leu Gly Ser Leu	
170 175 180	
tcg ttg agc agt tat aag gat tgc ttg atc gct ttc ata ggg cta tct	632
Ser Leu Ser Ser Tyr Lys Asp Cys Leu Ile Ala Phe Ile Gly Leu Ser	
185 190 195	
tta ggc ttt atc ccg ctt ttt ttg tta agg tgg cgc atc aat tta ttg	680
Leu Gly Phe Ile Pro Leu Phe Leu Leu Arg Trp Arg Ile Asn Leu Leu	
200 205 210	
agc ttg agc gat gcg caa agt ttg agc ttg ggg att aac ccg gtg ctg	728
Ser Leu Ser Asp Ala Gln Ser Leu Ser Leu Gly Ile Asn Pro Val Leu	
215 220 225 230	
ttg cga tcg ctt tgt ttg gtg tgc gtg agc gtt gcg agc gct tta gcg	776
Leu Arg Ser Leu Cys Leu Val Cys Val Ser Val Ala Ser Ala Leu Ala	
235 240 245	

gtg agc gtg tcc ggc acg att ggc tgg att ggg tta gtc att ccg cat	824
Val Ser Val Ser Gly Thr Ile Gly Trp Ile Gly Leu Val Ile Pro His	
250 255 260	
gtg gct agg ttg ttt ttt ggg gcg aat ttg caa aaa ctg ctt tta agt	872
Val Ala Arg Leu Phe Phe Gly Ala Asn Leu Gln Lys Leu Leu Leu Ser	
265 270 275	
tct ttg tta atg gga gcg ttt ttc ttg ctt cta gcg gat gtg gtg gct	920
Ser Leu Leu Met Gly Ala Phe Phe Leu Leu Leu Ala Asp Val Val Ala	
280 285 290	
aaa acc att acc ccc tat gat tta ccg gta ggc att gcg aca agc gtt	968
Lys Thr Ile Thr Pro Tyr Asp Leu Pro Val Gly Ile Ala Thr Ser Val	
295 300 305 310	
tta gga gcg cct ttc ttc ttg tgg ctt ttg ttt aga act agg ggg gtg	1016
Leu Gly Ala Pro Phe Phe Leu Trp Leu Leu Phe Arg Thr Arg Gly Val	
315 320 325	
tgatggtttt agaagttaaa aacctgtcct ttaaataattc tcaaaaactc attttggata	1076
aatt	1080

<210> 156
 <211> 326
 <212> PRT
 <213> *Helicobacter pylori*

<400> 156

Met	Leu	Lys	Thr	Tyr	His	Ile	Ala	Leu	Ala	Cys	Val	Ile	Leu	Ala	Val
1				5					10					15	
Val	Val	Leu	Leu	Phe	Gly	Gly	Glu	Ser	Leu	Ser	Leu	Glu	Glu	Trp	Gln
			20					25					30		
Glu	Val	Cys	Leu	Asn	Val	Lys	Asn	His	Phe	Leu	His	Asn	Glu	Glu	Leu
		35					40					45			
Ser	Ser	Leu	Ser	Ile	Ile	Ile	Leu	Glu	Ile	Arg	Leu	Pro	Arg	Val	Ile
		50				55					60				
Leu	Ala	Leu	Leu	Val	Gly	Ala	Ser	Leu	Ser	Gly	Ser	Gly	Val	Val	Met
65					70					75					80
Gln	Thr	Ile	Phe	Arg	Asn	Pro	Leu	Val	Asp	Pro	Phe	Leu	Leu	Gly	Ile
				85					90					95	
Ser	Ser	Gly	Ala	Met	Leu	Gly	Val	Ala	Met	Ala	Ile	Ala	Val	Val	Glu
			100					105					110		
Ser	Asn	Ile	Ala	Ile	Leu	Ala	Phe	Phe	Gly	Ala	Ile	Leu	Ala	Ser	Leu
			115					120					125		
Ala	Val	Leu	Ala	Met	Asn	Arg	Val	Leu	Gly	Asn	Ser	Val	Leu	Ser	Leu
			130			135					140				
Val	Leu	Ser	Gly	Val	Val	Leu	Ser	Ala	Phe	Leu	Ser	Ala	Leu	Ala	Gly
145					150					155					160
Ala	Ile	Lys	Phe	Phe	Val	Ile	Pro	Gln	Lys	Ala	Gln	Ala	Ile	Val	Val
				165					170					175	
Trp	Leu	Leu	Gly	Ser	Leu	Ser	Leu	Ser	Ser	Tyr	Lys	Asp	Cys	Leu	Ile
			180				185					190			
Ala	Phe	Ile	Gly	Leu	Ser	Leu	Gly	Phe	Ile	Pro	Leu	Phe	Leu	Leu	Arg
		195					200					205			
Trp	Arg	Ile	Asn	Leu	Leu	Ser	Leu	Ser	Asp	Ala	Gln	Ser	Leu	Ser	Leu
		210				215					220				
Gly	Ile	Asn	Pro	Val	Leu	Leu	Arg	Ser	Leu	Cys	Leu	Val	Cys	Val	Ser

<210> 158
 <211> 109
 <212> PRT
 <213> Helicobacter pylori

<400> 158
 Met Leu Asp Ser Thr Thr Ala Ile Ala Ile Ala Thr Pro Ser Ile Ala
 1 5 10 15
 Pro Leu Glu Ile Pro Ser Lys Lys Gly Ser Thr Lys Gly Phe Leu Lys
 20 25 30
 Ile Val Cys Ile Thr Thr Pro Leu Pro Asp Lys Leu Ala Pro Thr Arg
 35 40 45
 Ser Ala Lys Ile Thr Arg Gly Ser Arg Ile Ser Lys Ile Ile Ile Leu
 50 55 60
 Lys Glu Leu Ser Ser Ser Leu Cys Lys Lys Trp Phe Phe Thr Leu Arg
 65 70 75 80
 His Thr Ser Cys His Ser Ser Lys Leu Lys Asp Ser Pro Pro Asn Asn
 85 90 95
 Ser Thr Thr Thr Ala Lys Ile Thr Gln Ala Lys Ala Ile
 100 105

<210> 159
 <211> 711
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (39)...(662)

<400> 159
 aggaaaaaatg gctggggtgc aaggattcga acctcgga atg cca gga cca aaa cct 56
 Met Pro Gly Pro Lys Pro
 1 5
 ggt gcc tta ccg ctt ggc gac acc cca aaa act aaa gaa agc att ata 104
 Gly Ala Leu Pro Leu Gly Asp Thr Pro Lys Thr Lys Glu Ser Ile Ile
 10 15 20
 caa aag ctt ttt aaa aaa gtc aag cta aaa cgc tat aat ttt atc atg 152
 Gln Lys Leu Phe Lys Lys Val Lys Leu Lys Arg Tyr Asn Phe Ile Met
 25 30 35
 gaa aat gga ttt gac ccc atc att tat aaa cgc tat ttg aaa aag aaa 200
 Glu Asn Gly Phe Asp Pro Ile Ile Tyr Lys Arg Tyr Leu Lys Lys Lys
 40 45 50
 gaa acc ttt ttg ctg ttt aaa aaa atc gct caa gcg tct gcg ttt aaa 248
 Glu Thr Phe Leu Leu Phe Lys Lys Ile Ala Gln Ala Ser Ala Phe Lys
 55 60 65 70
 aat tta aaa ctc caa ctc aaa cga aga gaa ata atc aac cgc tat gtt 296
 Asn Leu Lys Leu Gln Leu Lys Arg Arg Glu Ile Ile Asn Arg Tyr Val
 75 80 85
 tct caa gct ttg ggg gat tta aaa aaa ggg ttt aga tac gct aaa gta 344
 Ser Gln Ala Leu Gly Asp Leu Lys Lys Gly Phe Arg Tyr Ala Lys Val
 90 95 100

gaa cac caa atc cta aaa atc tat ttc acg cac cct agc tat ttg aaa	392
Glu His Gln Ile Leu Lys Ile Tyr Phe Thr His Pro Ser Tyr Leu Lys	
105 110 115	
gcc ttt aaa ata gaa gaa gcc tat tac acc aac cac ctg aaa gcc cat	440
Ala Phe Lys Ile Glu Glu Ala Tyr Tyr Thr Asn His Leu Lys Ala His	
120 125 130	
tta aaa gaa acg caa aaa acc cta aaa gcc cta gat tac ccc ttt gat	488
Leu Lys Glu Thr Gln Lys Thr Leu Lys Ala Leu Asp Tyr Pro Phe Asp	
135 140 145 150	
ttt aag act atc caa gcg agc gtg aaa aaa agg gct tat caa aaa cca	536
Phe Lys Thr Ile Gln Ala Ser Val Lys Lys Arg Ala Tyr Gln Lys Pro	
155 160 165	
gtt gtt aaa aaa gaa aaa ccc cct aaa agc gtg aat gtc aat tgc gaa	584
Val Val Lys Lys Glu Lys Pro Pro Lys Ser Val Asn Val Asn Cys Glu	
170 175 180	
ggt ttg agc gat ttc act aaa aag caa ttt tta aag ctc aaa cgc gct	632
Gly Leu Ser Asp Phe Thr Lys Lys Gln Phe Leu Lys Leu Lys Arg Ala	
185 190 195	
tgt aac gat aat acg ctg cgc acg ccc cct tgagagctga ccatgcaact	682
Cys Asn Asp Asn Thr Leu Arg Thr Pro Pro	
200 205	
gccgatcggg ttttgcgggg tgcaagttt	711

<210> 160

<211> 208

<212> PRT

<213> Helicobacter pylori

<400> 160

Met Pro Gly Pro Lys Pro Gly Ala Leu Pro Leu Gly Asp Thr Pro Lys	
1 5 10 15	
Thr Lys Glu Ser Ile Ile Gln Lys Leu Phe Lys Lys Val Lys Leu Lys	
20 25 30	
Arg Tyr Asn Phe Ile Met Glu Asn Gly Phe Asp Pro Ile Ile Tyr Lys	
35 40 45	
Arg Tyr Leu Lys Lys Lys Glu Thr Phe Leu Leu Phe Lys Lys Ile Ala	
50 55 60	
Gln Ala Ser Ala Phe Lys Asn Leu Lys Leu Gln Leu Lys Arg Arg Glu	
65 70 75 80	
Ile Ile Asn Arg Tyr Val Ser Gln Ala Leu Gly Asp Leu Lys Lys Gly	
85 90 95	
Phe Arg Tyr Ala Lys Val Glu His Gln Ile Leu Lys Ile Tyr Phe Thr	
100 105 110	
His Pro Ser Tyr Leu Lys Ala Phe Lys Ile Glu Glu Ala Tyr Tyr Thr	
115 120 125	
Asn His Leu Lys Ala His Leu Lys Glu Thr Gln Lys Thr Leu Lys Ala	
130 135 140	
Leu Asp Tyr Pro Phe Asp Phe Lys Thr Ile Gln Ala Ser Val Lys Lys	
145 150 155 160	
Arg Ala Tyr Gln Lys Pro Val Val Lys Lys Glu Lys Pro Pro Lys Ser	
165 170 175	

Pro	Asn	Pro	Ser	Pro	Lys	Glu	Leu	Ala	Glu	Ile	Ala	Thr	Thr	Ser	Ala
			20					25					30		
Gln	Thr	Ala	Lys	Gln	Phe	Asn	Ile	Ala	Pro	Lys	Val	Ala	Leu	Leu	Ser
		35					40					45			
Tyr	Ala	Thr	Gly	Asp	Ser	Ala	Gln	Gly	Glu	Met	Ile	Asp	Lys	Ile	Asn
	50					55				60					
Glu	Ala	Leu	Thr	Ile	Ala	Gln	Lys	Leu	Asp	Pro	Gln	Leu	Glu	Ile	Asp
65					70				75					80	
Gly	Pro	Leu	Gln	Phe	Asp	Ala	Ser	Ile	Asp	Lys	Ser	Val	Ala	Lys	Lys
				85					90					95	
Lys	Cys	Leu	Thr	Ala	Lys	Trp	Leu	Gly	Lys	Leu	Ala	Phe	Leu	Phe	Ser
			100					105					110		
Arg	Ile														

<210> 163
 <211> 1151
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (38)...(1111)

<400> 163 agggcagggtt ttcaccccta aaaagatagt ggatttc atg ctc act ctc aaa cac 55 <div style="display: flex; justify-content: space-between; width: 100%;"> Met Leu Thr Leu Lys His 1 5 </div>														
aat cat ggg agt gtt tta gaa ccg agt gct ggc gat ggg agt ttt tta 103 <div style="display: flex; justify-content: space-between; width: 100%;"> Asn His Gly Ser Val Leu Glu Pro Ser Ala Gly Asp Gly Ser Phe Leu 10 15 20 </div>														
aag cgc tta aaa aag gcc gta agg att gaa atc gat cct aaa atc tgc 151 <div style="display: flex; justify-content: space-between; width: 100%;"> Lys Arg Leu Lys Lys Ala Val Arg Ile Glu Ile Asp Pro Lys Ile Cys 25 30 35 </div>														
cct aaa aat gcc ctt tgc atg gac ttt ttt gac tac cct tta gaa aat 199 <div style="display: flex; justify-content: space-between; width: 100%;"> Pro Lys Asn Ala Leu Cys Met Asp Phe Phe Asp Tyr Pro Leu Glu Asn 40 45 50 </div>														
caa ttt gac acc att att ggt aac ccg ccc tat gtc aag cac aag gat 247 <div style="display: flex; justify-content: space-between; width: 100%;"> Gln Phe Asp Thr Ile Ile Gly Asn Pro Pro Tyr Val Lys His Lys Asp 55 60 65 70 </div>														
att gcg cca agc acc aaa gaa aaa ctc cat tac agc ctt ttt gat gaa 295 <div style="display: flex; justify-content: space-between; width: 100%;"> Ile Ala Pro Ser Thr Lys Glu Lys Leu His Tyr Ser Leu Phe Asp Glu 75 80 85 </div>														
agg agt aat ctc tac ttg ttt ttc ata gaa aaa gcg atc aag cat tta 343 <div style="display: flex; justify-content: space-between; width: 100%;"> Arg Ser Asn Leu Tyr Leu Phe Phe Ile Glu Lys Ala Ile Lys His Leu 90 95 100 </div>														
aaa cct aaa ggc gaa ttg att ttc atc acc cca agg gat ttt tta aaa 391 <div style="display: flex; justify-content: space-between; width: 100%;"> Lys Pro Lys Gly Glu Leu Ile Phe Ile Thr Pro Arg Asp Phe Leu Lys 105 110 115 </div>														
tcc act tct agc gtg aaa tta aac gaa tgg att tat aaa gaa ggc acg 439														

Ser	Thr	Ser	Ser	Val	Lys	Leu	Asn	Glu	Trp	Ile	Tyr	Lys	Glu	Gly	Thr	
120						125					130					
ata	acg	cat	ttt	ttt	gaa	ctg	ggc	gat	caa	aag	gtt	ttc	cca	aac	gcc	487
Ile	Thr	His	Phe	Phe	Glu	Leu	Gly	Asp	Gln	Lys	Val	Phe	Pro	Asn	Ala	
135					140					145					150	
atg	cct	aat	tgc	gtg	att	ttt	cgt	ttt	tgt	aag	ggg	aat	ttc	agt	aga	535
Met	Pro	Asn	Cys	Val	Ile	Phe	Arg	Phe	Cys	Lys	Gly	Asn	Phe	Ser	Arg	
				155					160					165		
atc	acc	aac	gat	ggg	ttg	caa	ttt	ttg	tgc	aaa	aaa	ggc	att	ttg	tat	583
Ile	Thr	Asn	Asp	Gly	Leu	Gln	Phe	Leu	Cys	Lys	Lys	Gly	Ile	Leu	Tyr	
			170					175					180			
ttc	ctc	aac	caa	tct	tac	acg	caa	aaa	tta	agc	gag	gtt	ttt	aag	gtt	631
Phe	Leu	Asn	Gln	Ser	Tyr	Thr	Gln	Lys	Leu	Ser	Glu	Val	Phe	Lys	Val	
		185					190					195				
aaa	gtg	ggg	gca	gtg	agc	ggg	tgc	gat	aag	att	ttt	aaa	aat	gaa	aaa	679
Lys	Val	Gly	Ala	Val	Ser	Gly	Cys	Asp	Lys	Ile	Phe	Lys	Asn	Glu	Lys	
	200					205					210					
tac	ggg	aat	tta	gaa	ttt	gtc	acc	tca	atc	acg	aaa	aga	acc	aat	gct	727
Tyr	Gly	Asn	Leu	Glu	Phe	Val	Thr	Ser	Ile	Thr	Lys	Arg	Thr	Asn	Ala	
215					220					225					230	
tta	gaa	aaa	atg	gtt	ttt	gtc	aat	gag	cct	aat	gat	tat	tta	ctc	cag	775
Leu	Glu	Lys	Met	Val	Phe	Val	Asn	Glu	Pro	Asn	Asp	Tyr	Leu	Leu	Gln	
				235					240					245		
cat	aaa	gac	agc	tta	atg	caa	aga	aag	att	aaa	aaa	ttc	aat	gaa	aat	823
His	Lys	Asp	Ser	Leu	Met	Gln	Arg	Lys	Ile	Lys	Lys	Phe	Asn	Glu	Asn	
			250					255					260			
aac	tgg	ttt	gag	tgg	ggg	aga	atg	cat	cac	ata	tcc	cct	aaa	aaa	cgc	871
Asn	Trp	Phe	Glu	Trp	Gly	Arg	Met	His	His	Ile	Ser	Pro	Lys	Lys	Arg	
		265					270					275				
att	tat	gtc	aac	gcc	aaa	acg	cac	caa	aaa	aac	ccc	ttt	ttt	atc	cac	919
Ile	Tyr	Val	Asn	Ala	Lys	Thr	His	Gln	Lys	Asn	Pro	Phe	Phe	Ile	His	
	280					285					290					
caa	tgc	cct	aat	tat	gac	ggc	tct	att	tta	gcg	cta	ttc	cct	tat	aac	967
Gln	Cys	Pro	Asn	Tyr	Asp	Gly	Ser	Ile	Leu	Ala	Leu	Phe	Pro	Tyr	Asn	
295					300					305					310	
caa	aac	ctg	gac	tta	caa	aat	ctc	tgc	gac	aaa	ctc	aac	gct	atc	aac	1015
Gln	Asn	Leu	Asp	Leu	Gln	Asn	Leu	Cys	Asp	Lys	Leu	Asn	Ala	Ile	Asn	
				315					320					325		
tgg	caa	gaa	tta	ggc	ttt	gtg	tgc	ggc	ggg	cgt	ttt	ttg	ttt	tcg	cag	1063
Trp	Gln	Glu	Leu	Gly	Phe	Val	Cys	Gly	Gly	Arg	Phe	Leu	Phe	Ser	Gln	
			330					335					340			
cgc	tct	tta	gaa	aac	gcg	ctt	ttg	cct	aaa	gac	ttt	tta	aat	cta	gga	1111
Arg	Ser	Leu	Glu	Asn	Ala	Leu	Leu	Pro	Lys	Asp	Phe	Leu	Asn	Leu	Gly	
		345					350					355				

taaaacttgt tagaaacttt gcaattaaac cctgagcagc

1151

<210> 164

<211> 358

<212> PRT

<213> *Helicobacter pylori*

<400> 164

Met	Leu	Thr	Leu	Lys	His	Asn	His	Gly	Ser	Val	Leu	Glu	Pro	Ser	Ala	
1				5					10					15		
Gly	Asp	Gly	Ser	Phe	Leu	Lys	Arg	Leu	Lys	Lys	Ala	Val	Arg	Ile	Glu	
			20					25					30			
Ile	Asp	Pro	Lys	Ile	Cys	Pro	Lys	Asn	Ala	Leu	Cys	Met	Asp	Phe	Phe	
		35					40					45				
Asp	Tyr	Pro	Leu	Glu	Asn	Gln	Phe	Asp	Thr	Ile	Ile	Gly	Asn	Pro	Pro	
	50					55					60					
Tyr	Val	Lys	His	Lys	Asp	Ile	Ala	Pro	Ser	Thr	Lys	Glu	Lys	Leu	His	
65					70					75					80	
Tyr	Ser	Leu	Phe	Asp	Glu	Arg	Ser	Asn	Leu	Tyr	Leu	Phe	Phe	Ile	Glu	
			85					90						95		
Lys	Ala	Ile	Lys	His	Leu	Lys	Pro	Lys	Gly	Glu	Leu	Ile	Phe	Ile	Thr	
			100					105					110			
Pro	Arg	Asp	Phe	Leu	Lys	Ser	Thr	Ser	Ser	Val	Lys	Leu	Asn	Glu	Trp	
		115					120					125				
Ile	Tyr	Lys	Glu	Gly	Thr	Ile	Thr	His	Phe	Phe	Glu	Leu	Gly	Asp	Gln	
	130					135					140					
Lys	Val	Phe	Pro	Asn	Ala	Met	Pro	Asn	Cys	Val	Ile	Phe	Arg	Phe	Cys	
145					150				155						160	
Lys	Gly	Asn	Phe	Ser	Arg	Ile	Thr	Asn	Asp	Gly	Leu	Gln	Phe	Leu	Cys	
			165					170						175		
Lys	Lys	Gly	Ile	Leu	Tyr	Phe	Leu	Asn	Gln	Ser	Tyr	Thr	Gln	Lys	Leu	
		180					185						190			
Ser	Glu	Val	Phe	Lys	Val	Lys	Val	Gly	Ala	Val	Ser	Gly	Cys	Asp	Lys	
	195						200					205				
Ile	Phe	Lys	Asn	Glu	Lys	Tyr	Gly	Asn	Leu	Glu	Phe	Val	Thr	Ser	Ile	
	210					215					220					
Thr	Lys	Arg	Thr	Asn	Ala	Leu	Glu	Lys	Met	Val	Phe	Val	Asn	Glu	Pro	
225					230				235						240	
Asn	Asp	Tyr	Leu	Leu	Gln	His	Lys	Asp	Ser	Leu	Met	Gln	Arg	Lys	Ile	
			245					250						255		
Lys	Lys	Phe	Asn	Glu	Asn	Asn	Trp	Phe	Glu	Trp	Gly	Arg	Met	His	His	
		260						265					270			
Ile	Ser	Pro	Lys	Lys	Arg	Ile	Tyr	Val	Asn	Ala	Lys	Thr	His	Gln	Lys	
	275						280					285				
Asn	Pro	Phe	Phe	Ile	His	Gln	Cys	Pro	Asn	Tyr	Asp	Gly	Ser	Ile	Leu	
	290					295					300					
Ala	Leu	Phe	Pro	Tyr	Asn	Gln	Asn	Leu	Asp	Leu	Gln	Asn	Leu	Cys	Asp	
305					310				315						320	
Lys	Leu	Asn	Ala	Ile	Asn	Trp	Gln	Glu	Leu	Gly	Phe	Val	Cys	Gly	Gly	
			325					330						335		
Arg	Phe	Leu	Phe	Ser	Gln	Arg	Ser	Leu	Glu	Asn	Ala	Leu	Leu	Pro	Lys	
		340						345					350			
Asp	Phe	Leu	Asn	Leu	Gly											
		355														

<210> 165

<211> 1183

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(1130)

<221> misc_feature

<222> 1028

<223> n = A,T,C or G

<400> 165

```
cctaaagcgg agaataaagt tacagaagtc ctagcgagca aaacaatgtg atg gct 56
                                     Met Ala
                                     1

aag atc aat ggt tat ttg agc gaa agg gat att tta acg ctc agt tat 104
Lys Ile Asn Gly Tyr Leu Ser Glu Arg Asp Ile Leu Thr Leu Ser Tyr
      5                10                15

aac atg acc aga gac aac gct aac cgc cct tta aga gcg aat ttt aca 152
Asn Met Thr Arg Asp Asn Ala Asn Arg Pro Leu Arg Ala Asn Phe Thr
      20                25                30

ggc act ttt tta ccc tat tct tgc ggt gat ttt aac gct ttc cct aac 200
Gly Thr Phe Leu Pro Tyr Ser Cys Gly Asp Phe Asn Ala Phe Pro Asn
      35                40                45                50

gag aaa aac cct agc gat tgt ttg ttt gaa aac gac gct agt ttg ttt 248
Glu Lys Asn Pro Ser Asp Cys Leu Phe Glu Asn Asp Ala Ser Leu Phe
      55                60                65

aaa act tat agc gtc aat tta gtg cat aat gtg agt ttg aat tat gaa 296
Lys Thr Tyr Ser Val Asn Leu Val His Asn Val Ser Leu Asn Tyr Glu
      70                75                80

aga gaa ggg ggg agc cgt ttt ggt gat cct aaa tta aaa atc aat ggc 344
Arg Glu Gly Gly Ser Arg Phe Gly Asp Pro Lys Leu Lys Ile Asn Gly
      85                90                95

tat aca agc att agg aat gtc caa att gat ccg ctt ttt aag cct aac 392
Tyr Thr Ser Ile Arg Asn Val Gln Ile Asp Pro Leu Phe Lys Pro Asn
      100                105                110

gac ata gcg gct agt att cct ttc acc cca aac cca aaa ctt ggc gaa 440
Asp Ile Ala Ala Ser Ile Pro Phe Thr Pro Asn Pro Lys Leu Gly Glu
      115                120                125                130

gag aat gaa tgc gtg gcg caa ggg ggc att tat gac gct ctt aaa caa 488
Glu Asn Glu Cys Val Ala Gln Gly Gly Ile Tyr Asp Ala Leu Lys Gln
      135                140                145

act tgc tcc atc act ttt aaa agc ctt gga ggg ggt tct gtg gtg gct 536
Thr Cys Ser Ile Thr Phe Lys Ser Leu Gly Gly Gly Ser Val Val Ala
      150                155                160

aat aaa aat tta ttc atc atc aat tct ggg ttt aat gcg aac gtg atc 584
Asn Lys Asn Leu Phe Ile Ile Asn Ser Gly Phe Asn Ala Asn Val Ile
      165                170                175
```

cac acc ata gac cat aag aat gac aac ctt ttg gaa tac ggg ttg aat	632
His Thr Ile Asp His Lys Asn Asp Asn Leu Leu Glu Tyr Gly Leu Asn	
180 185 190	
tac caa aac tta acc act ttt gat aaa gcg atc cct aat agc gaa tta	680
Tyr Gln Asn Leu Thr Thr Phe Asp Lys Ala Ile Pro Asn Ser Glu Leu	
195 200 205 210	
gtc aaa ccc ggc gat gcc cct gac gca tgc tta agg gtt aca agc ccc	728
Val Lys Pro Gly Asp Ala Pro Asp Ala Cys Leu Arg Val Thr Ser Pro	
215 220 225	
aat gat ccc aac atg aac ggg cgt tgc caa cga aat ggc gct acg gcg	776
Asn Asp Pro Asn Met Asn Gly Arg Cys Gln Arg Asn Gly Ala Thr Ala	
230 235 240	
aat gtg att ggg gtg tat gcg caa gcg aat tac acc ttg cat cct atg	824
Asn Val Ile Gly Val Tyr Ala Gln Ala Asn Tyr Thr Leu His Pro Met	
245 250 255	
gta act tta ggg gca ggg act cgt tat gat gtc tat act tta gtg gat	872
Val Thr Leu Gly Ala Gly Thr Arg Tyr Asp Val Tyr Thr Leu Val Asp	
260 265 270	
aaa gac tgg caa ttg cac ata acc caa ggg ttt agc cct agc gcg gct	920
Lys Asp Trp Gln Leu His Ile Thr Gln Gly Phe Ser Pro Ser Ala Ala	
275 280 285 290	
tta aat gtc tcg cct tta gaa aat ttg aat ttc agg ctt tct tat gcg	968
Leu Asn Val Ser Pro Leu Glu Asn Leu Asn Phe Arg Leu Ser Tyr Ala	
295 300 305	
tat gta acc aga ggc cct atg cct gga ggt ttg gtg tgg atg cgt caa	1016
Tyr Val Thr Arg Gly Pro Met Pro Gly Gly Leu Val Trp Met Arg Gln	
310 315 320	
gat aat ttg cgn cta caa ccg caa ttt aaa gcc aga aat tgg gca aaa	1064
Asp Asn Leu Arg Leu Gln Pro Gln Phe Lys Ala Arg Asn Trp Ala Lys	
325 330 335	
tgt gga att tta aca ccg aat aca gca gtc agt att ttg att tta gag	1112
Cys Gly Ile Leu Thr Pro Asn Thr Ala Val Ser Ile Leu Ile Leu Glu	
340 345 350	
ccg ccg gtt ttg tcc aat tgatttctaa ttacatcaat caatttttctt	1160
Pro Pro Val Leu Ser Asn	
355 360	
caacgctttt tgtaaccaac ttg	1183

<210> 166

<211> 360

<212> PRT

<213> Helicobacter pylori

<220>

<221> VARIANT

<222> 326

<223> Xaa = Any Amino Acid

<400> 166

Met	Ala	Lys	Ile	Asn	Gly	Tyr	Leu	Ser	Glu	Arg	Asp	Ile	Leu	Thr	Leu
1				5					10					15	
Ser	Tyr	Asn	Met	Thr	Arg	Asp	Asn	Ala	Asn	Arg	Pro	Leu	Arg	Ala	Asn
		20						25					30		
Phe	Thr	Gly	Thr	Phe	Leu	Pro	Tyr	Ser	Cys	Gly	Asp	Phe	Asn	Ala	Phe
		35					40					45			
Pro	Asn	Glu	Lys	Asn	Pro	Ser	Asp	Cys	Leu	Phe	Glu	Asn	Asp	Ala	Ser
	50					55					60				
Leu	Phe	Lys	Thr	Tyr	Ser	Val	Asn	Leu	Val	His	Asn	Val	Ser	Leu	Asn
65					70					75					80
Tyr	Glu	Arg	Glu	Gly	Gly	Ser	Arg	Phe	Gly	Asp	Pro	Lys	Leu	Lys	Ile
				85					90					95	
Asn	Gly	Tyr	Thr	Ser	Ile	Arg	Asn	Val	Gln	Ile	Asp	Pro	Leu	Phe	Lys
			100					105						110	
Pro	Asn	Asp	Ile	Ala	Ala	Ser	Ile	Pro	Phe	Thr	Pro	Asn	Pro	Lys	Leu
		115					120					125			
Gly	Glu	Glu	Asn	Glu	Cys	Val	Ala	Gln	Gly	Gly	Ile	Tyr	Asp	Ala	Leu
	130					135					140				
Lys	Gln	Thr	Cys	Ser	Ile	Thr	Phe	Lys	Ser	Leu	Gly	Gly	Gly	Ser	Val
145					150					155					160
Val	Ala	Asn	Lys	Asn	Leu	Phe	Ile	Ile	Asn	Ser	Gly	Phe	Asn	Ala	Asn
				165					170					175	
Val	Ile	His	Thr	Ile	Asp	His	Lys	Asn	Asp	Asn	Leu	Leu	Glu	Tyr	Gly
			180					185					190		
Leu	Asn	Tyr	Gln	Asn	Leu	Thr	Thr	Phe	Asp	Lys	Ala	Ile	Pro	Asn	Ser
		195					200					205			
Glu	Leu	Val	Lys	Pro	Gly	Asp	Ala	Pro	Asp	Ala	Cys	Leu	Arg	Val	Thr
	210					215					220				
Ser	Pro	Asn	Asp	Pro	Asn	Met	Asn	Gly	Arg	Cys	Gln	Arg	Asn	Gly	Ala
225					230					235					240
Thr	Ala	Asn	Val	Ile	Gly	Val	Tyr	Ala	Gln	Ala	Asn	Tyr	Thr	Leu	His
				245					250						255
Pro	Met	Val	Thr	Leu	Gly	Ala	Gly	Thr	Arg	Tyr	Asp	Val	Tyr	Thr	Leu
			260					265					270		
Val	Asp	Lys	Asp	Trp	Gln	Leu	His	Ile	Thr	Gln	Gly	Phe	Ser	Pro	Ser
		275					280					285			
Ala	Ala	Leu	Asn	Val	Ser	Pro	Leu	Glu	Asn	Leu	Asn	Phe	Arg	Leu	Ser
	290					295					300				
Tyr	Ala	Tyr	Val	Thr	Arg	Gly	Pro	Met	Pro	Gly	Gly	Leu	Val	Trp	Met
305					310					315					320
Arg	Gln	Asp	Asn	Leu	Xaa	Leu	Gln	Pro	Gln	Phe	Lys	Ala	Arg	Asn	Trp
			325						330					335	
Ala	Lys	Cys	Gly	Ile	Leu	Thr	Pro	Asn	Thr	Ala	Val	Ser	Ile	Leu	Ile
			340					345					350		
Leu	Glu	Pro	Pro	Val	Leu	Ser	Asn								
		355					360								

<210> 167

<211> 431

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (31)...(387)

<400> 167

agactgaata aaatcgcaact cgctcccgca atg aca acc tgg aac atg ggg ctg 54
Met Thr Thr Trp Asn Met Gly Leu
1 5

ccc aaa aac aag tta atg agc gaa cac acc acc acc aca atc aaa gcg 102
Pro Lys Asn Lys Leu Met Ser Glu His Thr Thr Thr Thr Ile Lys Ala
10 15 20

atg aag agc att tta ccc ata ttc gct aga tgc ttt tta gtc tta agg 150
Met Lys Ser Ile Leu Pro Ile Phe Ala Arg Ser Phe Leu Val Leu Arg
25 30 35 40

gca tac acg ctc atc aaa cca aag aca ata gtt gtc atg ccc aaa gcc 198
Ala Tyr Thr Leu Ile Lys Pro Lys Thr Ile Val Val Met Pro Lys Ala
45 50 55

tgc caa atc gct cct aaa cca gct ttt gca atc acc ata ccc aac aaa 246
Cys Gln Ile Ala Pro Lys Pro Ala Phe Ala Ile Thr Ile Pro Asn Lys
60 65 70

ggc act agc gta acc cct gat aat gaa gtg aaa gca aac agc atg aac 294
Gly Thr Ser Val Thr Pro Asp Asn Glu Val Lys Ala Asn Ser Met Asn
75 80 85

aga ttc aat ccg ggt tta gat tta gaa aac atc aaa cca aaa aac gcc 342
Arg Phe Asn Pro Gly Leu Asp Leu Glu Asn Ile Lys Pro Lys Asn Ala
90 95 100

gca att tca gcg ata aaa aac acc cat tta tac tgc act acg gct 387
Ala Ile Ser Ala Ile Lys Asn Thr His Leu Tyr Cys Thr Thr Ala
105 110 115

tgaaaattca ttaaacctag taacgccccca atagtcgcta ataa 431

<210> 168

<211> 119

<212> PRT

<213> Helicobacter pylori

<400> 168

Met Thr Thr Trp Asn Met Gly Leu Pro Lys Asn Lys Leu Met Ser Glu
1 5 10 15
His Thr Thr Thr Thr Ile Lys Ala Met Lys Ser Ile Leu Pro Ile Phe
20 25 30
Ala Arg Ser Phe Leu Val Leu Arg Ala Tyr Thr Leu Ile Lys Pro Lys
35 40 45
Thr Ile Val Val Met Pro Lys Ala Cys Gln Ile Ala Pro Lys Pro Ala
50 55 60
Phe Ala Ile Thr Ile Pro Asn Lys Gly Thr Ser Val Thr Pro Asp Asn
65 70 75 80
Glu Val Lys Ala Asn Ser Met Asn Arg Phe Asn Pro Gly Leu Asp Leu
85 90 95
Glu Asn Ile Lys Pro Lys Asn Ala Ala Ile Ser Ala Ile Lys Asn Thr
100 105 110
His Leu Tyr Cys Thr Thr Ala
115

<210> 169

<400> 169																		
aagtttgata	tactaacaga	atg	aat	act	tat	aaa	aac	agc	ttg	aat	cac	ttt	53					
Met Asn Thr Tyr Lys Asn Ser Leu Asn His Phe																		
1													5		10			
tta	aat	tta	gtg	gat	tgt	tta	gaa	aaa	atc	ccc	aat	gtg	ggg	aaa	aag	101		
Leu	Asn	Leu	Val	Asp	Cys	Leu	Glu	Lys	Ile	Pro	Asn	Val	Gly	Lys	Lys			
15													20		25			
tcc	gcc	ttt	aaa	atg	gcg	tat	cat	ttg	ggg	tta	gaa	aac	ccc	tat	ctg	149		
Ser	Ala	Phe	Lys	Met	Ala	Tyr	His	Leu	Gly	Leu	Glu	Asn	Pro	Tyr	Leu			
30													35		40			
gcg	cta	aaa	atc	acg	cac	gct	tta	gag	aac	gcc	cta	gaa	aac	ctt	aaa	197		
Ala	Leu	Lys	Ile	Thr	His	Ala	Leu	Glu	Asn	Ala	Leu	Glu	Asn	Leu	Lys			
45													50		55			
aca	tgt	tca	tct	tgt	aac	gcg	ctc	agc	gag	agt	gag	gtt	tgt	gag	att	245		
Thr	Cys	Ser	Ser	Cys	Asn	Ala	Leu	Ser	Glu	Ser	Glu	Val	Cys	Glu	Ile			
60													65		70		75	
tgc	tct	gat	gaa	agc	cga	caa	aat	tct	cag	ctt	tgc	atg	gtt	tta	cac	293		
Cys	Ser	Asp	Glu	Ser	Arg	Gln	Asn	Ser	Gln	Leu	Cys	Met	Val	Leu	His			
80													85		90			
cca	aga	gat	gtg	ttt	att	tta	gaa	gat	tta	aag	gat	ttt	tta	ggg	cgc	341		
Pro	Arg	Asp	Val	Phe	Ile	Leu	Glu	Asp	Leu	Lys	Asp	Phe	Leu	Gly	Arg			
95													100		105			
tat	tat	gtg	tta	aac	tcc	ata	gaa	gaa	gtg	gat	ttt	aac	gcc	cta	gaa	389		
Tyr	Tyr	Val	Leu	Asn	Ser	Ile	Glu	Glu	Val	Asp	Phe	Asn	Ala	Leu	Glu			
110													115		120			
aaa	cgc	ctg	att	gaa	gaa	aac	att	aaa	gaa	atc	att	ttt	gct	ttc	cct	437		
Lys	Arg	Leu	Ile	Glu	Glu	Asn	Ile	Lys	Glu	Ile	Ile	Phe	Ala	Phe	Pro			
125													130		135			
ccc	act	tta	gct	aat	gat	tct	cta	atg	ctt	tat	att	gaa	gac	aaa	tta	485		
Pro	Thr	Leu	Ala	Asn	Asp	Ser	Leu	Met	Leu	Tyr	Ile	Glu	Asp	Lys	Leu			
140													145		150		155	
cag	cat	ttc	cac	ctc	act	ttc	act	aaa	atc	gct	caa	ggc	gtg	cct	act	533		
Gln	His	Phe	His	Leu	Thr	Phe	Thr	Lys	Ile	Ala	Gln	Gly	Val	Pro	Thr			
160													165		170			
gga	gtg	aat	ttt	gaa	aac	att	gac	tca	gtt	tcg	ctc	tca	agg	gcg	ttt	581		
Gly	Val	Asn	Phe	Glu	Asn	Ile	Asp	Ser	Val	Ser	Leu	Ser	Arg	Ala	Phe			
175													180		185			
aat	tca	agg	atc	aaa	gca	tgaatttaaa	ttttatgccc	ctattgcatg								629		
Asn	Ser	Arg	Ile	Lys	Ala													

190

cttataacca tgcgagcatt gatttttcatt tcaattctag tg

671

<210> 170
<211> 193
<212> PRT
<213> Helicobacter pylori

<400> 170
Met Asn Thr Tyr Lys Asn Ser Leu Asn His Phe Leu Asn Leu Val Asp
1 5 10 15
Cys Leu Glu Lys Ile Pro Asn Val Gly Lys Lys Ser Ala Phe Lys Met
20 25 30
Ala Tyr His Leu Gly Leu Glu Asn Pro Tyr Leu Ala Leu Lys Ile Thr
35 40 45
His Ala Leu Glu Asn Ala Leu Glu Asn Leu Lys Thr Cys Ser Ser Cys
50 55 60
Asn Ala Leu Ser Glu Ser Glu Val Cys Glu Ile Cys Ser Asp Glu Ser
65 70 75 80
Arg Gln Asn Ser Gln Leu Cys Met Val Leu His Pro Arg Asp Val Phe
85 90 95
Ile Leu Glu Asp Leu Lys Asp Phe Leu Gly Arg Tyr Tyr Val Leu Asn
100 105 110
Ser Ile Glu Glu Val Asp Phe Asn Ala Leu Glu Lys Arg Leu Ile Glu
115 120 125
Glu Asn Ile Lys Glu Ile Ile Phe Ala Phe Pro Pro Thr Leu Ala Asn
130 135 140
Asp Ser Leu Met Leu Tyr Ile Glu Asp Lys Leu Gln His Phe His Leu
145 150 155 160
Thr Phe Thr Lys Ile Ala Gln Gly Val Pro Thr Gly Val Asn Phe Glu
165 170 175
Asn Ile Asp Ser Val Ser Leu Ser Arg Ala Phe Asn Ser Arg Ile Lys
180 185 190
Ala

<210> 171
<211> 846
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (26)...(793)

<221> misc_feature
<222> 48
<223> n = A,T,C or G

<400> 171
aaaaaattca ggattaaaat ataaa atg aaa aaa gtt tta ttt ttg tng gta 52
Met Lys Lys Val Leu Phe Leu Xaa Val
1 5
ata agc ttt ttt ggg ggt ttt ttg aac gct tct agc ttg tat gaa aaa 100
Ile Ser Phe Phe Gly Gly Phe Leu Asn Ala Ser Ser Leu Tyr Glu Lys
10 15 20 25

ctg att aat aaa gaa acg atc agc gtt ggc aca gaa ggc att tac ccc	148
Leu Ile Asn Lys Glu Thr Ile Ser Val Gly Thr Glu Gly Ile Tyr Pro	
30 35 40	
cct ttc act tac cac aat aaa gaa ggc aag ctc acc ggc tat gat gtg	196
Pro Phe Thr Tyr His Asn Lys Glu Gly Lys Leu Thr Gly Tyr Asp Val	
45 50 55	
gaa gtg gct agg gag ttg gcc aaa gag ctt ggc gtg aag atc aaa ttc	244
Glu Val Ala Arg Glu Leu Ala Lys Glu Leu Gly Val Lys Ile Lys Phe	
60 65 70	
cac gaa act tca tgg gat atc atg ctg aca ggt ttg aaa tcg ggg cgt	292
His Glu Thr Ser Trp Asp Ile Met Leu Thr Gly Leu Lys Ser Gly Arg	
75 80 85	
ttt gat atg gtc gct aac caa gtg agt ttg gcg act aaa aaa cgc caa	340
Phe Asp Met Val Ala Asn Gln Val Ser Leu Ala Thr Lys Lys Arg Gln	
90 95 100 105	
gcg gct ttt gat aaa agc ttg cct tat agc tat tca ggc acg atc atg	388
Ala Ala Phe Asp Lys Ser Leu Pro Tyr Ser Tyr Ser Gly Thr Ile Met	
110 115 120	
ctg gtc agg aaa gat gaa aac cgc att aaa gat att aaa gac atc aag	436
Leu Val Arg Lys Asp Glu Asn Arg Ile Lys Asp Ile Lys Asp Ile Lys	
125 130 135	
ggt ttg aga gcg gct aac act tta agc tcc act tat ggg gaa atc gct	484
Gly Leu Arg Ala Ala Asn Thr Leu Ser Ser Thr Tyr Gly Glu Ile Ala	
140 145 150	
ttt aaa tac gac gct caa atc gtt tcg gtg gat tct atg gcg caa gct	532
Phe Lys Tyr Asp Ala Gln Ile Val Ser Val Asp Ser Met Ala Gln Ala	
155 160 165	
ttg ttg ctg gtg gcg caa aaa cga gcc gat ttg acc tta aat agt tct	580
Leu Leu Leu Val Ala Gln Lys Arg Ala Asp Leu Thr Leu Asn Ser Ser	
170 175 180 185	
tta gcg atc tta aac tac ctt aac acc cac aaa gat aac ccc ttt aaa	628
Leu Ala Ile Leu Asn Tyr Leu Asn Thr His Lys Asp Asn Pro Phe Lys	
190 195 200	
atc gca tgg gag tcc aaa gaa aaa gat ggg ggc gct tcc ttt gtt att	676
Ile Ala Trp Glu Ser Lys Glu Lys Asp Gly Gly Ala Ser Phe Val Ile	
205 210 215	
aac aag cac caa gaa aaa gcc tta gag ctt atc aac caa gcg atg caa	724
Asn Lys His Gln Glu Lys Ala Leu Glu Leu Ile Asn Gln Ala Met Gln	
220 225 230	
aga ttg atc aac aaa ggg gtt tta aaa cgc tta ggc gaa caa ttt ttt	772
Arg Leu Ile Asn Lys Gly Val Leu Lys Arg Leu Gly Glu Gln Phe Phe	
235 240 245	
gga aaa gat gtc agc cag ccc taatctgtct ttgttttttg aatctttaga	823
Gly Lys Asp Val Ser Gln Pro	

250

255

tttgagcaag gagcgtttgg aat

846

<210> 172

<211> 256

<212> PRT

<213> Helicobacter pylori

<220>

<221> VARIANT

<222> 8

<223> Xaa = Any Amino Acid

<400> 172

Met	Lys	Lys	Val	Leu	Phe	Leu	Xaa	Val	Ile	Ser	Phe	Phe	Gly	Gly	Phe
1				5					10					15	
Leu	Asn	Ala	Ser	Ser	Leu	Tyr	Glu	Lys	Leu	Ile	Asn	Lys	Glu	Thr	Ile
			20					25					30		
Ser	Val	Gly	Thr	Glu	Gly	Ile	Tyr	Pro	Pro	Phe	Thr	Tyr	His	Asn	Lys
		35					40					45			
Glu	Gly	Lys	Leu	Thr	Gly	Tyr	Asp	Val	Glu	Val	Ala	Arg	Glu	Leu	Ala
	50					55					60				
Lys	Glu	Leu	Gly	Val	Lys	Ile	Lys	Phe	His	Glu	Thr	Ser	Trp	Asp	Ile
65					70					75					80
Met	Leu	Thr	Gly	Leu	Lys	Ser	Gly	Arg	Phe	Asp	Met	Val	Ala	Asn	Gln
				85					90					95	
Val	Ser	Leu	Ala	Thr	Lys	Lys	Arg	Gln	Ala	Ala	Phe	Asp	Lys	Ser	Leu
			100					105					110		
Pro	Tyr	Ser	Tyr	Ser	Gly	Thr	Ile	Met	Leu	Val	Arg	Lys	Asp	Glu	Asn
		115					120					125			
Arg	Ile	Lys	Asp	Ile	Lys	Asp	Ile	Lys	Gly	Leu	Arg	Ala	Ala	Asn	Thr
		130				135					140				
Leu	Ser	Ser	Thr	Tyr	Gly	Glu	Ile	Ala	Phe	Lys	Tyr	Asp	Ala	Gln	Ile
145					150					155					160
Val	Ser	Val	Asp	Ser	Met	Ala	Gln	Ala	Leu	Leu	Leu	Val	Ala	Gln	Lys
				165					170					175	
Arg	Ala	Asp	Leu	Thr	Leu	Asn	Ser	Ser	Leu	Ala	Ile	Leu	Asn	Tyr	Leu
			180					185					190		
Asn	Thr	His	Lys	Asp	Asn	Pro	Phe	Lys	Ile	Ala	Trp	Glu	Ser	Lys	Glu
		195					200					205			
Lys	Asp	Gly	Gly	Ala	Ser	Phe	Val	Ile	Asn	Lys	His	Gln	Glu	Lys	Ala
	210					215					220				
Leu	Glu	Leu	Ile	Asn	Gln	Ala	Met	Gln	Arg	Leu	Ile	Asn	Lys	Gly	Val
225					230					235					240
Leu	Lys	Arg	Leu	Gly	Glu	Gln	Phe	Phe	Gly	Lys	Asp	Val	Ser	Gln	Pro
				245					250					255	

<210> 173

<211> 1423

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (23)...(1372)

<400> 173

cctagtttat taaggagttt tt atg gaa acg att gat tcg gtg gtg cgt ttg	52
Met Glu Thr Ile Asp Ser Val Val Arg Leu	
1 5 10	
tta tct aat ttg gtg tgg ggg att ccc atg caa att tta tta gta ggc	100
Leu Ser Asn Leu Val Trp Gly Ile Pro Met Gln Ile Leu Leu Val Gly	
15 20 25	
acc ggc ttg ttt tta acc ttt tat ctt agg ggt ttg caa ttc agt aag	148
Thr Gly Leu Phe Leu Thr Phe Tyr Leu Arg Gly Leu Gln Phe Ser Lys	
30 35 40	
att ttt tat gcg atc aaa atc ctt ttt gac aaa gag tcc caa tct aag	196
Ile Phe Tyr Ala Ile Lys Ile Leu Phe Asp Lys Glu Ser Gln Ser Lys	
45 50 55	
ggc gac att tca caa ttt tcc gct ctc atg ctc tct ttg ggg gcg act	244
Gly Asp Ile Ser Gln Phe Ser Ala Leu Met Leu Ser Leu Gly Ala Thr	
60 65 70	
gta ggc att ggg agt atc gta ggc gta gcg acc gct att agc atc gca	292
Val Gly Ile Gly Ser Ile Val Gly Val Ala Thr Ala Ile Ser Ile Ala	
75 80 85 90	
ggg cca gga gcg gtg ttt tgg atg tgg gtt act ggg ctt gtt ggc atg	340
Gly Pro Gly Ala Val Phe Trp Met Trp Val Thr Gly Leu Val Gly Met	
95 100 105	
gcg act aag tat tct gag ggg att tta gcg gtg aaa tac cgg gaa aaa	388
Ala Thr Lys Tyr Ser Glu Gly Ile Leu Ala Val Lys Tyr Arg Glu Lys	
110 115 120	
ggg gcg ttt gga tac aac gga ggg ccc atg tat tac atc aaa aac ggt	436
Gly Ala Phe Gly Tyr Asn Gly Gly Pro Met Tyr Tyr Ile Lys Asn Gly	
125 130 135	
ctt aac atg ccc aaa ctc gcc atg gcg ttt gcg att ttt acg att att	484
Leu Asn Met Pro Lys Leu Ala Met Ala Phe Ala Ile Phe Thr Ile Ile	
140 145 150	
gca agc att ggc acc ggt aac atg acg caa tct aat gcg gtt tct tcc	532
Ala Ser Ile Gly Thr Gly Asn Met Thr Gln Ser Asn Ala Val Ser Ser	
155 160 165 170	
att tta agc gaa caa gcg aac ctg cct aat tgg gtt tca ggt tta ttg	580
Ile Leu Ser Glu Gln Ala Asn Leu Pro Asn Trp Val Ser Gly Leu Leu	
175 180 185	
ctc act ctt tta acc gct ttc att gtc ata ggg ggg atc aaa tcc att	628
Leu Thr Leu Leu Thr Ala Phe Ile Val Ile Gly Gly Ile Lys Ser Ile	
190 195 200	
ggt aaa ttc act tct tac tta gct cct gtt atg gtg ctt tta tat ttg	676
Gly Lys Phe Thr Ser Tyr Leu Ala Pro Val Met Val Leu Leu Tyr Leu	
205 210 215	
atc gct att att tat att att gtt agc cat ttt gat tta gcc ctt caa	724
Ile Ala Ile Ile Tyr Ile Ile Val Ser His Phe Asp Leu Ala Leu Gln	
220 225 230	

gcg atc aaa ctc att ttt gaa gaa gcc ttt aac cct aaa ccc gtt gtg	772
Ala Ile Lys Leu Ile Phe Glu Glu Ala Phe Asn Pro Lys Pro Val Val	
235 240 245 250	
ggc gga gcg agc ggc gcg ttg ata gcg acg atg ata aaa acg ggc gtg	820
Gly Gly Ala Ser Gly Ala Leu Ile Ala Thr Met Ile Lys Thr Gly Val	
255 260 265	
gct agg ggg ttg tat tct aat gaa gcg ggg tta ggg agc tca gcc att	868
Ala Arg Gly Leu Tyr Ser Asn Glu Ala Gly Leu Gly Ser Ser Ala Ile	
270 275 280	
att gcc gcg agc gct caa aca cgc cac ccg gtg cgc caa gcc tta gtg	916
Ile Ala Ala Ser Ala Gln Thr Arg His Pro Val Arg Gln Ala Leu Val	
285 290 295	
tcc atg ctc caa act ttt att gta acc tta ata gtg tgt tcg gca aca	964
Ser Met Leu Gln Thr Phe Ile Val Thr Leu Ile Val Cys Ser Ala Thr	
300 305 310	
gcg agc gtg att tta atg gct cca gaa tac aac acc ttg ctc cct aat	1012
Ala Ser Val Ile Leu Met Ala Pro Glu Tyr Asn Thr Leu Leu Pro Asn	
315 320 325 330	
ggg gaa aaa tta agc gct aat ttg ctc act cta aaa agc acg gag tat	1060
Gly Glu Lys Leu Ser Ala Asn Leu Leu Thr Leu Lys Ser Thr Glu Tyr	
335 340 345	
ttt cta ggc tca tta ggg acg gtg gtg att ttt aca acc atg atc ttt	1108
Phe Leu Gly Ser Leu Gly Thr Val Val Ile Phe Thr Thr Met Ile Phe	
350 355 360	
ttt gcc tac tct acg atc att ggt tgg gct tat tat ggg gaa aaa tgc	1156
Phe Ala Tyr Ser Thr Ile Ile Gly Trp Ala Tyr Tyr Gly Glu Lys Cys	
365 370 375	
act gaa tac gcc ttt ggt gaa aaa aaa gtg aaa tat tac cgc ttg atc	1204
Thr Glu Tyr Ala Phe Gly Glu Lys Lys Val Lys Tyr Tyr Arg Leu Ile	
380 385 390	
ttt tta gcg agt gtg atg gtg ggg gct atg gcc aaa att gat ttt gtg	1252
Phe Leu Ala Ser Val Met Val Gly Ala Met Ala Lys Ile Asp Phe Val	
395 400 405 410	
tgg aat tta gcg gat ctt tct aac ggg ctt atg gct atc cct aat tta	1300
Trp Asn Leu Ala Asp Leu Ser Asn Gly Leu Met Ala Ile Pro Asn Leu	
415 420 425	
atc gct ttg att tta ttg cat aaa gtg gtt tat tct gaa act cgt tgg	1348
Ile Ala Leu Ile Leu Leu His Lys Val Val Tyr Ser Glu Thr Arg Trp	
430 435 440	
tat ttt agc aag cat tct aac aag taaaaatggca tgtaaaaaag ggcgagtttt	1402
Tyr Phe Ser Lys His Ser Asn Lys	
445 450	
gtagaagtgg ataccgcttc t	1423

<210> 174
 <211> 450
 <212> PRT
 <213> Helicobacter pylori

<400> 174
 Met Glu Thr Ile Asp Ser Val Val Arg Leu Leu Ser Asn Leu Val Trp
 1 5 10 15
 Gly Ile Pro Met Gln Ile Leu Leu Val Gly Thr Gly Leu Phe Leu Thr
 20 25 30
 Phe Tyr Leu Arg Gly Leu Gln Phe Ser Lys Ile Phe Tyr Ala Ile Lys
 35 40 45
 Ile Leu Phe Asp Lys Glu Ser Gln Ser Lys Gly Asp Ile Ser Gln Phe
 50 55 60
 Ser Ala Leu Met Leu Ser Leu Gly Ala Thr Val Gly Ile Gly Ser Ile
 65 70 75 80
 Val Gly Val Ala Thr Ala Ile Ser Ile Ala Gly Pro Gly Ala Val Phe
 85 90 95
 Trp Met Trp Val Thr Gly Leu Val Gly Met Ala Thr Lys Tyr Ser Glu
 100 105 110
 Gly Ile Leu Ala Val Lys Tyr Arg Glu Lys Gly Ala Phe Gly Tyr Asn
 115 120 125
 Gly Gly Pro Met Tyr Tyr Ile Lys Asn Gly Leu Asn Met Pro Lys Leu
 130 135 140
 Ala Met Ala Phe Ala Ile Phe Thr Ile Ile Ala Ser Ile Gly Thr Gly
 145 150 155 160
 Asn Met Thr Gln Ser Asn Ala Val Ser Ser Ile Leu Ser Glu Gln Ala
 165 170 175
 Asn Leu Pro Asn Trp Val Ser Gly Leu Leu Leu Thr Leu Leu Thr Ala
 180 185 190
 Phe Ile Val Ile Gly Gly Ile Lys Ser Ile Gly Lys Phe Thr Ser Tyr
 195 200 205
 Leu Ala Pro Val Met Val Leu Leu Tyr Leu Ile Ala Ile Ile Tyr Ile
 210 215 220
 Ile Val Ser His Phe Asp Leu Ala Leu Gln Ala Ile Lys Leu Ile Phe
 225 230 235 240
 Glu Glu Ala Phe Asn Pro Lys Pro Val Val Gly Gly Ala Ser Gly Ala
 245 250 255
 Leu Ile Ala Thr Met Ile Lys Thr Gly Val Ala Arg Gly Leu Tyr Ser
 260 265 270
 Asn Glu Ala Gly Leu Gly Ser Ser Ala Ile Ile Ala Ala Ser Ala Gln
 275 280 285
 Thr Arg His Pro Val Arg Gln Ala Leu Val Ser Met Leu Gln Thr Phe
 290 295 300
 Ile Val Thr Leu Ile Val Cys Ser Ala Thr Ala Ser Val Ile Leu Met
 305 310 315 320
 Ala Pro Glu Tyr Asn Thr Leu Leu Pro Asn Gly Glu Lys Leu Ser Ala
 325 330 335
 Asn Leu Leu Thr Leu Lys Ser Thr Glu Tyr Phe Leu Gly Ser Leu Gly
 340 345 350
 Thr Val Val Ile Phe Thr Thr Met Ile Phe Phe Ala Tyr Ser Thr Ile
 355 360 365
 Ile Gly Trp Ala Tyr Tyr Gly Glu Lys Cys Thr Glu Tyr Ala Phe Gly
 370 375 380
 Glu Lys Lys Val Lys Tyr Tyr Arg Leu Ile Phe Leu Ala Ser Val Met
 385 390 395 400
 Val Gly Ala Met Ala Lys Ile Asp Phe Val Trp Asn Leu Ala Asp Leu
 405 410 415
 Ser Asn Gly Leu Met Ala Ile Pro Asn Leu Ile Ala Leu Ile Leu Leu

Phe	Lys	Val	Asp	Leu	Ala	Leu	Ala	Met	Ser	Gly	Val	Ala	Gly	Pro	Asn		
				155					160					165			
ggg	ggg	aac	aag	gct	aat	cct	gta	ggc	acg	att	tac	att	ggc	gcg	caa		581
Gly	Gly	Asn	Lys	Ala	Asn	Pro	Val	Gly	Thr	Ile	Tyr	Ile	Gly	Ala	Gln		
			170					175					180				
aag	tta	gga	tct	caa	gct	tta	atc	gat	cgc	tgt	ttt	ttt	gaa	ggg	aac		629
Lys	Leu	Gly	Ser	Gln	Ala	Leu	Ile	Asp	Arg	Cys	Phe	Phe	Glu	Gly	Asn		
		185					190					195					
aga	gaa	agc	att	caa	aat	aaa	agc	gta	gag	cat	gcc	tta	aac	atg	ctc		677
Arg	Glu	Ser	Ile	Gln	Asn	Lys	Ser	Val	Glu	His	Ala	Leu	Asn	Met	Leu		
	200					205					210						
gct	aga	atg	cta	taaaactacc	ttaacgcaca	aacgctacca	aattcttttt										729
Ala	Arg	Met	Leu														
215																	
gagcgacctt	agcgatgtaa	gcgattt															756
<210>	178																
<211>	218																
<212>	PRT																
<213>	Helicobacter pylori																
<400>	178																
Met	Lys	Phe	Lys	Phe	Leu	Asn	Met	Asp	Asn	Glu	Ser	Gly	Phe	Ile	Leu		
1				5					10					15			
Ile	Glu	Lys	Glu	Leu	Lys	Arg	Leu	Asn	Ile	Leu	Ala	Gln	Val	Lys	Glu		
			20					25					30				
Asp	Cys	Ile	Glu	Leu	Lys	Gly	Glu	Asn	Thr	Glu	Gln	Ala	Arg	Ile	Tyr		
		35					40					45					
Leu	Lys	Thr	Leu	Phe	Asn	Ser	Asn	Ile	Val	Glu	Leu	Asp	Asp	His	Gln		
	50				55					60							
Lys	Ser	Ala	Asn	Ala	Leu	Ile	Glu	Arg	Leu	Lys	Ser	Leu	Asp	Leu	Lys		
65					70				75						80		
Ile	Ala	Val	Ala	Glu	Ser	Cys	Ser	Gly	Gly	Leu	Leu	Ser	His	Ala	Phe		
			85					90						95			
Thr	Ser	Ile	Ser	Gly	Ala	Ser	Ala	Val	Phe	Met	Gly	Gly	Ile	Val	Cys		
			100					105					110				
Tyr	Asn	Glu	Glu	Val	Lys	Arg	Glu	Leu	Leu	Lys	Val	Asn	Ala	Thr	Thr		
		115					120					125					
Leu	Lys	Val	Phe	Gly	Val	Tyr	Ser	Glu	Glu	Cys	Val	Lys	Glu	Met	Leu		
	130					135				140							
Leu	Gly	Val	Phe	Leu	Asn	Phe	Lys	Val	Asp	Leu	Ala	Leu	Ala	Met	Ser		
145					150				155						160		
Gly	Val	Ala	Gly	Pro	Asn	Gly	Gly	Asn	Lys	Ala	Asn	Pro	Val	Gly	Thr		
			165					170						175			
Ile	Tyr	Ile	Gly	Ala	Gln	Lys	Leu	Gly	Ser	Gln	Ala	Leu	Ile	Asp	Arg		
		180					185						190				
Cys	Phe	Phe	Glu	Gly	Asn	Arg	Glu	Ser	Ile	Gln	Asn	Lys	Ser	Val	Glu		
		195					200					205					
His	Ala	Leu	Asn	Met	Leu	Ala	Arg	Met	Leu								
	210					215											
<210>	179																
<211>	681																

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (28)...(657)

<400> 179

```
aaattctaaa aaaataaagg aaaatca atg aaa ttt ttg gat caa gaa aaa aga 54
                               Met Lys Phe Leu Asp Gln Glu Lys Arg
                               1           5

aga caa tta tta aac gag cgc cat tct tgc aag atg ttt gat agc cat 102
Arg Gln Leu Leu Asn Glu Arg His Ser Cys Lys Met Phe Asp Ser His
 10           15           20           25

tat gag ttt tct agc aca gaa tta gaa gaa atc gct gaa atc gcc agg 150
Tyr Glu Phe Ser Ser Thr Glu Leu Glu Glu Ile Ala Glu Ile Ala Arg
           30           35           40

cta tcg cca agc tct tac aac acg cag cca tgg cat ttt gtg atg gtt 198
Leu Ser Pro Ser Ser Tyr Asn Thr Gln Pro Trp His Phe Val Met Val
           45           50           55

act gat aag gat tta aaa aaa caa att gca gcg cac agc tat ttc aat 246
Thr Asp Lys Asp Leu Lys Lys Gln Ile Ala Ala His Ser Tyr Phe Asn
        60           65           70

gaa gag atg att aaa agc gct tca gcg tta atg gtg gta tgc tct tta 294
Glu Glu Met Ile Lys Ser Ala Ser Ala Leu Met Val Val Cys Ser Leu
        75           80           85

aga ccc agc gag ttg tta cca cac ggc cac tac atg caa aat ctc tat 342
Arg Pro Ser Glu Leu Leu Pro His Gly His Tyr Met Gln Asn Leu Tyr
 90           95          100          105

cgg gag tct tat aaa gtt aga gtg atc ccc tct ttt gct caa atg ctt 390
Pro Glu Ser Tyr Lys Val Arg Val Ile Pro Ser Phe Ala Gln Met Leu
        110          115          120

ggc gtg aga ttc aac cac agc atg caa aga tta gaa agc tat att tta 438
Gly Val Arg Phe Asn His Ser Met Gln Arg Leu Glu Ser Tyr Ile Leu
        125          130          135

gag caa tgc tat atc gct gtg ggg caa att tgc atg ggc gtg agc tta 486
Glu Gln Cys Tyr Ile Ala Val Gly Gln Ile Cys Met Gly Val Ser Leu
        140          145          150

atg gga ttg gat agt tgc att att gga ggc ttt gat cct tta aag gtg 534
Met Gly Leu Asp Ser Cys Ile Ile Gly Gly Phe Asp Pro Leu Lys Val
        155          160          165

ggc gaa gtt tta gaa gag cgt atc aat aag cct aaa atc gca tgc ttg 582
Gly Glu Val Leu Glu Glu Arg Ile Asn Lys Pro Lys Ile Ala Cys Leu
        170          175          180          185

atc gct ttg ggc aag agg gtg gca gaa gcg agt caa aaa tca aga aaa 630
Ile Ala Leu Gly Lys Arg Val Ala Glu Ala Ser Gln Lys Ser Arg Lys
        190          195          200
```

tca aaa gtt gat gcg att act tgg ttg tgattaaaca aaatcaaaaa 677
 Ser Lys Val Asp Ala Ile Thr Trp Leu
 205 210

cttt 681

<210> 180
 <211> 210
 <212> PRT
 <213> Helicobacter pylori

<400> 180
 Met Lys Phe Leu Asp Gln Glu Lys Arg Arg Gln Leu Leu Asn Glu Arg
 1 5 10 15
 His Ser Cys Lys Met Phe Asp Ser His Tyr Glu Phe Ser Ser Thr Glu
 20 25 30
 Leu Glu Glu Ile Ala Glu Ile Ala Arg Leu Ser Pro Ser Ser Tyr Asn
 35 40 45
 Thr Gln Pro Trp His Phe Val Met Val Thr Asp Lys Asp Leu Lys Lys
 50 55 60
 Gln Ile Ala Ala His Ser Tyr Phe Asn Glu Glu Met Ile Lys Ser Ala
 65 70 75 80
 Ser Ala Leu Met Val Val Cys Ser Leu Arg Pro Ser Glu Leu Leu Pro
 85 90 95
 His Gly His Tyr Met Gln Asn Leu Tyr Pro Glu Ser Tyr Lys Val Arg
 100 105 110
 Val Ile Pro Ser Phe Ala Gln Met Leu Gly Val Arg Phe Asn His Ser
 115 120 125
 Met Gln Arg Leu Glu Ser Tyr Ile Leu Glu Gln Cys Tyr Ile Ala Val
 130 135 140
 Gly Gln Ile Cys Met Gly Val Ser Leu Met Gly Leu Asp Ser Cys Ile
 145 150 155 160
 Ile Gly Gly Phe Asp Pro Leu Lys Val Gly Glu Val Leu Glu Glu Arg
 165 170 175
 Ile Asn Lys Pro Lys Ile Ala Cys Leu Ile Ala Leu Gly Lys Arg Val
 180 185 190
 Ala Glu Ala Ser Gln Lys Ser Arg Lys Ser Lys Val Asp Ala Ile Thr
 195 200 205
 Trp Leu
 210

<210> 181
 <211> 1490
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (99)...(1439)

<400> 181
 cttaaagaaa acatgcaaaa ttgcaaaat caagttcaaa acaaagagca atccatcgct 60
 caattagatg cacaaatcca agcttttaaag gggattca atg agc gtt aat ttt ttt 116
 Met Ser Val Asn Phe Phe
 1 5

aag ggc att ttt aat gac aat agc agg gct gaa aac cac caa gac aac 164

Lys	Gly	Ile	Phe	Asn	Asp	Asn	Ser	Arg	Ala	Glu	Asn	His	Gln	Asp	Asn	
			10					15					20			
cac	caa	aac	aac	cat	caa	gtg	ggc	tta	aaa	gag	cgt	tac	gat	ttg	atc	212
His	Gln	Asn	Asn	His	Gln	Val	Gly	Leu	Lys	Glu	Arg	Tyr	Asp	Leu	Ile	
		25					30				35					
gct	cgt	att	tta	aac	gcc	aga	att	gaa	aat	gaa	ggg	cta	gaa	gaa	tat	260
Ala	Arg	Ile	Leu	Asn	Ala	Arg	Ile	Glu	Asn	Glu	Gly	Leu	Glu	Glu	Tyr	
	40					45					50					
cag	agc	gtc	ttg	gat	aac	gag	ttt	tta	gag	ttc	gct	agc	ggc	gtg	gat	308
Gln	Ser	Val	Leu	Asp	Asn	Glu	Phe	Leu	Glu	Phe	Ala	Ser	Gly	Val	Asp	
	55				60					65					70	
tcg	ctc	aaa	gaa	aag	gaa	ata	gcg	tta	ctg	acg	ctc	caa	gaa	atc	caa	356
Ser	Leu	Lys	Glu	Lys	Glu	Ile	Ala	Leu	Leu	Thr	Leu	Gln	Glu	Ile	Gln	
				75				80						85		
aaa	gaa	ttg	caa	ttg	gta	gcg	agc	tac	cct	agt	ttg	ttc	caa	aaa	acc	404
Lys	Glu	Leu	Gln	Leu	Val	Ala	Ser	Tyr	Pro	Ser	Leu	Phe	Gln	Lys	Thr	
			90					95					100			
atc	gtt	gcg	gtg	ggg	gga	ggg	ttt	agc	gcg	ggc	aaa	tcc	act	ttt	tta	452
Ile	Val	Ala	Val	Gly	Gly	Gly	Phe	Ser	Ala	Gly	Lys	Ser	Thr	Phe	Leu	
	105						110					115				
aac	aac	ttg	ttg	ggc	ttg	aaa	tta	aaa	ctc	cct	gaa	gac	atg	aat	ccc	500
Asn	Asn	Leu	Leu	Gly	Leu	Lys	Leu	Lys	Leu	Pro	Glu	Asp	Met	Asn	Pro	
	120					125					130					
acc	aca	gct	atc	ccc	act	tat	tgc	tta	aag	ggc	aaa	aga	gaa	gtt	tta	548
Thr	Thr	Ala	Ile	Pro	Thr	Tyr	Cys	Leu	Lys	Gly	Lys	Arg	Glu	Val	Leu	
	135				140					145					150	
atg	ggg	ttt	tct	caa	aat	ggg	ggc	atg	gtg	gaa	ttg	cca	cat	ctc	gct	596
Met	Gly	Phe	Ser	Gln	Asn	Gly	Gly	Met	Val	Glu	Leu	Pro	His	Leu	Ala	
				155				160						165		
ttt	gac	cat	cag	ttt	tta	aac	tcc	ctt	ggc	ttt	aat	ttg	aaa	gag	atc	644
Phe	Asp	His	Gln	Phe	Leu	Asn	Ser	Leu	Gly	Phe	Asn	Leu	Lys	Glu	Ile	
			170					175					180			
atg	cct	ttc	atg	ctt	tta	agc	gct	cct	agc	gtg	cct	ttt	gaa	ttt	tta	692
Met	Pro	Phe	Met	Leu	Leu	Ser	Ala	Pro	Ser	Val	Pro	Phe	Glu	Phe	Leu	
		185					190					195				
tgc	ttc	ata	gac	acg	cct	ggc	ttt	aac	tcc	gcc	aag	caa	ggc	tat	acg	740
Cys	Phe	Ile	Asp	Thr	Pro	Gly	Phe	Asn	Ser	Ala	Lys	Gln	Gly	Tyr	Thr	
	200					205					210					
ggc	ggg	gat	aaa	gaa	gcc	tct	aaa	gaa	tcc	cta	aaa	cac	gcc	aaa	cac	788
Gly	Gly	Asp	Lys	Glu	Ala	Ser	Lys	Glu	Ser	Leu	Lys	His	Ala	Lys	His	
	215				220				225						230	
att	ctg	tgg	ctc	att	agt	tgc	gag	agt	ggg	gag	att	cac	gaa	gat	gat	836
Ile	Leu	Trp	Leu	Ile	Ser	Cys	Glu	Ser	Gly	Glu	Ile	His	Glu	Asp	Asp	
				235					240					245		

tta gaa tat ttg caa gaa tta tac gaa gaa ggc aag cag gtt ttt atc	884
Leu Glu Tyr Leu Gln Glu Leu Tyr Glu Glu Gly Lys Gln Val Phe Ile	
250 255 260	
gta ttg agt agg gct gat agg cgc aca aaa agg caa tta gaa gaa gtc	932
Val Leu Ser Arg Ala Asp Arg Arg Thr Lys Arg Gln Leu Glu Glu Val	
265 270 275	
gtt att aaa att aaa gag act tta aaa gat aat ggc att gaa ttt tta	980
Val Ile Lys Ile Lys Glu Thr Leu Lys Asp Asn Gly Ile Glu Phe Leu	
280 285 290	
ggg att ggt gct tat agt tct aca agg tat caa gaa tat aaa gaa ttc	1028
Gly Ile Gly Ala Tyr Ser Ser Thr Arg Tyr Gln Glu Tyr Lys Glu Phe	
295 300 305 310	
agc gaa aaa agc aaa gtt ttt aac tcg ctt gag gaa ttt cta atg aag	1076
Ser Glu Lys Ser Lys Val Phe Asn Ser Leu Glu Glu Phe Leu Met Lys	
315 320 325	
tta aat caa agg agc gag aaa caa aac gaa att tta gga tat tta tac	1124
Leu Asn Gln Arg Ser Glu Lys Gln Asn Glu Ile Leu Gly Tyr Leu Tyr	
330 335 340	
gag gtg cat tcc atg tat gaa aag gct att gag caa gac gct aac caa	1172
Glu Val His Ser Met Tyr Glu Lys Ala Ile Glu Gln Asp Ala Asn Gln	
345 350 355	
ttc aaa cgc tac caa agc gaa ttg cat tct gtt aga ttg gat ttg atg	1220
Phe Lys Arg Tyr Gln Ser Glu Leu His Ser Val Arg Leu Asp Leu Met	
360 365 370	
caa aaa ggc ttt gat gat ttt agc gat aaa att ttt aga aga att gag	1268
Gln Lys Gly Phe Asp Asp Phe Ser Asp Lys Ile Phe Arg Arg Ile Glu	
375 380 385 390	
aat tta gaa aaa gaa ttt tcc gag caa gag cga tcc aaa aga gag agt	1316
Asn Leu Glu Lys Glu Phe Ser Glu Gln Glu Arg Ser Lys Arg Glu Ser	
395 400 405	
tta gcg cga ttg aat gaa gtg att gac ttg ttt aaa gaa ggt att gat	1364
Leu Ala Arg Leu Asn Glu Val Ile Asp Leu Phe Lys Glu Gly Ile Asp	
410 415 420	
aag gtt ttt gat cgc gtg agc gct ttc act tgg gaa aaa tac aaa gaa	1412
Lys Val Phe Asp Arg Val Ser Ala Phe Thr Trp Glu Lys Tyr Lys Glu	
425 430 435	
caa aat gac gat gaa gag gac gat gat tgaagaaaac tacaaagaag	1459
Gln Asn Asp Asp Glu Glu Asp Asp Asp	
440 445	
agcggttacac cgaaaggggtg aatcaaggcg g	1490
<210> 182	
<211> 447	
<212> PRT	
<213> Helicobacter pylori	

<400> 182

Met	Ser	Val	Asn	Phe	Phe	Lys	Gly	Ile	Phe	Asn	Asp	Asn	Ser	Arg	Ala	
1				5					10					15		
Glu	Asn	His	Gln	Asp	Asn	His	Gln	Asn	Asn	His	Gln	Val	Gly	Leu	Lys	
			20					25					30			
Glu	Arg	Tyr	Asp	Leu	Ile	Ala	Arg	Ile	Leu	Asn	Ala	Arg	Ile	Glu	Asn	
		35					40					45				
Glu	Gly	Leu	Glu	Glu	Tyr	Gln	Ser	Val	Leu	Asp	Asn	Glu	Phe	Leu	Glu	
	50					55					60					
Phe	Ala	Ser	Gly	Val	Asp	Ser	Leu	Lys	Glu	Lys	Glu	Ile	Ala	Leu	Leu	
65				70						75					80	
Thr	Leu	Gln	Glu	Ile	Gln	Lys	Glu	Leu	Gln	Leu	Val	Ala	Ser	Tyr	Pro	
				85					90					95		
Ser	Leu	Phe	Gln	Lys	Thr	Ile	Val	Ala	Val	Gly	Gly	Gly	Phe	Ser	Ala	
			100					105					110			
Gly	Lys	Ser	Thr	Phe	Leu	Asn	Asn	Leu	Leu	Gly	Leu	Lys	Leu	Lys	Leu	
		115					120					125				
Pro	Glu	Asp	Met	Asn	Pro	Thr	Thr	Ala	Ile	Pro	Thr	Tyr	Cys	Leu	Lys	
	130					135					140					
Gly	Lys	Arg	Glu	Val	Leu	Met	Gly	Phe	Ser	Gln	Asn	Gly	Gly	Met	Val	
145				150						155					160	
Glu	Leu	Pro	His	Leu	Ala	Phe	Asp	His	Gln	Phe	Leu	Asn	Ser	Leu	Gly	
				165				170						175		
Phe	Asn	Leu	Lys	Glu	Ile	Met	Pro	Phe	Met	Leu	Leu	Ser	Ala	Pro	Ser	
			180					185					190			
Val	Pro	Phe	Glu	Phe	Leu	Cys	Phe	Ile	Asp	Thr	Pro	Gly	Phe	Asn	Ser	
		195					200					205				
Ala	Lys	Gln	Gly	Tyr	Thr	Gly	Gly	Asp	Lys	Glu	Ala	Ser	Lys	Glu	Ser	
	210					215					220					
Leu	Lys	His	Ala	Lys	His	Ile	Leu	Trp	Leu	Ile	Ser	Cys	Glu	Ser	Gly	
225					230					235					240	
Glu	Ile	His	Glu	Asp	Leu	Glu	Tyr	Leu	Gln	Glu	Leu	Tyr	Glu	Glu		
				245				250						255		
Gly	Lys	Gln	Val	Phe	Ile	Val	Leu	Ser	Arg	Ala	Asp	Arg	Arg	Thr	Lys	
			260					265					270			
Arg	Gln	Leu	Glu	Glu	Val	Val	Ile	Lys	Ile	Lys	Glu	Thr	Leu	Lys	Asp	
			275				280					285				
Asn	Gly	Ile	Glu	Phe	Leu	Gly	Ile	Gly	Ala	Tyr	Ser	Ser	Thr	Arg	Tyr	
	290					295					300					
Gln	Glu	Tyr	Lys	Glu	Phe	Ser	Glu	Lys	Ser	Lys	Val	Phe	Asn	Ser	Leu	
305					310					315					320	
Glu	Glu	Phe	Leu	Met	Lys	Leu	Asn	Gln	Arg	Ser	Glu	Lys	Gln	Asn	Glu	
				325				330						335		
Ile	Leu	Gly	Tyr	Leu	Tyr	Glu	Val	His	Ser	Met	Tyr	Glu	Lys	Ala	Ile	
			340					345					350			
Glu	Gln	Asp	Ala	Asn	Gln	Phe	Lys	Arg	Tyr	Gln	Ser	Glu	Leu	His	Ser	
			355				360					365				
Val	Arg	Leu	Asp	Leu	Met	Gln	Lys	Gly	Phe	Asp	Asp	Phe	Ser	Asp	Lys	
	370					375					380					
Ile	Phe	Arg	Arg	Ile	Glu	Asn	Leu	Glu	Lys	Glu	Phe	Ser	Glu	Gln	Glu	
385					390					395					400	
Arg	Ser	Lys	Arg	Glu	Ser	Leu	Ala	Arg	Leu	Asn	Glu	Val	Ile	Asp	Leu	
				405				410						415		
Phe	Lys	Glu	Gly	Ile	Asp	Lys	Val	Phe	Asp	Arg	Val	Ser	Ala	Phe	Thr	
			420					425					430			
Trp	Glu	Lys	Tyr	Lys	Glu	Gln	Asn	Asp	Asp	Glu	Glu	Asp	Asp	Asp		
		435					440					445				

ttt	gtg	gag	ttt	tta	gaa	cag	gtt	tta	gaa	gtt	tta	aaa	gaa	gtg	gag	102
Phe	Val	Glu	Phe	Leu	Glu	Gln	Val	Leu	Glu	Val	Leu	Lys	Glu	Val	Glu	
10					15					20				25		
atc	gat	aaa	aca	gaa	tgc	tcc	acg	ctt	tta	gca	agc	gtt	caa	aaa	caa	150
Ile	Asp	Lys	Thr	Glu	Cys	Ser	Thr	Leu	Leu	Ala	Ser	Val	Gln	Lys	Gln	
				30					35					40		
cag	cta	gtg	ata	ccc	gtt	gtg	ggg	aat	ttt	agc	gca	ggg	aaa	agc	acg	198
Gln	Leu	Val	Ile	Pro	Val	Val	Gly	Asn	Phe	Ser	Ala	Gly	Lys	Ser	Thr	
			45					50					55			
cta	tta	aac	cgc	ttt	tta	ggc	agc	agc	gtt	ttg	cct	acc	ggg	atc	acg	246
Leu	Leu	Asn	Arg	Phe	Leu	Gly	Ser	Ser	Val	Leu	Pro	Thr	Gly	Ile	Thr	
		60					65					70				
cca	gag	act	tct	tta	gcc	act	gag	ttg	cac	tat	agc	gct	aag	gaa	cgc	294
Pro	Glu	Thr	Ser	Leu	Ala	Thr	Glu	Leu	His	Tyr	Ser	Ala	Lys	Glu	Arg	
	75					80					85					
ata	gag	gct	ttt	tca	aac	aat	gat	gaa	aaa	aca	gag	agt	ttt	gaa	ctg	342
Ile	Glu	Ala	Phe	Ser	Asn	Asn	Asp	Glu	Lys	Thr	Glu	Ser	Phe	Glu	Leu	
90					95					100				105		
aat	gag	caa	agt	ttt	gaa	gcg	att	aaa	gag	aat	gcc	acg	aag	tat	tcc	390
Asn	Glu	Gln	Ser	Phe	Glu	Ala	Ile	Lys	Glu	Asn	Ala	Thr	Lys	Tyr	Ser	
				110					115					120		
tac	ctt	aag	gtt	tat	ttg	aat	aat	gaa	gct	ttg	aaa	aac	agc	gct	cct	438
Tyr	Leu	Lys	Val	Tyr	Leu	Asn	Asn	Glu	Ala	Leu	Lys	Asn	Ser	Ala	Pro	
			125					130					135			
tta	gtg	ttt	gtg	gat	atg	cca	ggc	ttt	gat	agc	ccc	att	tca	agc	cac	486
Leu	Val	Phe	Val	Asp	Met	Pro	Gly	Phe	Asp	Ser	Pro	Ile	Ser	Ser	His	
		140					145					150				
acc	cat	gcc	att	ttg	gaa	tat	tta	gaa	agg	ggc	gtg	cat	ttt	gtc	att	534
Thr	His	Ala	Ile	Leu	Glu	Tyr	Leu	Glu	Arg	Gly	Val	His	Phe	Val	Ile	
	155					160					165					
ctc	aca	agc	gta	gaa	gag	ggc	aat	ctc	act	aaa	cgc	atg	gtt	agg	gag	582
Leu	Thr	Ser	Val	Glu	Glu	Gly	Asn	Leu	Thr	Lys	Arg	Met	Val	Arg	Glu	
170					175					180					185	
tta	aaa	aac	ctt	tta	gag	ttt	gac	aaa	ggc	ctt	agc	ttt	att	ttg	agt	630

Leu	Lys	Asn	Leu	Leu	Glu	Phe	Asp	Lys	Gly	Leu	Ser	Phe	Ile	Leu	Ser	
			190						195					200		
aaa	acg	aat	tta	aga	acg	cct	tcg	caa	gtg	gga	gaa	atc	tct	cac	tac	678
Lys	Thr	Asn	Leu	Arg	Thr	Pro	Ser	Gln	Val	Gly	Glu	Ile	Ser	His	Tyr	
			205					210					215			
att	caa	gat	caa	atc	cag	gat	cac	ctt	gat	ttg	aca	acg	cac	ctc	atc	726
Ile	Gln	Asp	Gln	Ile	Gln	Asp	His	Leu	Asp	Leu	Thr	Thr	His	Leu	Ile	
			220				225						230			
cat	tcc	aat	aaa	gac	aat	aac	gcc	ctt	tta	gag	gta	gcg	gat	aaa	ata	774
His	Ser	Asn	Lys	Asp	Asn	Asn	Ala	Leu	Leu	Glu	Val	Ala	Asp	Lys	Ile	
			235			240					245					
gac	gct	gaa	aag	ctt	ttt	agc	gct	ttg	tat	ttg	aaa	cga	ttg	aag	ttt	822
Asp	Ala	Glu	Lys	Leu	Phe	Ser	Ala	Leu	Tyr	Leu	Lys	Arg	Leu	Lys	Phe	
			250		255					260					265	
tta	aat	tct	aag	tta	caa	aat	agc	cta	aaa	agc	gtg	atg	gaa	agc	ttt	870
Leu	Asn	Ser	Lys	Leu	Gln	Asn	Ser	Leu	Lys	Ser	Val	Met	Glu	Ser	Phe	
				270					275					280		
gat	tat	tct	aaa	gaa	aag	gct	tta	gaa	gaa	ata	caa	gct	ttg	gat	ttg	918
Asp	Tyr	Ser	Lys	Glu	Lys	Ala	Leu	Glu	Glu	Ile	Gln	Ala	Leu	Asp	Leu	
			285					290					295			
ggc	gtt	aaa	gac	att	gaa	aaa	acc	tat	gaa	aaa	tta	agg	gct	aat	tta	966
Gly	Val	Lys	Asp	Ile	Glu	Lys	Thr	Tyr	Glu	Lys	Leu	Arg	Ala	Asn	Leu	
			300				305					310				
gaa	gaa	gaa	tat	tct	agc	gtg	gct	gtg	gga	tcg	gtg	gtt	aaa	aaa	gta	1014
Glu	Glu	Glu	Tyr	Ser	Ser	Val	Ala	Val	Gly	Ser	Val	Val	Lys	Lys	Val	
			315			320					325					
gta	gaa	gag	gtt	agg	gat	caa	aaa	tcc	tat	tta	gcc	tct	tta	atc	aac	1062
Val	Glu	Glu	Val	Arg	Asp	Gln	Lys	Ser	Tyr	Leu	Ala	Ser	Leu	Ile	Asn	
			330		335					340					345	
aag	cct	aac	gag	ttc	aat	agc	gaa	ata	gaa	agc	atc	atg	caa	caa	agc	1110
Lys	Pro	Asn	Glu	Phe	Asn	Ser	Glu	Ile	Glu	Ser	Ile	Met	Gln	Gln	Ser	
				350					355					360		
ttg	atc	aaa	aac	gct	aaa	tta	gag	att	gaa	aag	atc	aac	ctt	tct	ttt	1158
Leu	Ile	Lys	Asn	Ala	Lys	Leu	Glu	Ile	Glu	Lys	Ile	Asn	Leu	Ser	Phe	
			365					370					375			
tca	aaa	gat	ttc	cat	gcg	gaa	ttt	gaa	agc	ctg	aac	aag	ctt	tct	agc	1206
Ser	Lys	Asp	Phe	His	Ala	Glu	Phe	Glu	Ser	Leu	Asn	Lys	Leu	Ser	Ser	
			380				385					390				
gat	ctg	tct	gtg	aat	tta	gag	cat	ggg	att	gaa	tta	ggg	atc	aac	gct	1254
Asp	Leu	Ser	Val	Asn	Leu	Glu	His	Gly	Ile	Glu	Leu	Gly	Ile	Asn	Ala	
			395			400					405					
tta	agc	gtg	att	ttt	tcc	aag	aat	ccg	gtt	aca	agg	cca	ttc	gcg	ctg	1302
Leu	Ser	Val	Ile	Phe	Ser	Lys	Asn	Pro	Val	Thr	Arg	Pro	Phe	Ala	Leu	
					415					420					425	

att ttg caa ggg tta aaa tct ctt tta aaa gat tta ctg aca ttg ttg 1350
 Ile Leu Gln Gly Leu Lys Ser Leu Leu Lys Asp Leu Leu Thr Leu Leu
 430 435 440

cct aat atc atc gct tca ttc ttt agg aat gaa gaa aaa gag cgg gcg 1398
 Pro Asn Ile Ile Ala Ser Phe Phe Arg Asn Glu Glu Lys Glu Arg Ala
 445 450 455

aaa tta gaa aat ctg att gaa gtc aga gtg att cca gaa atc caa tac 1446
 Lys Leu Glu Asn Leu Ile Glu Val Arg Val Ile Pro Glu Ile Gln Tyr
 460 465 470

aag ctt aaa aaa gtt tta ccg gga ttg ttt aat gaa gct ttg caa aat 1494
 Lys Leu Lys Lys Val Leu Pro Gly Leu Phe Asn Glu Ala Leu Gln Asn
 475 480 485

tcc cta aaa tct cta aaa gat cgg tgc gag cta gaa atc acg cat aaa 1542
 Ser Leu Lys Ser Leu Lys Asp Arg Cys Glu Leu Glu Ile Thr His Lys
 490 495 500 505

aaa caa gaa atc gcg ctc gct caa aag gaa aaa gaa aaa cac cta aac 1590
 Lys Gln Glu Ile Ala Leu Ala Gln Lys Glu Lys Glu Lys His Leu Asn
 510 515 520

gat tta gaa gat caa aaa caa atc tta gaa aat aag atc aac gct tta 1638
 Asp Leu Glu Asp Gln Lys Gln Ile Leu Glu Asn Lys Ile Asn Ala Leu
 525 530 535

agc gat tta gaa caa caa tat tta aag gat caa caa tgaacgagca 1684
 Ser Asp Leu Glu Gln Gln Tyr Leu Lys Asp Gln Gln
 540 545

agaactcatt caaaaaagcg ctttaattga aaaa 1718

<210> 184

<211> 549

<212> PRT

<213> Helicobacter pylori

<400> 184

Met Met Val Leu Arg Thr Gln Thr Asn Phe Val Glu Phe Leu Glu Gln
 1 5 10 15
 Val Leu Glu Val Leu Lys Glu Val Glu Ile Asp Lys Thr Glu Cys Ser
 20 25 30
 Thr Leu Leu Ala Ser Val Gln Lys Gln Gln Leu Val Ile Pro Val Val
 35 40 45
 Gly Asn Phe Ser Ala Gly Lys Ser Thr Leu Leu Asn Arg Phe Leu Gly
 50 55 60
 Ser Ser Val Leu Pro Thr Gly Ile Thr Pro Glu Thr Ser Leu Ala Thr
 65 70 75 80
 Glu Leu His Tyr Ser Ala Lys Glu Arg Ile Glu Ala Phe Ser Asn Asn
 85 90 95
 Asp Glu Lys Thr Glu Ser Phe Glu Leu Asn Glu Gln Ser Phe Glu Ala
 100 105 110
 Ile Lys Glu Asn Ala Thr Lys Tyr Ser Tyr Leu Lys Val Tyr Leu Asn
 115 120 125
 Asn Glu Ala Leu Lys Asn Ser Ala Pro Leu Val Phe Val Asp Met Pro
 130 135 140
 Gly Phe Asp Ser Pro Ile Ser Ser His Thr His Ala Ile Leu Glu Tyr

145					150				155				160
Leu	Glu	Arg	Gly	Val	His	Phe	Val	Ile	Leu	Thr	Ser	Val	Glu
				165					170				175
Asn	Leu	Thr	Lys	Arg	Met	Val	Arg	Glu	Leu	Lys	Asn	Leu	Glu
			180					185				190	Phe
Asp	Lys	Gly	Leu	Ser	Phe	Ile	Leu	Ser	Lys	Thr	Asn	Leu	Arg
		195					200				205	Thr	Pro
Ser	Gln	Val	Gly	Glu	Ile	Ser	His	Tyr	Ile	Gln	Asp	Gln	Ile
	210					215				220			Asp
His	Leu	Asp	Leu	Thr	Thr	His	Leu	Ile	His	Ser	Asn	Lys	Asp
225				230					235				Asn
Ala	Leu	Leu	Glu	Val	Ala	Asp	Lys	Ile	Asp	Ala	Glu	Lys	Leu
			245					250					Phe
Ala	Leu	Tyr	Leu	Lys	Arg	Leu	Lys	Phe	Leu	Asn	Ser	Lys	Leu
		260					265					270	Gln
Ser	Leu	Lys	Ser	Val	Met	Glu	Ser	Phe	Asp	Tyr	Ser	Lys	Glu
	275						280				285	Lys	Ala
Leu	Glu	Glu	Ile	Gln	Ala	Leu	Asp	Leu	Gly	Val	Lys	Asp	Ile
	290					295			300				Glu
Thr	Tyr	Glu	Lys	Leu	Arg	Ala	Asn	Leu	Glu	Glu	Glu	Tyr	Ser
305				310					315				Ser
Ala	Val	Gly	Ser	Val	Val	Lys	Lys	Val	Val	Glu	Glu	Val	Arg
			325					330					Asp
Lys	Ser	Tyr	Leu	Ala	Ser	Leu	Ile	Asn	Lys	Pro	Asn	Glu	Phe
		340					345				350	Asn	Ser
Glu	Ile	Glu	Ser	Ile	Met	Gln	Gln	Ser	Leu	Ile	Lys	Asn	Ala
	355					360					365	Lys	Leu
Glu	Ile	Glu	Lys	Ile	Asn	Leu	Ser	Phe	Ser	Lys	Asp	Phe	His
	370				375				380				Ala
Phe	Glu	Ser	Leu	Asn	Lys	Leu	Ser	Ser	Asp	Leu	Ser	Val	Asn
385				390					395				Leu
His	Gly	Ile	Glu	Leu	Gly	Ile	Asn	Ala	Leu	Ser	Val	Ile	Phe
			405					410					Ser
Asn	Pro	Val	Thr	Arg	Pro	Phe	Ala	Leu	Ile	Leu	Gln	Gly	Leu
		420					425					430	Lys
Leu	Leu	Lys	Asp	Leu	Leu	Thr	Leu	Leu	Pro	Asn	Ile	Ile	Ala
	435					440					445	Ser	Phe
Phe	Arg	Asn	Glu	Glu	Lys	Glu	Arg	Ala	Lys	Leu	Glu	Asn	Leu
	450				455				460				Ile
Val	Arg	Val	Ile	Pro	Glu	Ile	Gln	Tyr	Lys	Leu	Lys	Lys	Val
465				470					475				Leu
Gly	Leu	Phe	Asn	Glu	Ala	Leu	Gln	Asn	Ser	Leu	Lys	Ser	Leu
			485					490					Lys
Arg	Cys	Glu	Leu	Glu	Ile	Thr	His	Lys	Lys	Gln	Glu	Ile	Ala
		500					505					510	Leu
Gln	Lys	Glu	Lys	Glu	Lys	His	Leu	Asn	Asp	Leu	Glu	Asp	Gln
	515					520			525				Lys
Ile	Leu	Glu	Asn	Lys	Ile	Asn	Ala	Leu	Ser	Asp	Leu	Glu	Gln
	530				535					540			Tyr
Leu	Lys	Asp	Gln	Gln									
545													

<210> 185
 <211> 360
 <212> DNA
 <213> Helicobacter pylori

<220>

<221> CDS
 <222> (31)...(348)

<400> 185

```

tcttttttctt cattcctaaa gaatgaagcg atg ata tta ggc aac aat gtc agt 54
                               Met Ile Leu Gly Asn Asn Val Ser
                               1           5

aaa tct ttt aaa aga gat ttt aac cct tgc aaa atc agc gcg aat ggc 102
Lys Ser Phe Lys Arg Asp Phe Asn Pro Cys Lys Ile Ser Ala Asn Gly
    10           15           20

ctt gta acc gga ttc ttg gaa aaa atc acg ctt aaa gcg ttg atc cct 150
Leu Val Thr Gly Phe Leu Glu Lys Ile Thr Leu Lys Ala Leu Ile Pro
    25           30           35           40

aat tca atc cca tgc tct aaa ttc aca gac aga tcg cta gaa agc ttg 198
Asn Ser Ile Pro Cys Ser Lys Phe Thr Asp Arg Ser Leu Glu Ser Leu
           45           50           55

ttc agg ctt tca aat tcc gca tgg aaa tct ttt gaa aaa gaa agg ttg 246
Phe Arg Leu Ser Asn Ser Ala Trp Lys Ser Phe Glu Lys Glu Arg Leu
           60           65           70

atc ttt tca atc tct aat tta gcg ttt ttg atc aag ctt tgt tgc atg 294
Ile Phe Ser Ile Ser Asn Leu Ala Phe Leu Ile Lys Leu Cys Cys Met
           75           80           85

atg ctt tct att tcg cta ttg aac tcg tta ggc ttg ttg att aaa gag 342
Met Leu Ser Ile Ser Leu Leu Asn Ser Leu Gly Leu Leu Ile Lys Glu
           90           95          100

gct aaa taggattttt ga 360
Ala Lys
105
  
```

<210> 186
 <211> 106
 <212> PRT
 <213> Helicobacter pylori

<400> 186

```

Met Ile Leu Gly Asn Asn Val Ser Lys Ser Phe Lys Arg Asp Phe Asn
 1           5           10           15
Pro Cys Lys Ile Ser Ala Asn Gly Leu Val Thr Gly Phe Leu Glu Lys
           20           25           30
Ile Thr Leu Lys Ala Leu Ile Pro Asn Ser Ile Pro Cys Ser Lys Phe
           35           40           45
Thr Asp Arg Ser Leu Glu Ser Leu Phe Arg Leu Ser Asn Ser Ala Trp
           50           55           60
Lys Ser Phe Glu Lys Glu Arg Leu Ile Phe Ser Ile Ser Asn Leu Ala
65           70           75           80
Phe Leu Ile Lys Leu Cys Cys Met Met Leu Ser Ile Ser Leu Leu Asn
           85           90           95
Ser Leu Gly Leu Leu Ile Lys Glu Ala Lys
           100          105
  
```


<210> 187
 <211> 3179
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (61)...(3120)

```

<400> 187
cagcgtggca gtgggggtcat tgataggggtt aaaaggcatg atcaacaatt taggggagga 60
atg atg ctc gct tcc att att gaa ttt tcc tta cgc caa aga gtg atc 108
Met Met Leu Ala Ser Ile Ile Glu Phe Ser Leu Arg Gln Arg Val Ile
  1             5             10             15

gtg att gtt ggt gcg att ctt att tta ttt ttt ggg act tat agt ttt 156
Val Ile Val Gly Ala Ile Leu Ile Leu Phe Phe Gly Thr Tyr Ser Phe
      20             25             30

atc aac act cca gtg gac gct ttc ccg gat att tcg ccc act caa gtt 204
Ile Asn Thr Pro Val Asp Ala Phe Pro Asp Ile Ser Pro Thr Gln Val
      35             40             45

aaa atc att tta aaa ctc ccc ggc tct agc cct gaa gaa atg gaa aac 252
Lys Ile Ile Leu Lys Leu Pro Gly Ser Ser Pro Glu Glu Met Glu Asn
      50             55             60

aac atc gtg cgc cct tta gaa ttg gag ctt tta ggc ttg aaa ggg caa 300
Asn Ile Val Arg Pro Leu Glu Leu Glu Leu Leu Gly Leu Lys Gly Gln
      65             70             75             80

aaa tct tta agg agt gtt tca aaa tat tct att tca gat att acg ata 348
Lys Ser Leu Arg Ser Val Ser Lys Tyr Ser Ile Ser Asp Ile Thr Ile
      85             90             95

gat ttt gat gac agc gtg gat att tat tta gcc agg aat att gtc aat 396
Asp Phe Asp Asp Ser Val Asp Ile Tyr Leu Ala Arg Asn Ile Val Asn
      100            105            110

gag cgc ttg agc agc gtg atg aaa gat tta ccc gtg ggg gtt gag ggg 444
Glu Arg Leu Ser Ser Val Met Lys Asp Leu Pro Val Gly Val Glu Gly
      115            120            125

ggc atg gcg ccc att gtt acg ccg cta tca gat atc ttt atg ttc act 492
Gly Met Ala Pro Ile Val Thr Pro Leu Ser Asp Ile Phe Met Phe Thr
      130            135            140

att gat ggc aat atc act gag ata gaa aaa cga cag ctt tta gat ttt 540
Ile Asp Gly Asn Ile Thr Glu Ile Glu Lys Arg Gln Leu Leu Asp Phe
      145            150            155            160

gtg atc cgc cca caa tta aga atg att agc ggc gta gca gat gtc aat 588
Val Ile Arg Pro Gln Leu Arg Met Ile Ser Gly Val Ala Asp Val Asn
      165            170            175

tcc att gga ggc ttt agc aga gcg ttt gtg atc gtg ccg gat ttt aat 636
Ser Ile Gly Gly Phe Ser Arg Ala Phe Val Ile Val Pro Asp Phe Asn
      180            185            190

```

gac atg gca agg ctt ggg gtg agt att tct gat tta gaa tcg gct gtg	684
Asp Met Ala Arg Leu Gly Val Ser Ile Ser Asp Leu Glu Ser Ala Val	
195 200 205	
aga gtg aat tta aga aac agc gga gcg ggg cgc gtg gat aga gat ggc	732
Arg Val Asn Leu Arg Asn Ser Gly Ala Gly Arg Val Asp Arg Asp Gly	
210 215 220	
gaa acc ttt tta gtc aaa atc caa acc gct tct ttg agt tta gaa gac	780
Glu Thr Phe Leu Val Lys Ile Gln Thr Ala Ser Leu Ser Leu Glu Asp	
225 230 235 240	
att ggc aaa atc acc gtt tcc act aat tta ggg cat ttg cac att aag	828
Ile Gly Lys Ile Thr Val Ser Thr Asn Leu Gly His Leu His Ile Lys	
245 250 255	
gat ttt gcg aaa gtc atc agc cag tct cgc acc cgt ttg ggg ttt gtt	876
Asp Phe Ala Lys Val Ile Ser Gln Ser Arg Thr Arg Leu Gly Phe Val	
260 265 270	
act aaa gat ggc gtg ggc gag acc aca gaa ggc ttg gtg ctt tct tta	924
Thr Lys Asp Gly Val Gly Glu Thr Thr Glu Gly Leu Val Leu Ser Leu	
275 280 285	
aaa gac gct aac acc aaa gaa atc atc act caa gtg tat caa aaa cta	972
Lys Asp Ala Asn Thr Lys Glu Ile Ile Thr Gln Val Tyr Gln Lys Leu	
290 295 300	
gaa gaa tta aaa ccc ttt tta ccg aat ggc gtg tcc att aat gtt ttt	1020
Glu Glu Leu Lys Pro Phe Leu Pro Asn Gly Val Ser Ile Asn Val Phe	
305 310 315 320	
tat gat cgc tca gaa ttt acg caa aaa gcc att gcc acc gtt tct aaa	1068
Tyr Asp Arg Ser Glu Phe Thr Gln Lys Ala Ile Ala Thr Val Ser Lys	
325 330 335	
acc ctc att gaa gcc gtt gtt tta atc atc atc acg ctc ttt tta ttt	1116
Thr Leu Ile Glu Ala Val Val Leu Ile Ile Ile Thr Leu Phe Leu Phe	
340 345 350	
tta ggg aat ttg agg gcg agc gtg gct gtg ggg gtg att tta cct tta	1164
Leu Gly Asn Leu Arg Ala Ser Val Ala Val Gly Val Ile Leu Pro Leu	
355 360 365	
agc ttg tcc gtg gcg ttt att ttt atc aag ttt agc gat ctg act tta	1212
Ser Leu Ser Val Ala Phe Ile Phe Ile Lys Phe Ser Asp Leu Thr Leu	
370 375 380	
aat ttg atg agt tta ggg gga ttg gtt atc gct ata ggc atg ctc att	1260
Asn Leu Met Ser Leu Gly Gly Leu Val Ile Ala Ile Gly Met Leu Ile	
385 390 395 400	
gac tca gcc gtg gtg gtg gtg gaa aac gct ttt gaa aaa tta agc gct	1308
Asp Ser Ala Val Val Val Val Glu Asn Ala Phe Glu Lys Leu Ser Ala	
405 410 415	
aac act aaa acc act aaa ctc cat gca atc tat cgt tcg tgt aaa gaa	1356
Asn Thr Lys Thr Thr Lys Leu His Ala Ile Tyr Arg Ser Cys Lys Glu	
420 425 430	

atc gct gtt tca gtg gtg agc ggg gtg gtg atc atc att gtg ttt ttt	1404
Ile Ala Val Ser Val Val Ser Gly Val Val Ile Ile Ile Val Phe Phe	
435 440 445	
gtg ccg att tta acc tta cag ggg tta gag ggt aag atg ttt agg cct	1452
Val Pro Ile Leu Thr Leu Gln Gly Leu Glu Gly Lys Met Phe Arg Pro	
450 455 460	
tta gcg caa agc att gtg tat gcg ctt tta ggc act tta gtt cta tct	1500
Leu Ala Gln Ser Ile Val Tyr Ala Leu Leu Gly Thr Leu Val Leu Ser	
465 470 475 480	
att aca atc att cct gta gtc agc tct ctt gtc tta aaa gcc acg ccc	1548
Ile Thr Ile Ile Pro Val Val Ser Ser Leu Val Leu Lys Ala Thr Pro	
485 490 495	
cat agc gaa acc ttt tta acg agg ttt tta aac aga atc tac gcc cct	1596
His Ser Glu Thr Phe Leu Thr Arg Phe Leu Asn Arg Ile Tyr Ala Pro	
500 505 510	
tta ttg gaa ttt ttt gtg cat aac cct aaa aaa gtg att tta gga gcg	1644
Leu Leu Glu Phe Phe Val His Asn Pro Lys Lys Val Ile Leu Gly Ala	
515 520 525	
ttt gtt ttt tta atc gca agc ctt tct tta ttc cct ttt gtg ggg aag	1692
Phe Val Phe Leu Ile Ala Ser Leu Ser Leu Phe Pro Phe Val Gly Lys	
530 535 540	
aat ttc atg ccc gtt tta gat gag ggc gat gtg gtt ttg agc gtg gaa	1740
Asn Phe Met Pro Val Leu Asp Glu Gly Asp Val Val Leu Ser Val Glu	
545 550 555 560	
acc acc cct tct att tct tta gat caa tct agg gat ctc atg cta aac	1788
Thr Thr Pro Ser Ile Ser Leu Asp Gln Ser Arg Asp Leu Met Leu Asn	
565 570 575	
att gag agc gcg att aaa aag cat gtc aag gaa gtt aaa agc att gtc	1836
Ile Glu Ser Ala Ile Lys Lys His Val Lys Glu Val Lys Ser Ile Val	
580 585 590	
gcg cgc aca ggg agc gat gaa ttg ggg ctg gat tta gga ggt ttg aat	1884
Ala Arg Thr Gly Ser Asp Glu Leu Gly Leu Asp Leu Gly Gly Leu Asn	
595 600 605	
caa acc gat act ttt att tct ttt att cct aaa aaa gaa tgg agc gtt	1932
Gln Thr Asp Thr Phe Ile Ser Phe Ile Pro Lys Lys Glu Trp Ser Val	
610 615 620	
aaa acc aaa gat gaa tta tta gaa aaa atc atg gat tct tta aaa gac	1980
Lys Thr Lys Asp Glu Leu Leu Glu Lys Ile Met Asp Ser Leu Lys Asp	
625 630 635 640	
ttt aag ggg att aac ttt tct ttc acc caa ccc att gaa atg aga att	2028
Phe Lys Gly Ile Asn Phe Ser Phe Thr Gln Pro Ile Glu Met Arg Ile	
645 650 655	
tct gaa atg ctg aca ggg gtt agg ggg gat tta gcg gtt aag att ttt	2076
Ser Glu Met Leu Thr Gly Val Arg Gly Asp Leu Ala Val Lys Ile Phe	

660					665					670					
gga gat ggt att agc gaa ttg aat gaa ttg agt ttt caa atc gcg caa	2124														
Gly Asp Gly Ile Ser Glu Leu Asn Glu Leu Ser Phe Gln Ile Ala Gln															
675	680														
gct cta aaa ggg att aaa gga tct agt gaa gtt tta acc acg ctt aat	2172														
Ala Leu Lys Gly Ile Lys Gly Ser Ser Glu Val Leu Thr Thr Leu Asn															
690	695														
gag ggc gtg aat tat ttg tat gta acc cct aat aaa gaa tcg atg gcg	2220														
Glu Gly Val Asn Tyr Leu Tyr Val Thr Pro Asn Lys Glu Ser Met Ala															
705	710														
gat gtg ggg atc act agc gat gaa ttt tcc aag ttt tta aaa tcc gct	2268														
Asp Val Gly Ile Thr Ser Asp Glu Phe Ser Lys Phe Leu Lys Ser Ala															
725	730														
tta gag ggc ttg gtt gta gat gtg atc cct aca ggg att tca cgc acg	2316														
Leu Glu Gly Leu Val Val Asp Val Ile Pro Thr Gly Ile Ser Arg Thr															
740	745														
cca gtg atg atc cgc caa gag agc gat ttt gca agc tct atc act aaa	2364														
Pro Val Met Ile Arg Gln Glu Ser Asp Phe Ala Ser Ser Ile Thr Lys															
755	760														
atc aaa agt tta gcc ttg act tca aaa tat ggc gtt tta gtg cct atc	2412														
Ile Lys Ser Leu Ala Leu Thr Ser Lys Tyr Gly Val Leu Val Pro Ile															
770	775														
act tct atc gcc aaa att gaa gaa gtg gat ggc cct gtt tct gtt gtg	2460														
Thr Ser Ile Ala Lys Ile Glu Glu Val Asp Gly Pro Val Ser Val Val															
785	790														
cgt gaa aat tca atg cgc atg agc gtg gtt cgc agt aat gtg gtg ggg	2508														
Arg Glu Asn Ser Met Arg Met Ser Val Val Arg Ser Asn Val Val Gly															
805	810														
cgc gat ttg aaa tct ttt gta gaa gag gct aaa aaa gtg atc gct caa	2556														
Arg Asp Leu Lys Ser Phe Val Glu Glu Ala Lys Lys Val Ile Ala Gln															
820	825														
aac atc aaa ctc cct ccc agc tac tat atc act tat ggg ggg cag ttt	2604														
Asn Ile Lys Leu Pro Pro Ser Tyr Tyr Ile Thr Tyr Gly Gly Gln Phe															
835	840														
gaa aac cag caa cgg gcc aat aaa agg ctc tcc acc gtt atc cct tta	2652														
Glu Asn Gln Gln Arg Ala Asn Lys Arg Leu Ser Thr Val Ile Pro Leu															
850	855														
agc atc tta gcg att ttt ttc att ctt ttt ttc act ttt aaa agc att	2700														
Ser Ile Leu Ala Ile Phe Phe Ile Leu Phe Phe Thr Phe Lys Ser Ile															
865	870														
cct tta gcc ttg ctc att ctt ttg aat atc cct ttt gcg gtt acc gga	2748														
Pro Leu Ala Leu Leu Ile Leu Leu Asn Ile Pro Phe Ala Val Thr Gly															
885	890														
ggc ctt att gcg ttg ttt gcg gtc ggg gag tat att tca gtg cca gcg	2796														

Gly	Leu	Ile	Ala	Leu	Phe	Ala	Val	Gly	Glu	Tyr	Ile	Ser	Val	Pro	Ala		
			900					905					910				
agc	gtg	ggc	ttt	atc	gct	ctt	ttt	ggg	att	gcg	gtt	tta	aat	ggc	gtg	2844	
Ser	Val	Gly	Phe	Ile	Ala	Leu	Phe	Gly	Ile	Ala	Val	Leu	Asn	Gly	Val		
		915					920					925					
gtg	atg	ata	ggc	tat	ttt	aaa	gag	ctt	ctc	ttg	caa	ggg	aaa	agc	gta	2892	
Val	Met	Ile	Gly	Tyr	Phe	Lys	Glu	Leu	Leu	Leu	Gln	Gly	Lys	Ser	Val		
	930					935					940						
gaa	gaa	tgc	gtt	tta	ttg	ggc	gct	aaa	agg	cgt	ttg	aga	ccg	gtt	tta	2940	
Glu	Glu	Cys	Val	Leu	Leu	Gly	Ala	Lys	Arg	Arg	Leu	Arg	Pro	Val	Leu		
945					950				955						960		
atg	acc	gct	tgc	att	gcc	ggg	ttg	ggg	ttg	ctc	cct	tta	tta	ttt	tct	2988	
Met	Thr	Ala	Cys	Ile	Ala	Gly	Leu	Gly	Leu	Leu	Pro	Leu	Leu	Phe	Ser		
				965					970						975		
cat	agc	gtg	gga	tca	gaa	gtc	caa	aaa	cct	tta	gcg	atc	gtg	gtg	ctt	3036	
His	Ser	Val	Gly	Ser	Glu	Val	Gln	Lys	Pro	Leu	Ala	Ile	Val	Val	Leu		
			980					985					990				
gga	ggc	ttg	gtt	acc	tca	agc	gct	cta	acc	tta	ctc	cta	ctg	ccg	cca	3084	
Gly	Gly	Leu	Val	Thr	Ser	Ser	Ala	Leu	Thr	Leu	Leu	Leu	Leu	Pro	Pro		
		995					1000					1005					
atg	ttt	atg	ctc	atc	gct	aaa	aag	att	aaa	atc	gtt	tgagttaaag				3130	
Met	Phe	Met	Leu	Ile	Ala	Lys	Lys	Ile	Lys	Ile	Val						
	1010					1015					1020						
gatttcacat	gctcgcttta	gaaatttata	ttgatatttg	tttgaaaga												3179	
<210> 188																	
<211> 1020																	
<212> PRT																	
<213> Helicobacter pylori																	
<400> 188																	
Met	Met	Leu	Ala	Ser	Ile	Ile	Glu	Phe	Ser	Leu	Arg	Gln	Arg	Val	Ile		
1				5					10					15			
Val	Ile	Val	Gly	Ala	Ile	Leu	Ile	Leu	Phe	Phe	Gly	Thr	Tyr	Ser	Phe		
			20					25					30				
Ile	Asn	Thr	Pro	Val	Asp	Ala	Phe	Pro	Asp	Ile	Ser	Pro	Thr	Gln	Val		
	35					40					45						
Lys	Ile	Ile	Leu	Lys	Leu	Pro	Gly	Ser	Ser	Pro	Glu	Glu	Met	Glu	Asn		
	50				55					60							
Asn	Ile	Val	Arg	Pro	Leu	Glu	Leu	Glu	Leu	Leu	Gly	Leu	Lys	Gly	Gln		
65				70					75					80			
Lys	Ser	Leu	Arg	Ser	Val	Ser	Lys	Tyr	Ser	Ile	Ser	Asp	Ile	Thr	Ile		
			85					90					95				
Asp	Phe	Asp	Asp	Ser	Val	Asp	Ile	Tyr	Leu	Ala	Arg	Asn	Ile	Val	Asn		
		100					105					110					
Glu	Arg	Leu	Ser	Ser	Val	Met	Lys	Asp	Leu	Pro	Val	Gly	Val	Glu	Gly		
		115					120					125					
Gly	Met	Ala	Pro	Ile	Val	Thr	Pro	Leu	Ser	Asp	Ile	Phe	Met	Phe	Thr		
	130				135					140							
Ile	Asp	Gly	Asn	Ile	Thr	Glu	Ile	Glu	Lys	Arg	Gln	Leu	Leu	Asp	Phe		
145				150					155						160		

Val	Ile	Arg	Pro	Gln	Leu	Arg	Met	Ile	Ser	Gly	Val	Ala	Asp	Val	Asn
				165					170					175	
Ser	Ile	Gly	Gly	Phe	Ser	Arg	Ala	Phe	Val	Ile	Val	Pro	Asp	Phe	Asn
			180					185					190		
Asp	Met	Ala	Arg	Leu	Gly	Val	Ser	Ile	Ser	Asp	Leu	Glu	Ser	Ala	Val
		195					200					205			
Arg	Val	Asn	Leu	Arg	Asn	Ser	Gly	Ala	Gly	Arg	Val	Asp	Arg	Asp	Gly
	210					215					220				
Glu	Thr	Phe	Leu	Val	Lys	Ile	Gln	Thr	Ala	Ser	Leu	Ser	Leu	Glu	Asp
225					230					235					240
Ile	Gly	Lys	Ile	Thr	Val	Ser	Thr	Asn	Leu	Gly	His	Leu	His	Ile	Lys
				245						250				255	
Asp	Phe	Ala	Lys	Val	Ile	Ser	Gln	Ser	Arg	Thr	Arg	Leu	Gly	Phe	Val
			260					265					270		
Thr	Lys	Asp	Gly	Val	Gly	Glu	Thr	Thr	Glu	Gly	Leu	Val	Leu	Ser	Leu
		275					280					285			
Lys	Asp	Ala	Asn	Thr	Lys	Glu	Ile	Ile	Thr	Gln	Val	Tyr	Gln	Lys	Leu
	290					295					300				
Glu	Glu	Leu	Lys	Pro	Phe	Leu	Pro	Asn	Gly	Val	Ser	Ile	Asn	Val	Phe
305					310					315					320
Tyr	Asp	Arg	Ser	Glu	Phe	Thr	Gln	Lys	Ala	Ile	Ala	Thr	Val	Ser	Lys
				325					330					335	
Thr	Leu	Ile	Glu	Ala	Val	Val	Leu	Ile	Ile	Ile	Thr	Leu	Phe	Leu	Phe
			340					345					350		
Leu	Gly	Asn	Leu	Arg	Ala	Ser	Val	Ala	Val	Gly	Val	Ile	Leu	Pro	Leu
		355					360					365			
Ser	Leu	Ser	Val	Ala	Phe	Ile	Phe	Ile	Lys	Phe	Ser	Asp	Leu	Thr	Leu
	370					375					380				
Asn	Leu	Met	Ser	Leu	Gly	Gly	Leu	Val	Ile	Ala	Ile	Gly	Met	Leu	Ile
385					390					395					400
Asp	Ser	Ala	Val	Val	Val	Val	Glu	Asn	Ala	Phe	Glu	Lys	Leu	Ser	Ala
			405						410					415	
Asn	Thr	Lys	Thr	Thr	Lys	Leu	His	Ala	Ile	Tyr	Arg	Ser	Cys	Lys	Glu
			420					425					430		
Ile	Ala	Val	Ser	Val	Val	Ser	Gly	Val	Val	Ile	Ile	Ile	Val	Phe	Phe
		435					440					445			
Val	Pro	Ile	Leu	Thr	Leu	Gln	Gly	Leu	Glu	Gly	Lys	Met	Phe	Arg	Pro
	450					455					460				
Leu	Ala	Gln	Ser	Ile	Val	Tyr	Ala	Leu	Leu	Gly	Thr	Leu	Val	Leu	Ser
465					470					475					480
Ile	Thr	Ile	Ile	Pro	Val	Val	Ser	Ser	Leu	Val	Leu	Lys	Ala	Thr	Pro
				485					490					495	
His	Ser	Glu	Thr	Phe	Leu	Thr	Arg	Phe	Leu	Asn	Arg	Ile	Tyr	Ala	Pro
			500					505					510		
Leu	Leu	Glu	Phe	Phe	Val	His	Asn	Pro	Lys	Lys	Val	Ile	Leu	Gly	Ala
		515					520					525			
Phe	Val	Phe	Leu	Ile	Ala	Ser	Leu	Ser	Leu	Phe	Pro	Phe	Val	Gly	Lys
	530					535					540				
Asn	Phe	Met	Pro	Val	Leu	Asp	Glu	Gly	Asp	Val	Val	Leu	Ser	Val	Glu
545					550					555					560
Thr	Thr	Pro	Ser	Ile	Ser	Leu	Asp	Gln	Ser	Arg	Asp	Leu	Met	Leu	Asn
			565						570					575	
Ile	Glu	Ser	Ala	Ile	Lys	Lys	His	Val	Lys	Glu	Val	Lys	Ser	Ile	Val
			580					585					590		
Ala	Arg	Thr	Gly	Ser	Asp	Glu	Leu	Gly	Leu	Asp	Leu	Gly	Gly	Leu	Asn
		595				600						605			
Gln	Thr	Asp	Thr	Phe	Ile	Ser	Phe	Ile	Pro	Lys	Lys	Glu	Trp	Ser	Val
	610					615					620				
Lys	Thr	Lys	Asp	Glu	Leu	Leu	Glu	Lys	Ile	Met	Asp	Ser	Leu	Lys	Asp

625					630					635					640
Phe	Lys	Gly	Ile	Asn	Phe	Ser	Phe	Thr	Gln	Pro	Ile	Glu	Met	Arg	Ile
				645					650					655	
Ser	Glu	Met	Leu	Thr	Gly	Val	Arg	Gly	Asp	Leu	Ala	Val	Lys	Ile	Phe
			660					665					670		
Gly	Asp	Gly	Ile	Ser	Glu	Leu	Asn	Glu	Leu	Ser	Phe	Gln	Ile	Ala	Gln
		675					680					685			
Ala	Leu	Lys	Gly	Ile	Lys	Gly	Ser	Ser	Glu	Val	Leu	Thr	Thr	Leu	Asn
	690					695					700				
Glu	Gly	Val	Asn	Tyr	Leu	Tyr	Val	Thr	Pro	Asn	Lys	Glu	Ser	Met	Ala
705					710					715					720
Asp	Val	Gly	Ile	Thr	Ser	Asp	Glu	Phe	Ser	Lys	Phe	Leu	Lys	Ser	Ala
				725					730					735	
Leu	Glu	Gly	Leu	Val	Val	Asp	Val	Ile	Pro	Thr	Gly	Ile	Ser	Arg	Thr
			740					745					750		
Pro	Val	Met	Ile	Arg	Gln	Glu	Ser	Asp	Phe	Ala	Ser	Ser	Ile	Thr	Lys
		755					760					765			
Ile	Lys	Ser	Leu	Ala	Leu	Thr	Ser	Lys	Tyr	Gly	Val	Leu	Val	Pro	Ile
	770					775					780				
Thr	Ser	Ile	Ala	Lys	Ile	Glu	Glu	Val	Asp	Gly	Pro	Val	Ser	Val	Val
785					790					795					800
Arg	Glu	Asn	Ser	Met	Arg	Met	Ser	Val	Val	Arg	Ser	Asn	Val	Val	Gly
				805					810					815	
Arg	Asp	Leu	Lys	Ser	Phe	Val	Glu	Glu	Ala	Lys	Lys	Val	Ile	Ala	Gln
		820						825					830		
Asn	Ile	Lys	Leu	Pro	Pro	Ser	Tyr	Ile	Thr	Tyr	Gly	Gly	Gln	Phe	
		835					840				845				
Glu	Asn	Gln	Gln	Arg	Ala	Asn	Lys	Arg	Leu	Ser	Thr	Val	Ile	Pro	Leu
	850					855					860				
Ser	Ile	Leu	Ala	Ile	Phe	Phe	Ile	Leu	Phe	Phe	Thr	Phe	Lys	Ser	Ile
865					870					875					880
Pro	Leu	Ala	Leu	Leu	Ile	Leu	Leu	Asn	Ile	Pro	Phe	Ala	Val	Thr	Gly
				885					890					895	
Gly	Leu	Ile	Ala	Leu	Phe	Ala	Val	Gly	Glu	Tyr	Ile	Ser	Val	Pro	Ala
			900					905					910		
Ser	Val	Gly	Phe	Ile	Ala	Leu	Phe	Gly	Ile	Ala	Val	Leu	Asn	Gly	Val
		915					920					925			
Val	Met	Ile	Gly	Tyr	Phe	Lys	Glu	Leu	Leu	Leu	Gln	Gly	Lys	Ser	Val
	930					935					940				
Glu	Glu	Cys	Val	Leu	Leu	Gly	Ala	Lys	Arg	Arg	Leu	Arg	Pro	Val	Leu
945					950					955					960
Met	Thr	Ala	Cys	Ile	Ala	Gly	Leu	Gly	Leu	Leu	Pro	Leu	Leu	Phe	Ser
				965					970					975	
His	Ser	Val	Gly	Ser	Glu	Val	Gln	Lys	Pro	Leu	Ala	Ile	Val	Val	Leu
			980					985					990		
Gly	Gly	Leu	Val	Thr	Ser	Ser	Ala	Leu	Thr	Leu	Leu	Leu	Leu	Pro	Pro
		995					1000					1005			
Met	Phe	Met	Leu	Ile	Ala	Lys	Lys	Ile	Lys	Ile	Val				
	1010					1015					1020				

<210> 189
 <211> 720
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (33)...(638)

<400> 189

aagcttataa aatcatcaaa aagagtgtctg aa atg aat gtt tta atc aga ttg	53
Met Asn Val Leu Ile Arg Leu	
1 5	
tgc ttt att ttt ttg att ggg ttt ttt ggc gcg aat aaa acc cta aac	101
Cys Phe Ile Phe Leu Ile Gly Phe Phe Gly Ala Asn Lys Thr Leu Asn	
10 15 20	
gca aca gcc att ctt tct ctt gac ttt ggc tct ttt tcc atg cca atc	149
Ala Thr Ala Ile Leu Ser Leu Asp Phe Gly Ser Phe Ser Met Pro Ile	
25 30 35	
act gcc aat ttc tca gat ggt gcg tta aat gta ttc aaa tgg ttt gaa	197
Thr Ala Asn Phe Ser Asp Gly Ala Leu Asn Val Phe Lys Trp Phe Glu	
40 45 50 55	
aaa cac cca tca gtg ggt gtt aaa gtt ggt cgg ctt gca aat caa gac	245
Lys His Pro Ser Val Gly Val Lys Val Gly Arg Leu Ala Asn Gln Asp	
60 65 70	
gac act atc ttt act cta gtt ttc att gtg ata gtt gtc gca ata att	293
Asp Thr Ile Phe Thr Leu Val Phe Ile Val Ile Val Val Ala Ile Ile	
75 80 85	
gcc ctt atc gct att ttt ata agg agt ata tta cta aac aca att ttt	341
Ala Leu Ile Ala Ile Phe Ile Arg Ser Ile Leu Leu Asn Thr Ile Phe	
90 95 100	
gta gga tcg ctc ata gga tcc tta tgg ttg tat atg gta ggg ttt tat	389
Val Gly Ser Leu Ile Gly Ser Leu Trp Leu Tyr Met Val Gly Phe Tyr	
105 110 115	
tat ttt tat ggt gtt ccc ttt ttg agt tat ttg agc ggt tgt tat gaa	437
Tyr Phe Tyr Gly Val Pro Phe Leu Ser Tyr Leu Ser Gly Cys Tyr Glu	
120 125 130 135	
tcg ttt tct ttc tcc gca tgc tat cct cat agt ttg cag cta ctc ccc	485
Ser Phe Ser Phe Ser Ala Cys Tyr Pro His Ser Leu Gln Leu Leu Pro	
140 145 150	
acc ctt atg cag tat tcg ccc att tac tcc ata atc aaa ctt ctt gct	533
Thr Leu Met Gln Tyr Ser Pro Ile Tyr Ser Ile Ile Lys Leu Leu Ala	
155 160 165	
cat ttt aat ata gag atc act tct aag att atc att tct ctt gtt tgg	581
His Phe Asn Ile Glu Ile Thr Ser Lys Ile Ile Ile Ser Leu Val Trp	
170 175 180	
gtg tgt ata ggg ctg tat ttt ttg tta ttg caa gcg ttt ttt agt ctt	629
Val Cys Ile Gly Leu Tyr Phe Leu Leu Leu Gln Ala Phe Phe Ser Leu	
185 190 195	
aca aat tat tagttgcaga aaattcaaga aggcaaaaaa ttatcttttt	678
Thr Asn Tyr	
200	
tcctcgaatc aatcattagg ttatttttttg gttttatgat ag	720

<210> 190
 <211> 202
 <212> PRT
 <213> Helicobacter pylori

<400> 190
 Met Asn Val Leu Ile Arg Leu Cys Phe Ile Phe Leu Ile Gly Phe Phe
 1 5 10 15
 Gly Ala Asn Lys Thr Leu Asn Ala Thr Ala Ile Leu Ser Leu Asp Phe
 20 25 30
 Gly Ser Phe Ser Met Pro Ile Thr Ala Asn Phe Ser Asp Gly Ala Leu
 35 40 45
 Asn Val Phe Lys Trp Phe Glu Lys His Pro Ser Val Gly Val Lys Val
 50 55 60
 Gly Arg Leu Ala Asn Gln Asp Asp Thr Ile Phe Thr Leu Val Phe Ile
 65 70 75 80
 Val Ile Val Val Ala Ile Ile Ala Leu Ile Ala Ile Phe Ile Arg Ser
 85 90 95
 Ile Leu Leu Asn Thr Ile Phe Val Gly Ser Leu Ile Gly Ser Leu Trp
 100 105 110
 Leu Tyr Met Val Gly Phe Tyr Tyr Phe Tyr Gly Val Pro Phe Leu Ser
 115 120 125
 Tyr Leu Ser Gly Cys Tyr Glu Ser Phe Ser Phe Ser Ala Cys Tyr Pro
 130 135 140
 His Ser Leu Gln Leu Leu Pro Thr Leu Met Gln Tyr Ser Pro Ile Tyr
 145 150 155 160
 Ser Ile Ile Lys Leu Leu Ala His Phe Asn Ile Glu Ile Thr Ser Lys
 165 170 175
 Ile Ile Ile Ser Leu Val Trp Val Cys Ile Gly Leu Tyr Phe Leu Leu
 180 185 190
 Leu Gln Ala Phe Phe Ser Leu Thr Asn Tyr
 195 200

<210> 191
 <211> 310
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (65)...(280)

<400> 191
 aattcaagaa ggcaaaaaat tatctttttt cctcgaatca atcattaggt tatttttttg 60
 tttt atg ata gtt tct ttt att gcc gtt cca tgc tac tat gtt tta ttg 109
 Met Ile Val Ser Phe Ile Ala Val Pro Cys Tyr Tyr Val Leu Leu
 1 5 10 15
 gcg atg gaa tac caa ata gcc tat gaa cac cca gga gaa tta ata agc 157
 Ala Met Glu Tyr Gln Ile Ala Tyr Glu His Pro Gly Glu Leu Ile Ser
 20 25 30
 acg att ggt ttt gtt gcg tta gca gtg ctt gtg tat tac tta tgg ggt 205
 Thr Ile Gly Phe Val Ala Leu Ala Val Leu Val Tyr Tyr Leu Trp Gly
 35 40 45
 aaa tgg gag aag ttg cta tgg ggc gca cct tcc aat caa gag caa caa 253
 Lys Trp Glu Lys Leu Leu Trp Gly Ala Pro Ser Asn Gln Glu Gln Gln

```

50              55              60
ctc tcc aat caa ggc aac caa aat caa tgattgtgat tgatcgctag      300
Leu Ser Asn Gln Gly Asn Gln Asn Gln
65              70

gtcaatctga      310

<210> 192
<211> 72
<212> PRT
<213> Helicobacter pylori

<400> 192
Met Ile Val Ser Phe Ile Ala Val Pro Cys Tyr Tyr Val Leu Leu Ala
1      5      10      15
Met Glu Tyr Gln Ile Ala Tyr Glu His Pro Gly Glu Leu Ile Ser Thr
20      25      30
Ile Gly Phe Val Ala Leu Ala Val Leu Val Tyr Tyr Leu Trp Gly Lys
35      40      45
Trp Glu Lys Leu Leu Trp Gly Ala Pro Ser Asn Gln Glu Gln Gln Leu
50      55      60
Ser Asn Gln Gly Asn Gln Asn Gln
65      70

<210> 193
<211> 311
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (60)...(287)

<400> 193
taggaaaaaag actatcatgc gagctatcca aattagatcc gatcaaaaac tacccttta      59
atg gtt gta tca atg aac tgc atc ggc tct aaa tac aaa ctc att gcc      107
Met Val Val Ser Met Asn Cys Ile Gly Ser Lys Tyr Lys Leu Ile Ala
1      5      10      15

ttt att caa gaa aat atc cat gcg gtt gtg ggg caa cct ttt ggg tgt      155
Phe Ile Gln Glu Asn Ile His Ala Val Val Gly Gln Pro Phe Gly Cys
20      25      30

gat ttt ttg cga tct gtt cgc tgg gac ggg tat cgt ggg gtg tgc gta      203
Asp Phe Leu Arg Ser Val Arg Trp Asp Gly Tyr Arg Gly Val Cys Val
35      40      45

aag tgg tct cta ggt tca aca cta aaa aac att ttt tca tta gac agc      251
Lys Trp Ser Leu Gly Ser Thr Leu Lys Asn Ile Phe Ser Leu Asp Ser
50      55      60

gtg tta aaa gcc aat caa gtt atc cct aaa gat gct taacatgtta      297
Val Leu Lys Ala Asn Gln Val Ile Pro Lys Asp Ala
65      70      75

aaataatctc atac      311

```

<210> 194
 <211> 76
 <212> PRT
 <213> Helicobacter pylori

<400> 194
 Met Val Val Ser Met Asn Cys Ile Gly Ser Lys Tyr Lys Leu Ile Ala
 1 5 10 15
 Phe Ile Gln Glu Asn Ile His Ala Val Val Gly Gln Pro Phe Gly Cys
 20 25 30
 Asp Phe Leu Arg Ser Val Arg Trp Asp Gly Tyr Arg Gly Val Cys Val
 35 40 45
 Lys Trp Ser Leu Gly Ser Thr Leu Lys Asn Ile Phe Ser Leu Asp Ser
 50 55 60
 Val Leu Lys Ala Asn Gln Val Ile Pro Lys Asp Ala
 65 70 75

<210> 195
 <211> 900
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(872)

<400> 195
 aaaattaagt tgtttgatcg cttttaaacg atttttaaaa ggaaaaattt atg gat 56
 Met Asp
 1
 gaa att aaa acg ctg tta gtg gat ttt ttt ccg cag gca aag cat ttt 104
 Glu Ile Lys Thr Leu Leu Val Asp Phe Phe Pro Gln Ala Lys His Phe
 5 10 15
 ggg ata atc tta atc aag gct att gtt gtc ttt tgt ata ggt ttt tat 152
 Gly Ile Ile Leu Ile Lys Ala Ile Val Val Phe Cys Ile Gly Phe Tyr
 20 25 30
 ttt tca ttt ttc tta caa aaa aaa acc atg aaa ttt tta tcc aaa aag 200
 Phe Ser Phe Phe Leu Gln Lys Lys Thr Met Lys Phe Leu Ser Lys Lys
 35 40 45 50
 gat gag att tta gcg aat ttt gtc gca cag gtt act ttt atc tta atc 248
 Asp Glu Ile Leu Ala Asn Phe Val Ala Gln Val Thr Phe Ile Leu Ile
 55 60 65
 ctt atc atc acc aca atc att gcg ctc agc acg cta ggc gtg caa acc 296
 Leu Ile Ile Thr Thr Ile Ile Ala Leu Ser Thr Leu Gly Val Gln Thr
 70 75 80
 acc tct att atc act gtt tta gga acg gta ggg att gct gtg gcg ttg 344
 Thr Ser Ile Ile Thr Val Leu Gly Thr Val Gly Ile Ala Val Ala Leu
 85 90 95
 gct tta aaa gat tat ctt tca agc att gct gga ggg ata atc ctt att 392
 Ala Leu Lys Asp Tyr Leu Ser Ser Ile Ala Gly Gly Ile Ile Leu Ile
 100 105 110

atc ttg cac cct ttc aaa aaa gga gac atc att gaa atc tct ggc cta	440
Ile Leu His Pro Phe Lys Lys Gly Asp Ile Ile Glu Ile Ser Gly Leu	
115 120 125 130	
gag ggc aaa gta gaa gcg ctt aat ttt ttt aac act tct tta cgc ttg	488
Glu Gly Lys Val Glu Ala Leu Asn Phe Phe Asn Thr Ser Leu Arg Leu	
135 140 145	
cat gac gga cgc ttg gcg gtt tta ccc aat aga agt gtc gct aat tct	536
His Asp Gly Arg Leu Ala Val Leu Pro Asn Arg Ser Val Ala Asn Ser	
150 155 160	
aat att atc aat agc aat aac acg gcg tgt cgg cgc att gaa tgg gtt	584
Asn Ile Ile Asn Ser Asn Asn Thr Ala Cys Arg Arg Ile Glu Trp Val	
165 170 175	
tgt ggg gta ggg tat ggg agc gat att gaa ctg gtg cat aag act ata	632
Cys Gly Val Gly Tyr Gly Ser Asp Ile Glu Leu Val His Lys Thr Ile	
180 185 190	
aaa gat gtt att gat gca atg gaa aaa att gat aaa aac atg ccc act	680
Lys Asp Val Ile Asp Ala Met Glu Lys Ile Asp Lys Asn Met Pro Thr	
195 200 205 210	
ttt att ggg atc acg gat ttt gga caa agt tcg ctg aat ttc acc att	728
Phe Ile Gly Ile Thr Asp Phe Gly Gln Ser Ser Leu Asn Phe Thr Ile	
215 220 225	
agg gtt tgg gca aag att gaa gac gga atc ttt aat gtg cgc agc gaa	776
Arg Val Trp Ala Lys Ile Glu Asp Gly Ile Phe Asn Val Arg Ser Glu	
230 235 240	
ctc att gaa cgc atc aaa aac gcc cta gac gct aac cac att gaa atc	824
Leu Ile Glu Arg Ile Lys Asn Ala Leu Asp Ala Asn His Ile Glu Ile	
245 250 255	
cct ttc aac aag cta gat att gct att aaa aat caa gac tct cct aaa	872
Pro Phe Asn Lys Leu Asp Ile Ala Ile Lys Asn Gln Asp Ser Pro Lys	
260 265 270	
tgattggtgt gagatgtatt gattgtag	900

<210> 196

<211> 274

<212> PRT

<213> Helicobacter pylori

<400> 196

Met Asp Glu Ile Lys Thr Leu Leu Val Asp Phe Phe Pro Gln Ala Lys	
1 5 10 15	
His Phe Gly Ile Ile Leu Ile Lys Ala Ile Val Val Phe Cys Ile Gly	
20 25 30	
Phe Tyr Phe Ser Phe Phe Leu Gln Lys Lys Thr Met Lys Phe Leu Ser	
35 40 45	
Lys Lys Asp Glu Ile Leu Ala Asn Phe Val Ala Gln Val Thr Phe Ile	
50 55 60	
Leu Ile Leu Ile Ile Thr Thr Ile Ile Ala Leu Ser Thr Leu Gly Val	
65 70 75 80	

Gln	Thr	Thr	Ser	Ile	Ile	Thr	Val	Leu	Gly	Thr	Val	Gly	Ile	Ala	Val
				85					90					95	
Ala	Leu	Ala	Leu	Lys	Asp	Tyr	Leu	Ser	Ser	Ile	Ala	Gly	Gly	Ile	Ile
			100					105					110		
Leu	Ile	Ile	Leu	His	Pro	Phe	Lys	Lys	Gly	Asp	Ile	Ile	Glu	Ile	Ser
		115					120					125			
Gly	Leu	Glu	Gly	Lys	Val	Glu	Ala	Leu	Asn	Phe	Phe	Asn	Thr	Ser	Leu
	130					135					140				
Arg	Leu	His	Asp	Gly	Arg	Leu	Ala	Val	Leu	Pro	Asn	Arg	Ser	Val	Ala
145					150					155					160
Asn	Ser	Asn	Ile	Ile	Asn	Ser	Asn	Asn	Thr	Ala	Cys	Arg	Arg	Ile	Glu
				165					170					175	
Trp	Val	Cys	Gly	Val	Gly	Tyr	Gly	Ser	Asp	Ile	Glu	Leu	Val	His	Lys
			180					185					190		
Thr	Ile	Lys	Asp	Val	Ile	Asp	Ala	Met	Glu	Lys	Ile	Asp	Lys	Asn	Met
		195					200					205			
Pro	Thr	Phe	Ile	Gly	Ile	Thr	Asp	Phe	Gly	Gln	Ser	Ser	Leu	Asn	Phe
	210					215					220				
Thr	Ile	Arg	Val	Trp	Ala	Lys	Ile	Glu	Asp	Gly	Ile	Phe	Asn	Val	Arg
225					230					235					240
Ser	Glu	Leu	Ile	Glu	Arg	Ile	Lys	Asn	Ala	Leu	Asp	Ala	Asn	His	Ile
				245					250					255	
Glu	Ile	Pro	Phe	Asn	Lys	Leu	Asp	Ile	Ala	Ile	Lys	Asn	Gln	Asp	Ser
			260					265					270		
Pro	Lys														

<210> 197
 <211> 833
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (52)...(762)

<400> 197	
tagcggttgg gtaattcact ccaatctcta agtggcagtg gctatgaaaa c atg caa	57
	Met Gln
	1
tca ctt gct ggg gga ttg agt ggt aga gcg tgg gga gaa atg ttg tgt	105
Ser Leu Ala Gly Gly Leu Ser Gly Arg Ala Trp Gly Glu Met Leu Cys	
	5 10 15
aaa atg gta aac gat agt aat tat gaa agc gag caa gct ctt tta gca	153
Lys Met Val Asn Asp Ser Asn Tyr Glu Ser Glu Gln Ala Leu Leu Ala	
	20 25 30
aca ggc aat agc tca gaa gag caa aaa cga aga ttt ttg ctt aga gta	201
Thr Gly Asn Ser Ser Glu Glu Gln Lys Arg Arg Phe Leu Leu Arg Val	
	35 40 45 50
aag aaa aag gtt aat gat aat agg cag tta aaa aag aaa ctt gac cca	249
Lys Lys Lys Val Asn Asp Asn Arg Gln Leu Lys Lys Lys Leu Asp Pro	
	55 60 65
ttt cta aaa aga ctt gat gtc cta caa act gag ttt ggt gta act gac	297

Phe	Leu	Lys	Arg	Leu	Asp	Val	Leu	Gln	Thr	Glu	Phe	Gly	Val	Thr	Asp		
			70					75					80				
cct	aca	gct	aac	cat	aat	aag	caa	ggg	ata	cat	tat	tgc	aca	gaa	aat	345	
Pro	Thr	Ala	Asn	His	Asn	Lys	Gln	Gly	Ile	His	Tyr	Cys	Thr	Glu	Asn		
		85					90					95					
aaa	aag	aca	ggt	aaa	tgc	gac	cct	att	gat	aat	gta	ttt	agg	aca	act	393	
Lys	Lys	Thr	Gly	Lys	Cys	Asp	Pro	Ile	Asp	Asn	Val	Phe	Arg	Thr	Thr		
	100					105					110						
cgc	tta	gat	aac	gaa	tta	gaa	caa	gaa	atc	caa	acg	ctc	aca	ctt	gat	441	
Arg	Leu	Asp	Asn	Glu	Leu	Glu	Gln	Glu	Ile	Gln	Thr	Leu	Thr	Leu	Asp		
115					120					125					130		
tta	acc	aaa	gcc	ccc	aat	aaa	gac	gct	caa	agc	caa	gcc	tac	gca	aat	489	
Leu	Thr	Lys	Ala	Pro	Asn	Lys	Asp	Ala	Gln	Ser	Gln	Ala	Tyr	Ala	Asn		
				135					140					145			
ttc	aat	caa	agg	att	aaa	tta	ctt	act	cta	aaa	tat	tta	aaa	gaa	att	537	
Phe	Asn	Gln	Arg	Ile	Lys	Leu	Leu	Thr	Leu	Lys	Tyr	Leu	Lys	Glu	Ile		
			150					155					160				
acc	aat	caa	atg	ctc	ttt	tta	aat	caa	aca	atg	gca	atg	caa	agc	gag	585	
Thr	Asn	Gln	Met	Leu	Phe	Leu	Asn	Gln	Thr	Met	Ala	Met	Gln	Ser	Glu		
		165					170					175					
att	atg	gca	gat	gat	tat	ttt	agg	caa	aat	aat	gat	ggc	ttt	ggg	aaa	633	
Ile	Met	Ala	Asp	Asp	Tyr	Phe	Arg	Gln	Asn	Asn	Asp	Gly	Phe	Gly	Lys		
	180					185					190						
gaa	gaa	aac	cat	ata	gac	aaa	caa	tta	acg	caa	aaa	aga	ata	aac	gaa	681	
Glu	Glu	Asn	His	Ile	Asp	Lys	Gln	Leu	Thr	Gln	Lys	Arg	Ile	Asn	Glu		
195					200					205					210		
aga	gaa	aga	gcc	aga	ata	tac	ttt	caa	aac	cct	aat	gtt	aaa	ttt	gac	729	
Arg	Glu	Arg	Ala	Arg	Ile	Tyr	Phe	Gln	Asn	Pro	Asn	Val	Lys	Phe	Asp		
			215						220					225			
caa	ttt	ggt	ttt	ccc	att	ttt	agt	ata	tgg	gat	taagggttta	gtgatgagag	782				
Gln	Phe	Gly	Phe	Pro	Ile	Phe	Ser	Ile	Trp	Asp							
			230					235									
atagaataag	tat	tttttttt	ccaaactatt	cctatttttag	tggtagtgtt	g	833										

<210> 198

<211> 237

<212> PRT

<213> Helicobacter pylori

<400> 198

Met	Gln	Ser	Leu	Ala	Gly	Gly	Leu	Ser	Gly	Arg	Ala	Trp	Gly	Glu	Met
1				5					10					15	
Leu	Cys	Lys	Met	Val	Asn	Asp	Ser	Asn	Tyr	Glu	Ser	Glu	Gln	Ala	Leu
			20					25					30		
Leu	Ala	Thr	Gly	Asn	Ser	Ser	Glu	Glu	Gln	Lys	Arg	Arg	Phe	Leu	Leu
		35					40					45			
Arg	Val	Lys	Lys	Lys	Val	Asn	Asp	Asn	Arg	Gln	Leu	Lys	Lys	Lys	Leu
	50					55					60				

Asp	Pro	Phe	Leu	Lys	Arg	Leu	Asp	Val	Leu	Gln	Thr	Glu	Phe	Gly	Val
65					70					75					80
Thr	Asp	Pro	Thr	Ala	Asn	His	Asn	Lys	Gln	Gly	Ile	His	Tyr	Cys	Thr
				85					90					95	
Glu	Asn	Lys	Lys	Thr	Gly	Lys	Cys	Asp	Pro	Ile	Asp	Asn	Val	Phe	Arg
			100					105					110		
Thr	Thr	Arg	Leu	Asp	Asn	Glu	Leu	Glu	Gln	Glu	Ile	Gln	Thr	Leu	Thr
			115				120					125			
Leu	Asp	Leu	Thr	Lys	Ala	Pro	Asn	Lys	Asp	Ala	Gln	Ser	Gln	Ala	Tyr
	130					135					140				
Ala	Asn	Phe	Asn	Gln	Arg	Ile	Lys	Leu	Leu	Thr	Leu	Lys	Tyr	Leu	Lys
145					150					155					160
Glu	Ile	Thr	Asn	Gln	Met	Leu	Phe	Leu	Asn	Gln	Thr	Met	Ala	Met	Gln
				165					170					175	
Ser	Glu	Ile	Met	Ala	Asp	Asp	Tyr	Phe	Arg	Gln	Asn	Asn	Asp	Gly	Phe
			180					185					190		
Gly	Lys	Glu	Glu	Asn	His	Ile	Asp	Lys	Gln	Leu	Thr	Gln	Lys	Arg	Ile
		195					200					205			
Asn	Glu	Arg	Glu	Arg	Ala	Arg	Ile	Tyr	Phe	Gln	Asn	Pro	Asn	Val	Lys
	210					215					220				
Phe	Asp	Gln	Phe	Gly	Phe	Pro	Ile	Phe	Ser	Ile	Trp	Asp			
225					230					235					

<210> 199
 <211> 351
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (63)...(311)

<400> 199
 tcaaaccacaa accaacacaa aatttgctaa actacaatca aatcaattta gggaggataa 60
 aa atg tca ttt gcc cct atg tta tta gct aca atc aat aac tct att 107
 Met Ser Phe Ala Pro Met Leu Leu Ala Thr Ile Asn Asn Ser Ile
 1 5 10 15

 ggc aat aaa gat aag cat gtg agt tta gag tat ctt ata ggg ctt ttt 155
 Gly Asn Lys Asp Lys His Val Ser Leu Glu Tyr Leu Ile Gly Leu Phe
 20 25 30

 atg gat aaa aaa aca act aat cta agc aat act gac aag tat att ata 203
 Met Asp Lys Lys Thr Thr Asn Leu Ser Asn Thr Asp Lys Tyr Ile Ile
 35 40 45

 ggc aca att caa aca gag gca cta gag caa gaa ata gaa tgg ttt tca 251
 Gly Thr Ile Gln Thr Glu Ala Leu Glu Gln Glu Ile Glu Trp Phe Ser
 50 55 60

 caa gac tat cac att cct atg gag aat att tta cat gtc ctt tct atc 299
 Gln Asp Tyr His Ile Pro Met Glu Asn Ile Leu His Val Leu Ser Ile
 65 70 75

 aat ccc tat caa tgaaaagagc cttagtttta tcaaaaacaa ctttcaagct 351
 Asn Pro Tyr Gln
 80

<210> 200
 <211> 83
 <212> PRT
 <213> Helicobacter pylori

<400> 200
 Met Ser Phe Ala Pro Met Leu Leu Ala Thr Ile Asn Asn Ser Ile Gly
 1 5 10 15
 Asn Lys Asp Lys His Val Ser Leu Glu Tyr Leu Ile Gly Leu Phe Met
 20 25 30
 Asp Lys Lys Thr Thr Asn Leu Ser Asn Thr Asp Lys Tyr Ile Ile Gly
 35 40 45
 Thr Ile Gln Thr Glu Ala Leu Glu Gln Glu Ile Glu Trp Phe Ser Gln
 50 55 60
 Asp Tyr His Ile Pro Met Glu Asn Ile Leu His Val Leu Ser Ile Asn
 65 70 75 80
 Pro Tyr Gln

<210> 201
 <211> 1934
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (67)...(1866)

<400> 201
 aaacataggg caaatctagt tggcacaaaa acagctagtc ctgtgcttat taaaaacata 60
 gggcaaa atg aaa cgc tcc cac tta gaa aat gcc cta aat tat gct tta 108
 Met Lys Arg Ser His Leu Glu Asn Ala Leu Asn Tyr Ala Leu
 1 5 10
 gaa aat agc gaa aca gct tac aat gaa atg ttt tta gaa tgc gat aag 156
 Glu Asn Ser Glu Thr Ala Tyr Asn Glu Met Phe Leu Glu Cys Asp Lys
 15 20 25 30
 caa ttc atc tta gag agt tgg ctc aat gac ttt gat ttg act aaa gat 204
 Gln Phe Ile Leu Glu Ser Trp Leu Asn Asp Phe Asp Leu Thr Lys Asp
 35 40 45
 tat aac gag act atg cac tta gtt ttt tct atc aaa gat aag cca gat 252
 Tyr Asn Glu Thr Met His Leu Val Phe Ser Ile Lys Asp Lys Pro Asp
 50 55 60
 gaa gag aca atg caa ggg ctt tta cat tct act tgg gag agc tta aaa 300
 Glu Glu Thr Met Gln Gly Leu Leu His Ser Thr Trp Glu Ser Leu Lys
 65 70 75
 ata aga ttg cct gaa tac aag ttt gcc ctt gtg cca cac gct cat caa 348
 Ile Arg Leu Pro Glu Tyr Lys Phe Ala Leu Val Pro His Ala His Gln
 80 85 90
 gac cat gcc cat atc cat tgt ttt atc aat aag act aat cag ctc aca 396
 Asp His Ala His Ile His Cys Phe Ile Asn Lys Thr Asn Gln Leu Thr
 95 100 105 110

cga aga aga ctg cgt ttt aag ggg cat gaa gat tgt aaa gaa ttt ttt	444
Arg Arg Arg Leu Arg Phe Lys Gly His Glu Asp Cys Lys Glu Phe Phe	
115 120 125	
aat gaa tta aga agt gag ttt gct tat agg ttg aat gac cac tta ttg	492
Asn Glu Leu Arg Ser Glu Phe Ala Tyr Arg Leu Asn Asp His Leu Leu	
130 135 140	
agc gaa gaa tac ttg tat gtc aat gag cca aaa ctt aaa gag cta gac	540
Ser Glu Glu Tyr Leu Tyr Val Asn Glu Pro Lys Leu Lys Glu Leu Asp	
145 150 155	
aat atc aaa caa caa tta caa gac ttg gaa aaa gaa gaa aaa gcc tta	588
Asn Ile Lys Gln Gln Leu Gln Asp Leu Glu Lys Glu Glu Lys Ala Leu	
160 165 170	
gaa caa atc aaa tcc cca caa gat gag tgg gac tta aac aag gct tta	636
Glu Gln Ile Lys Ser Pro Gln Asp Glu Trp Asp Leu Asn Lys Ala Leu	
175 180 185 190	
caa agc gag tat tta caa gaa ctc aaa tat aaa aac aaa gca aaa gcc	684
Gln Ser Glu Tyr Leu Gln Glu Leu Lys Tyr Lys Asn Lys Ala Lys Ala	
195 200 205	
cta gac att caa aat aac cac agc acc cct tta aaa caa aag att tct	732
Leu Asp Ile Gln Asn Asn His Ser Thr Pro Leu Lys Gln Lys Ile Ser	
210 215 220	
gaa ttt aaa atc gct ctg ttt aat cac aaa gac aca agc gat gat gaa	780
Glu Phe Lys Ile Ala Leu Phe Asn His Lys Asp Thr Ser Asp Asp Glu	
225 230 235	
aaa gaa cag cta gat att gac agg ata gat aag aga aaa cca gta agc	828
Lys Glu Gln Leu Asp Ile Asp Arg Ile Asp Lys Arg Lys Pro Val Ser	
240 245 250	
gaa cac tta aaa aac act aac aaa cac gag cta tac gaa ctc tta ggc	876
Glu His Leu Lys Asn Thr Asn Lys His Glu Leu Tyr Glu Leu Leu Gly	
255 260 265 270	
ttt tat caa aaa gaa tta gat aaa aaa caa aac cat tca gcc ttt aag	924
Phe Tyr Gln Lys Glu Leu Asp Lys Lys Gln Asn His Ser Ala Phe Lys	
275 280 285	
aat ttt gct att ctc aat ggt tta gac aga gac ttt gaa aga gag act	972
Asn Phe Ala Ile Leu Asn Gly Leu Asp Arg Asp Phe Glu Arg Glu Thr	
290 295 300	
aat ggc tat tct gtt tta aag aaa aaa gaa atg ctt tta aat aag ctt	1020
Asn Gly Tyr Ser Val Leu Lys Lys Lys Glu Met Leu Leu Asn Lys Leu	
305 310 315	
gaa cac cta gac aaa cgc ctt tta gat aaa aac tca cac tta cta tta	1068
Glu His Leu Asp Lys Arg Leu Leu Asp Lys Asn Ser His Leu Leu Leu	
320 325 330	
gcc cag cta aga aat gaa gtt aaa acc aag caa aac atc caa tac aac	1116
Ala Gln Leu Arg Asn Glu Val Lys Thr Lys Gln Asn Ile Gln Tyr Asn	

335	340	345	350	
act cta act aat cct att ctt tta gcc aaa gcc tta gaa ctt tct aaa	1164			
Thr Leu Thr Asn Pro Ile Leu Leu Ala Lys Ala Leu Glu Leu Ser Lys				
355 360 365				
gat aaa cgc ccc act ctc aaa act ttt aaa aac gct tat ttt agt gct	1212			
Asp Lys Arg Pro Thr Leu Lys Thr Phe Lys Asn Ala Tyr Phe Ser Ala				
370 375 380				
aga aaa tat caa ttc atg cta gag agc ttt aaa act aag caa aat gac	1260			
Arg Lys Tyr Gln Phe Met Leu Glu Ser Phe Lys Thr Lys Gln Asn Asp				
385 390 395				
ccc act tac aag ctt aat gat aac act tat gag cta gtg agt aag caa	1308			
Pro Thr Tyr Lys Leu Asn Asp Asn Thr Tyr Glu Leu Val Ser Lys Gln				
400 405 410				
cta caa gac tat caa aac acc atg ctt tta tta gcc aaa gag aga tta	1356			
Leu Gln Asp Tyr Gln Asn Thr Met Leu Leu Leu Ala Lys Glu Arg Leu				
415 420 425 430				
ctt ttt tta gaa caa gat tta aaa caa aaa gaa gaa gag ttt gaa aga	1404			
Leu Phe Leu Glu Gln Asp Leu Lys Gln Lys Glu Glu Glu Phe Glu Arg				
435 440 445				
gcc aaa gaa cat tat gtg aaa tct tca aaa cat tat aga gaa act tca	1452			
Ala Lys Glu His Tyr Val Lys Ser Ser Lys His Tyr Arg Glu Thr Ser				
450 455 460				
ttg tct cca aaa gaa aaa caa ggc ttt ctc aaa caa att aaa caa ttt	1500			
Leu Ser Pro Lys Glu Lys Gln Gly Phe Leu Lys Gln Ile Lys Gln Phe				
465 470 475				
tct aaa att tct aag gat att ctc tat act tgt aat gag atc ata gga	1548			
Ser Lys Ile Ser Lys Asp Ile Leu Tyr Thr Cys Asn Glu Ile Ile Gly				
480 485 490				
gct aat agg ttt tta acc cac tat gac aac cta aac ctt gaa aaa gtc	1596			
Ala Asn Arg Phe Leu Thr His Tyr Asp Asn Leu Asn Leu Glu Lys Val				
495 500 505 510				
cta gaa cac gct aaa gat act aag cta gag caa aaa gaa att caa gct	1644			
Leu Glu His Ala Lys Asp Thr Lys Leu Glu Gln Lys Glu Ile Gln Ala				
515 520 525				
atc aca aaa gag cct aat aac gat gag cct tgg att gag ttt ggt aaa	1692			
Ile Thr Lys Glu Pro Asn Asn Asp Glu Pro Trp Ile Glu Phe Gly Lys				
530 535 540				
aaa gaa caa gct aga gct aaa gca cac tat caa gct atg cta gaa aaa	1740			
Lys Glu Gln Ala Arg Ala Lys Ala His Tyr Gln Ala Met Leu Glu Lys				
545 550 555				
gaa aaa gct aaa gaa tta gct aaa caa caa gct aac acc ttg cac tct	1788			
Glu Lys Ala Lys Glu Leu Ala Lys Gln Gln Ala Asn Thr Leu His Ser				
560 565 570				
aat gag ctt gat gat gac cct aaa gct cat gct gga tta aaa caa aat	1836			

tgccctttaat gttcttaata aagaatatac cctttgaaag gggtttat 1934

```
<210> 202
<211> 600
<212> PRT
<213> Helicobacter pylori
```

<400>	202														
Met 1	Lys	Arg	Ser	His 5	Leu	Glu	Asn	Ala	Leu 10	Asn	Tyr	Ala	Leu	Glu 15	Asn
Ser	Glu	Thr	Ala 20	Tyr	Asn	Glu	Met	Phe 25	Leu	Glu	Cys	Asp	Lys 30	Gln	Phe
Ile	Leu	Glu 35	Ser	Trp	Leu	Asn	Asp 40	Phe	Asp	Leu	Thr	Lys 45	Asp	Tyr	Asn
Glu	Thr 50	Met	His	Leu	Val	Phe 55	Ser	Ile	Lys	Asp	Lys 60	Pro	Asp	Glu	Glu
Thr 65	Met	Gln	Gly	Leu	Leu 70	His	Ser	Thr	Trp	Glu 75	Ser	Leu	Lys	Ile	Arg 80
Leu	Pro	Glu	Tyr	Lys 85	Phe	Ala	Leu	Val	Pro 90	His	Ala	His	Gln	Asp 95	His
Ala	His	Ile	His 100	Cys	Phe	Ile	Asn	Lys 105	Thr	Asn	Gln	Leu	Thr	Arg	Arg
Arg	Leu	Arg 115	Phe	Lys	Gly	His	Glu 120	Asp	Cys	Lys	Glu	Phe 125	Phe	Asn	Glu
Leu	Arg 130	Ser	Glu	Phe	Ala	Tyr 135	Arg	Leu	Asn	Asp	His 140	Leu	Leu	Ser	Glu
Glu 145	Tyr	Leu	Tyr	Val	Asn 150	Glu	Pro	Lys	Leu	Lys 155	Glu	Leu	Asp	Asn	Ile 160
Lys	Gln	Gln	Leu	Gln 165	Asp	Leu	Glu	Lys	Glu 170	Glu	Lys	Ala	Leu	Glu 175	Gln
Ile	Lys	Ser	Pro 180	Gln	Asp	Glu	Trp	Asp 185	Leu	Asn	Lys	Ala	Leu 190	Gln	Ser
Glu	Tyr 195	Leu	Gln	Glu	Leu	Lys	Tyr 200	Lys	Asn	Lys	Ala	Lys 205	Ala	Leu	Asp
Ile	Gln 210	Asn	Asn	His	Ser	Thr 215	Pro	Leu	Lys	Gln	Lys 220	Ile	Ser	Glu	Phe
Lys 225	Ile	Ala	Leu	Phe	Asn 230	His	Lys	Asp	Thr	Ser	Asp 235	Asp	Glu	Lys	Glu 240
Gln	Leu	Asp	Ile	Asp 245	Arg	Ile	Asp	Lys	Arg 250	Lys	Pro	Val	Ser	Glu 255	His
Leu	Lys	Asn	Thr 260	Asn	Lys	His	Glu	Leu 265	Tyr	Glu	Leu	Leu	Gly 270	Phe	Tyr
Gln	Lys	Glu 275	Leu	Asp	Lys	Lys	Gln	Asn 280	His	Ser	Ala	Phe 285	Lys	Asn	Phe
Ala	Ile 290	Leu	Asn	Gly	Leu	Asp 295	Arg	Asp	Phe	Glu	Arg 300	Glu	Thr	Asn	Gly
Tyr 305	Ser	Val	Leu	Lys	Lys 310	Lys	Glu	Met	Leu	Leu	Asn 315	Lys	Leu	Glu	His 320
Leu	Asp	Lys	Arg	Leu 325	Leu	Asp	Lys	Asn	Ser 330	His	Leu	Leu	Leu	Ala 335	Gln
Leu	Arg	Asn	Glu 340	Val	Lys	Thr	Lys	Gln 345	Asn	Ile	Gln	Tyr	Asn 350	Thr	Leu

Thr	Asn	Pro	Ile	Leu	Leu	Ala	Lys	Ala	Leu	Glu	Leu	Ser	Lys	Asp	Lys
		355					360					365			
Arg	Pro	Thr	Leu	Lys	Thr	Phe	Lys	Asn	Ala	Tyr	Phe	Ser	Ala	Arg	Lys
		370				375					380				
Tyr	Gln	Phe	Met	Leu	Glu	Ser	Phe	Lys	Thr	Lys	Gln	Asn	Asp	Pro	Thr
385					390					395					400
Tyr	Lys	Leu	Asn	Asp	Asn	Thr	Tyr	Glu	Leu	Val	Ser	Lys	Gln	Leu	Gln
			405					410						415	
Asp	Tyr	Gln	Asn	Thr	Met	Leu	Leu	Leu	Ala	Lys	Glu	Arg	Leu	Leu	Phe
			420					425					430		
Leu	Glu	Gln	Asp	Leu	Lys	Gln	Lys	Glu	Glu	Glu	Phe	Glu	Arg	Ala	Lys
		435					440					445			
Glu	His	Tyr	Val	Lys	Ser	Ser	Lys	His	Tyr	Arg	Glu	Thr	Ser	Leu	Ser
450						455					460				
Pro	Lys	Glu	Lys	Gln	Gly	Phe	Leu	Lys	Gln	Ile	Lys	Gln	Phe	Ser	Lys
465					470					475					480
Ile	Ser	Lys	Asp	Ile	Leu	Tyr	Thr	Cys	Asn	Glu	Ile	Ile	Gly	Ala	Asn
			485					490						495	
Arg	Phe	Leu	Thr	His	Tyr	Asp	Asn	Leu	Asn	Leu	Glu	Lys	Val	Leu	Glu
			500					505					510		
His	Ala	Lys	Asp	Thr	Lys	Leu	Glu	Gln	Lys	Glu	Ile	Gln	Ala	Ile	Thr
		515					520					525			
Lys	Glu	Pro	Asn	Asn	Asp	Glu	Pro	Trp	Ile	Glu	Phe	Gly	Lys	Lys	Glu
530						535					540				
Gln	Ala	Arg	Ala	Lys	Ala	His	Tyr	Gln	Ala	Met	Leu	Glu	Lys	Glu	Lys
545					550					555					560
Ala	Lys	Glu	Leu	Ala	Lys	Gln	Gln	Ala	Asn	Thr	Leu	His	Ser	Asn	Glu
			565					570						575	
Leu	Asp	Asp	Asp	Pro	Lys	Ala	His	Ala	Gly	Leu	Lys	Gln	Asn	Asp	Asn
			580					585					590		
Thr	Asn	Phe	Lys	Gly	Arg	Asn	Arg								
		595					600								

<210> 203
 <211> 884
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (22)...(840)

<400> 203																
ggagaataaaa	attacaataa	a	atg	gcg	tta	gaa	aaa	agt	tat	agt	aaa	aac			51	
			Met	Ala	Leu	Glu	Lys	Ser	Tyr	Ser	Lys	Asn				
			1				5					10				
ttt	gaa	agc	gat	gag	ctt	ttt	gat	tat	gag	atc	atc	aag	ccc	aaa	aag	99
Phe	Glu	Ser	Asp	Glu	Leu	Phe	Asp	Tyr	Glu	Ile	Ile	Lys	Pro	Lys	Lys	
			15					20					25			
acg	ctt	aag	ata	caa	tac	act	tat	gct	aaa	cgc	tac	tat	aaa	gaa	gta	147
Thr	Leu	Lys	Ile	Gln	Tyr	Thr	Tyr	Ala	Lys	Arg	Tyr	Tyr	Lys	Glu	Val	
			30					35					40			
gaa	aag	ttt	gct	aaa	aat	tta	acc	caa	ctg	aca	caa	gaa	gaa	ttc	atg	195
Glu	Lys	Phe	Ala	Lys	Asn	Leu	Thr	Gln	Leu	Thr	Gln	Glu	Glu	Phe	Met	
		45					50					55				

cg	t	a	a	g	a	g	a	c	a	a	a	a	a	a	a	a	a	243
Arg	Leu	Arg	Glu	Pro	Gln	Lys	Gln	Val	Val	Ile	Lys	Asn	Ile	Gly	Asn			
	60					65					70							
at	a	c	a	c	a	c	a	a	a	a	a	a	a	a	a	a	291	
Met	Thr	Arg	Leu	His	Ser	Lys	Arg	Ala	Met	Asp	Tyr	Ile	Ala	Lys	His			
	75				80					85					90			
gg	a	a	c	a	a	a	a	a	a	a	a	a	a	a	a	a	339	
Gly	Glu	Leu	Val	Arg	Asp	Glu	Phe	Phe	Asn	Glu	Val	Asn	Tyr	Asn	Asp			
				95					100					105				
at	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	387	
Ile	Ala	Glu	Gln	Trp	Asn	Glu	Gln	Phe	Glu	Lys	Leu	Leu	Glu	Asn	Lys			
			110					115					120					
ag	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	435	
Ser	Arg	Val	Lys	Asn	Cys	Ala	Leu	His	Leu	Val	Phe	Ser	Ile	Asp	Glu			
		125					130					135						
aa	t	g	a	a	a	a	a	a	a	a	a	a	a	a	a	a	483	
Asn	Cys	Asn	Glu	Lys	Asn	Leu	Lys	Ala	Leu	Glu	Leu	Ser	Val	Tyr	Gln			
	140					145				150								
ac	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	531	
Thr	Leu	Thr	Asn	Thr	Leu	Gly	Tyr	Asp	Tyr	Pro	Phe	Ile	Met	Lys	Leu			
	155				160					165					170			
ca	a	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	579	
His	Thr	His	Gln	Asn	Asn	Pro	His	Ala	His	Val	Ile	Ile	Asn	Lys	Thr			
				175					180					185				
aa	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	627	
Asn	Lys	Ile	Thr	Asn	Lys	Gln	Leu	Cys	Phe	Asn	Ser	Lys	Asp	Ser	Cys			
			190					195					200					
aa	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	675	
Lys	Glu	Phe	Tyr	His	Thr	Leu	Arg	Glu	Thr	Phe	Lys	Asp	Tyr	Leu	Phe			
		205					210					215						
gc	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	723	
Ala	Asn	Ser	Lys	Gly	Glu	Leu	Gln	Tyr	Ser	Asn	Thr	Pro	Asn	Ile	Tyr			
	220					225					230							
aa	g	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	771	
Lys	Ala	Ile	Lys	Asp	Ile	Glu	Thr	Glu	Leu	Asp	Ala	Leu	Glu	Asn	Arg			
	235				240					245					250			
ct	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	819	
Leu	Glu	Thr	Ile	Arg	Val	Leu	Gly	Met	Lys	Thr	Ile	Phe	Ile	Lys	Phe			
			255						260					265				
tg	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	870	
Trp	Val	Val	Gln	Leu	Leu	Lys												
			270															
tatttgatca	t	t	t	a													884	

<210> 204
 <211> 273
 <212> PRT
 <213> Helicobacter pylori

<400> 204
 Met Ala Leu Glu Lys Ser Tyr Ser Lys Asn Phe Glu Ser Asp Glu Leu
 1 5 10 15
 Phe Asp Tyr Glu Ile Ile Lys Pro Lys Lys Thr Leu Lys Ile Gln Tyr
 20 25 30
 Thr Tyr Ala Lys Arg Tyr Tyr Lys Glu Val Glu Lys Phe Ala Lys Asn
 35 40 45
 Leu Thr Gln Leu Thr Gln Glu Glu Phe Met Arg Leu Arg Glu Pro Gln
 50 55 60
 Lys Gln Val Val Ile Lys Asn Ile Gly Asn Met Thr Arg Leu His Ser
 65 70 75 80
 Lys Arg Ala Met Asp Tyr Ile Ala Lys His Gly Glu Leu Val Arg Asp
 85 90 95
 Glu Phe Phe Asn Glu Val Asn Tyr Asn Asp Ile Ala Glu Gln Trp Asn
 100 105 110
 Glu Gln Phe Glu Lys Leu Leu Glu Asn Lys Ser Arg Val Lys Asn Cys
 115 120 125
 Ala Leu His Leu Val Phe Ser Ile Asp Glu Asn Cys Asn Glu Lys Asn
 130 135 140
 Leu Lys Ala Leu Glu Leu Ser Val Tyr Gln Thr Leu Thr Asn Thr Leu
 145 150 155 160
 Gly Tyr Asp Tyr Pro Phe Ile Met Lys Leu His Thr His Gln Asn Asn
 165 170 175
 Pro His Ala His Val Ile Ile Asn Lys Thr Asn Lys Ile Thr Asn Lys
 180 185 190
 Gln Leu Cys Phe Asn Ser Lys Asp Ser Cys Lys Glu Phe Tyr His Thr
 195 200 205
 Leu Arg Glu Thr Phe Lys Asp Tyr Leu Phe Ala Asn Ser Lys Gly Glu
 210 215 220
 Leu Gln Tyr Ser Asn Thr Pro Asn Ile Tyr Lys Ala Ile Lys Asp Ile
 225 230 235 240
 Glu Thr Glu Leu Asp Ala Leu Glu Asn Arg Leu Glu Thr Ile Arg Val
 245 250 255
 Leu Gly Met Lys Thr Ile Phe Ile Lys Phe Trp Val Val Gln Leu Leu
 260 265 270
 Lys

<210> 205
 <211> 557
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (49)...(519)

<400> 205
 ataaacaacc atgacaaact aacggacttt aagcaatacc aaacagac atg aaa gaa 57
 Met Lys Glu
 1
 tta cta ggg ata gaa ata gat gaa gag ctg gat act aaa cga ctt atc 105

Leu	Leu	Gly	Ile	Glu	Ile	Asp	Glu	Glu	Leu	Asp	Thr	Lys	Arg	Leu	Ile		
	5					10					15						
cct	act	tat	tcc	aaa	ttg	tat	tct	tta	aaa	aaa	tac	tct	aaa	aaa	ttt	153	
Pro	Thr	Tyr	Ser	Lys	Leu	Tyr	Ser	Leu	Lys	Lys	Tyr	Ser	Lys	Lys	Phe		
	20				25				30						35		
aaa	aga	tta	caa	aga	aaa	caa	agc	cgt	agg	gtg	tta	aag	tct	aaa	caa	201	
Lys	Arg	Leu	Gln	Arg	Lys	Gln	Ser	Arg	Arg	Val	Leu	Lys	Ser	Lys	Gln		
			40					45						50			
aac	aaa	acc	aaa	tta	gga	ggg	aat	ttt	tac	aaa	acc	caa	aag	aaa	tta	249	
Asn	Lys	Thr	Lys	Leu	Gly	Gly	Asn	Phe	Tyr	Lys	Thr	Gln	Lys	Lys	Leu		
			55					60					65				
aac	caa	gcc	ttt	gac	aag	tct	agt	cat	caa	aaa	aca	gac	aga	tac	cat	297	
Asn	Gln	Ala	Phe	Asp	Lys	Ser	Ser	His	Gln	Lys	Thr	Asp	Arg	Tyr	His		
		70					75					80					
aaa	atc	aca	agc	gaa	ctt	tca	aag	caa	ttt	gaa	ttg	ata	gta	gtt	gaa	345	
Lys	Ile	Thr	Ser	Glu	Leu	Ser	Lys	Gln	Phe	Glu	Leu	Ile	Val	Val	Glu		
	85				90					95							
gat	ttg	caa	gta	aaa	aac	atg	act	aaa	aga	gct	aaa	ctc	aaa	aat	gtt	393	
Asp	Leu	Gln	Val	Lys	Asn	Met	Thr	Lys	Arg	Ala	Lys	Leu	Lys	Asn	Val		
	100				105					110					115		
aaa	caa	aag	agt	ggg	ctt	aat	caa	tct	att	tta	aac	gct	tca	ttc	tat	441	
Lys	Gln	Lys	Ser	Gly	Leu	Asn	Gln	Ser	Ile	Leu	Asn	Ala	Ser	Phe	Tyr		
				120					125					130			
caa	atc	atc	tct	ttt	tta	gac	tac	aaa	caa	cag	cat	aat	ggc	aaa	ttg	489	
Gln	Ile	Ile	Ser	Phe	Leu	Asp	Tyr	Lys	Gln	Gln	His	Asn	Gly	Lys	Leu		
			135					140					145				
tta	gtg	aaa	gtt	tcc	ccc	aca	ata	tac	gag	taaaaacttgc	cattgttgtg					539	
Leu	Val	Lys	Val	Ser	Pro	Thr	Ile	Tyr	Glu								
	150						155										
ggaatatcaa	ccacaagc																557

<210> 206

<211> 157

<212> PRT

<213> Helicobacter pylori

<400> 206

Met	Lys	Glu	Leu	Leu	Gly	Ile	Glu	Ile	Asp	Glu	Glu	Leu	Asp	Thr	Lys		
1				5					10					15			
Arg	Leu	Ile	Pro	Thr	Tyr	Ser	Lys	Leu	Tyr	Ser	Leu	Lys	Lys	Tyr	Ser		
			20					25					30				
Lys	Lys	Phe	Lys	Arg	Leu	Gln	Arg	Lys	Gln	Ser	Arg	Arg	Val	Leu	Lys		
		35					40					45					
Ser	Lys	Gln	Asn	Lys	Thr	Lys	Leu	Gly	Gly	Asn	Phe	Tyr	Lys	Thr	Gln		
		50				55				60							
Lys	Lys	Leu	Asn	Gln	Ala	Phe	Asp	Lys	Ser	Ser	His	Gln	Lys	Thr	Asp		
				70					75					80			
Arg	Tyr	His	Lys	Ile	Thr	Ser	Glu	Leu	Ser	Lys	Gln	Phe	Glu	Leu	Ile		
				85				90						95			

ctt aaa aat ata gcc ttt gct aaa cac aag gat aat ttg cct aag cat	537
Leu Lys Asn Ile Ala Phe Ala Lys His Lys Asp Asn Leu Pro Lys His	
150 155 160	
cta aat tca aaa gat tta aaa tct ttt ata tat act ctt ata aac tat	585
Leu Asn Ser Lys Asp Leu Lys Ser Phe Ile Tyr Thr Leu Ile Asn Tyr	
165 170 175	
aga act aga agc agt tat gaa aag aga aat aag tgt att ttg ctc ttg	633
Arg Thr Arg Ser Ser Tyr Glu Lys Arg Asn Lys Cys Ile Leu Leu Leu	
180 185 190	
att att ttg ggt ggt ttg aga aaa tct gag gtt ttt aat tta gaa ttg	681
Ile Ile Leu Gly Gly Leu Arg Lys Ser Glu Val Phe Asn Leu Glu Leu	
195 200 205 210	
aga aat att gtt tta gag aaa gag cat tat atc ttg ctt ata aaa ggc	729
Arg Asn Ile Val Leu Glu Lys Glu His Tyr Ile Leu Leu Ile Lys Gly	
215 220 225	
aaa aac aat aaa gag cga aaa gcg ttc att aaa atc gct caa aca gat	777
Lys Asn Asn Lys Glu Arg Lys Ala Phe Ile Lys Ile Ala Gln Thr Asp	
230 235 240	
att gac aca ctc gca ccg ctt atc cgt atc ctt ttg gaa agt att gct	825
Ile Asp Thr Leu Ala Pro Leu Ile Arg Ile Leu Leu Glu Ser Ile Ala	
245 250 255	
aaa aat ctt tta tcc cac tagcgcgaaa aactccgtcc tttagggcgg	873
Lys Asn Leu Leu Ser His	
260	
agatgtaagc gtttag	889
<210> 208	
<211> 264	
<212> PRT	
<213> Helicobacter pylori	
<400> 208	
Met Lys Lys Ser Asn Asp Asn Asn Ala Leu Ala Arg Ser Gln Arg Glu	
1 5 10 15	
Leu Phe Val Gly Ile Arg Asp Phe Ile Val Phe Lys Phe Lys Arg Met	
20 25 30	
Val Val Phe Asn Gly Val Arg Asp Phe Thr Lys Met Arg Phe Leu Ser	
35 40 45	
Ile Glu Leu Glu Lys Cys Glu Asn Ile Lys Asp Leu Glu Lys Leu Cys	
50 55 60	
His Thr Ile Tyr Asn Gln Gly Thr Lys His Ile Leu Met Met Arg Val	
65 70 75 80	
Leu Phe Leu Phe Phe Asp Tyr Phe Cys Lys His Leu Lys Val Lys Arg	
85 90 95	
Leu Arg Leu Leu Asn Glu Glu Met Leu Val Asn Phe Leu Phe Glu Leu	
100 105 110	
Ala Lys Gln Arg Lys Ile Asn Ser Met Ala Lys Tyr Val Met Tyr Ile	
115 120 125	
Arg Gln Phe Phe Asp Tyr Leu Asp Arg Thr Lys His Tyr Glu Phe Tyr	
130 135 140	

Phe	Ser	Leu	Lys	Asn	Ile	Ala	Phe	Ala	Lys	His	Lys	Asp	Asn	Leu	Pro
145					150					155					160
Lys	His	Leu	Asn	Ser	Lys	Asp	Leu	Lys	Ser	Phe	Ile	Tyr	Thr	Leu	Ile
			165						170						175
Asn	Tyr	Arg	Thr	Arg	Ser	Ser	Tyr	Glu	Lys	Arg	Asn	Lys	Cys	Ile	Leu
			180					185					190		
Leu	Leu	Ile	Ile	Leu	Gly	Gly	Leu	Arg	Lys	Ser	Glu	Val	Phe	Asn	Leu
		195					200					205			
Glu	Leu	Arg	Asn	Ile	Val	Leu	Glu	Lys	Glu	His	Tyr	Ile	Leu	Leu	Ile
	210					215					220				
Lys	Gly	Lys	Asn	Asn	Lys	Glu	Arg	Lys	Ala	Phe	Ile	Lys	Ile	Ala	Gln
225				230						235					240
Thr	Asp	Ile	Asp	Thr	Leu	Ala	Pro	Leu	Ile	Arg	Ile	Leu	Leu	Glu	Ser
			245					250						255	
Ile	Ala	Lys	Asn	Leu	Leu	Ser	His								
			260												

<210> 209
 <211> 546
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (75)...(530)

<400> 209
 ttgacagagt ggattttttt atttctaacg ctattattta tgggcgttct gtcgtggggg 60
 gatttgcacc gttt atg cga tta aaa cct aag ggg tta aac aac att tac 110
 Met Arg Leu Lys Pro Lys Gly Leu Asn Asn Ile Tyr
 1 5 10

aca gcc acc gtg tta gcg ttc gtc gta ggg gct caa gaa gcg gca aaa 158
 Thr Ala Thr Val Leu Ala Phe Val Val Gly Ala Gln Glu Ala Ala Lys
 15 20 25

cgc atg caa aaa ata ggc ggt ggg gcg atc gtg agc tta agt tct acc 206
 Arg Met Gln Lys Ile Gly Gly Gly Ala Ile Val Ser Leu Ser Ser Thr
 30 35 40

ggg aat cta gtt tat atg cct aat tac gcc ggg cat ggc aat tcc aaa 254
 Gly Asn Leu Val Tyr Met Pro Asn Tyr Ala Gly His Gly Asn Ser Lys
 45 50 55 60

aac gcc gta gaa acc atg gtc aaa tac gct gcc gtg gat tta ggc gaa 302
 Asn Ala Val Glu Thr Met Val Lys Tyr Ala Ala Val Asp Leu Gly Glu
 65 70 75

ttt aac att aga gtg aat gcg gtt agt ggc ggg cct att gat acg gac 350
 Phe Asn Ile Arg Val Asn Ala Val Ser Gly Gly Pro Ile Asp Thr Asp
 80 85 90

gct ttg aaa gcc ttc cct gat tat gtg gag att aaa gaa aaa gta gaa 398
 Ala Leu Lys Ala Phe Pro Asp Tyr Val Glu Ile Lys Glu Lys Val Glu
 95 100 105

gag caa tcg ccc cta aaa cgc atg ggc aat cct aac gat cta gcc gga 446
 Glu Gln Ser Pro Leu Lys Arg Met Gly Asn Pro Asn Asp Leu Ala Gly

110	115	120	
gcg gct tat ttt tta tgc gat gag acc caa agc ggt tgg ctt aca ggg			494
Ala Ala Tyr Phe Leu Cys Asp Glu Thr Gln Ser Gly Trp Leu Thr Gly			
125	130	135	140
caa acg atc gtt gta gat ggc ggg act act ttt aaa taaagatatatt			540
Gln Thr Ile Val Val Asp Gly Gly Thr Thr Phe Lys			
	145	150	
tcttgc			546

<210> 210
 <211> 152
 <212> PRT
 <213> Helicobacter pylori

<400> 210

Met Arg Leu Lys Pro Lys Gly Leu Asn Asn Ile Tyr Thr Ala Thr Val			
1	5	10	15
Leu Ala Phe Val Val Gly Ala Gln Glu Ala Ala Lys Arg Met Gln Lys			
	20	25	30
Ile Gly Gly Gly Ala Ile Val Ser Leu Ser Ser Thr Gly Asn Leu Val			
	35	40	45
Tyr Met Pro Asn Tyr Ala Gly His Gly Asn Ser Lys Asn Ala Val Glu			
	50	55	60
Thr Met Val Lys Tyr Ala Ala Val Asp Leu Gly Glu Phe Asn Ile Arg			
	65	70	75
Val Asn Ala Val Ser Gly Gly Pro Ile Asp Thr Asp Ala Leu Lys Ala			
	85	90	95
Phe Pro Asp Tyr Val Glu Ile Lys Glu Lys Val Glu Glu Gln Ser Pro			
	100	105	110
Leu Lys Arg Met Gly Asn Pro Asn Asp Leu Ala Gly Ala Ala Tyr Phe			
	115	120	125
Leu Cys Asp Glu Thr Gln Ser Gly Trp Leu Thr Gly Gln Thr Ile Val			
	130	135	140
Val Asp Gly Gly Thr Thr Phe Lys			
145	150		

<210> 211
 <211> 644
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (2)...(616)

<400> 211

a aga tat ttc ttg caa aac att atc cac atc cac caa aac aaa gag ttg	49
Arg Tyr Phe Leu Gln Asn Ile Ile His Ile His Gln Asn Lys Glu Leu	
1	5
caa ttc att aaa aaa tgc ttg ttg ggc tat ttt ttc gcc cct ttg tgt	97
Gln Phe Ile Lys Lys Cys Leu Leu Gly Tyr Phe Phe Ala Pro Leu Cys	
	20
ggg gct att ctg tta gtg ctt ttt att gtt tca agc ggg gca aaa tcg	145

Gly	Ala	Ile	Leu	Leu	Val	Leu	Phe	Ile	Val	Ser	Ser	Gly	Ala	Lys	Ser		
		35					40					45					
ttt	caa	att	tct	aat	ctc	ttt	aac	aat	caa	cta	gcc	tat	atc	gtt	ttg	193	
Phe	Gln	Ile	Ser	Asn	Leu	Phe	Asn	Asn	Gln	Leu	Ala	Tyr	Ile	Val	Leu		
	50					55					60						
ttg	tct	ctt	ttt	ttg	tgc	gcg	ctt	ggg	ttt	att	gcc	gga	gcg	att	ggt	241	
Leu	Ser	Leu	Phe	Leu	Cys	Ala	Leu	Gly	Phe	Ile	Ala	Gly	Ala	Ile	Gly		
	65				70					75					80		
ttt	tat	agg	ctt	tct	aaa	atc	aca	cgc	cat	ctg	agt	ttt	ttt	gaa	aat	289	
Phe	Tyr	Arg	Leu	Ser	Lys	Ile	Thr	Arg	His	Leu	Ser	Phe	Phe	Glu	Asn		
				85					90					95			
ttc	gct	ttc	agt	ttt	tta	gcg	gtg	att	tta	tgc	gct	att	tta	agc	tat	337	
Phe	Ala	Phe	Ser	Phe	Leu	Ala	Val	Ile	Leu	Cys	Ala	Ile	Leu	Ser	Tyr		
			100					105					110				
ctt	gtc	cct	aac	gcc	agt	aac	gct	ctt	tcg	cta	atc	ggt	aat	ggc	gtt	385	
Leu	Val	Pro	Asn	Ala	Ser	Asn	Ala	Leu	Ser	Leu	Ile	Gly	Asn	Gly	Val		
		115					120					125					
tct	att	ttt	tat	ttg	cac	aaa	ctc	tat	aga	gaa	ttg	agc	ctt	tac	acg	433	
Ser	Ile	Phe	Tyr	Leu	His	Lys	Leu	Tyr	Arg	Glu	Leu	Ser	Leu	Tyr	Thr		
	130					135					140						
caa	gaa	agg	ttt	ttt	tta	agc	ggg	ttt	agg	ttg	ttg	ctt	ttt	agt	ttc	481	
Gln	Glu	Arg	Phe	Phe	Leu	Ser	Gly	Phe	Arg	Leu	Leu	Leu	Phe	Ser	Phe		
	145				150					155					160		
atg	ctg	gct	ctt	tta	ggg	att	tta	gtg	caa	gcg	tta	gtt	atc	att	ttt	529	
Met	Leu	Ala	Leu	Leu	Gly	Ile	Leu	Val	Gln	Ala	Leu	Val	Ile	Ile	Phe		
				165					170					175			
tta	acg	acc	gct	gtg	gtt	tta	atg	tgt	gtg	gcg	ctt	ggt	ttt	ttg	gcg	577	
Leu	Thr	Thr	Ala	Val	Val	Leu	Met	Cys	Val	Ala	Leu	Gly	Phe	Leu	Ala		
			180					185					190				
cgc	gcg	ttt	ttg	aat	ttt	tca	caa	gtc	ttt	ttg	aaa	gca	tgaaa	gtttt		626	
Arg	Ala	Phe	Leu	Asn	Phe	Ser	Gln	Val	Phe	Leu	Lys	Ala					
		195					200					205					
aaaactcctg	cctaattt															644	
<210>	212																
<211>	205																
<212>	PRT																
<213>	Helicobacter pylori																
<400>	212																
Arg	Tyr	Phe	Leu	Gln	Asn	Ile	Ile	His	Ile	His	Gln	Asn	Lys	Glu	Leu		
	1			5					10					15			
Gln	Phe	Ile	Lys	Lys	Cys	Leu	Leu	Gly	Tyr	Phe	Phe	Ala	Pro	Leu	Cys		
			20					25				30					
Gly	Ala	Ile	Leu	Leu	Val	Leu	Phe	Ile	Val	Ser	Ser	Gly	Ala	Lys	Ser		
		35					40					45					
Phe	Gln	Ile	Ser	Asn	Leu	Phe	Asn	Asn	Gln	Leu	Ala	Tyr	Ile	Val	Leu		
	50					55					60						

Leu Ser Leu Phe Leu Cys Ala Leu Gly Phe Ile Ala Gly Ala Ile Gly
 65 70 75 80
 Phe Tyr Arg Leu Ser Lys Ile Thr Arg His Leu Ser Phe Phe Glu Asn
 85 90 95
 Phe Ala Phe Ser Phe Leu Ala Val Ile Leu Cys Ala Ile Leu Ser Tyr
 100 105 110
 Leu Val Pro Asn Ala Ser Asn Ala Leu Ser Leu Ile Gly Asn Gly Val
 115 120 125
 Ser Ile Phe Tyr Leu His Lys Leu Tyr Arg Glu Leu Ser Leu Tyr Thr
 130 135 140
 Gln Glu Arg Phe Phe Leu Ser Gly Phe Arg Leu Leu Leu Phe Ser Phe
 145 150 155 160
 Met Leu Ala Leu Leu Gly Ile Leu Val Gln Ala Leu Val Ile Ile Phe
 165 170 175
 Leu Thr Thr Ala Val Val Leu Met Cys Val Ala Leu Gly Phe Leu Ala
 180 185 190
 Arg Ala Phe Leu Asn Phe Ser Gln Val Phe Leu Lys Ala
 195 200 205

<210> 213
 <211> 630
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (62)...(598)

<400> 213
 gtgtggcgct tggttttttg gcgcgcgcggt ttttgaattt ttcacaagtc tttttgaaag 60
 c atg aaa gtt tta aaa ctc ctg cct aat ttt tta aca att tta cgc att 109
 Met Lys Val Leu Lys Leu Leu Pro Asn Phe Leu Thr Ile Leu Arg Ile
 1 5 10 15

 gtc tta tcc tta ttt tta tta ttt tta ttg tta aac acg cgc act tat 157
 Val Leu Ser Leu Phe Leu Leu Phe Leu Leu Leu Asn Thr Arg Thr Tyr
 20 25 30

 ttt agt ttt tta acc ccc ttt caa acc aat atg atc tct tca ttg gtt 205
 Phe Ser Phe Leu Thr Pro Phe Gln Thr Asn Met Ile Ser Ser Leu Val
 35 40 45

 ttt ttg ttt gcc gcg ctc acg gat tta ttg gac ggc tac atc gct aga 253
 Phe Leu Phe Ala Ala Leu Thr Asp Leu Leu Asp Gly Tyr Ile Ala Arg
 50 55 60

 agc tat aaa gcc aaa tcg cgc ttt ggg gaa atc ttt gat cct tta gcg 301
 Ser Tyr Lys Ala Lys Ser Arg Phe Gly Glu Ile Phe Asp Pro Leu Ala
 65 70 75 80

 gat aaa atc ctt att ttg agc gcg ttt tta ggg tta gtt tat ttg gat 349
 Asp Lys Ile Leu Ile Leu Ser Ala Phe Leu Gly Leu Val Tyr Leu Asp
 85 90 95

 cgt gtg aat gcg tgg atc ccg ttt gtg att tta ggg cgt gaa ttt ttt 397
 Arg Val Asn Ala Trp Ile Pro Phe Val Ile Leu Gly Arg Glu Phe Phe
 100 105 110

att tca ggg ctt aga gtc tta gcc gct aat gag aaa aag gat att cct	445
Ile Ser Gly Leu Arg Val Leu Ala Ala Asn Glu Lys Lys Asp Ile Pro	
115 120 125	
gtc aat gcg tta ggc aag tat aaa acc gtt tct caa gtc gtg gcg att	493
Val Asn Ala Leu Gly Lys Tyr Lys Thr Val Ser Gln Val Val Ala Ile	
130 135 140	
ggg gct tta ttg gct gat gta act tac tct tat gcg ctt gtg gct ata	541
Gly Ala Leu Leu Ala Asp Val Thr Tyr Ser Tyr Ala Leu Val Ala Ile	
145 150 155 160	
gcg gtt ttt tta acc ctt tat tcg ggg ata gat tac acc att aaa tat	589
Ala Val Phe Leu Thr Leu Tyr Ser Gly Ile Asp Tyr Thr Ile Lys Tyr	
165 170 175	
tat aaa tct taatatttta aaagaagttt ttagcgttct tt	630
Tyr Lys Ser	

<210> 214
 <211> 179
 <212> PRT
 <213> Helicobacter pylori

<400> 214
Met Lys Val Leu Lys Leu Leu Pro Asn Phe Leu Thr Ile Leu Arg Ile
1 5 10 15
Val Leu Ser Leu Phe Leu Leu Phe Leu Leu Asn Thr Arg Thr Tyr
20 25 30
Phe Ser Phe Leu Thr Pro Phe Gln Thr Asn Met Ile Ser Ser Leu Val
35 40 45
Phe Leu Phe Ala Ala Leu Thr Asp Leu Leu Asp Gly Tyr Ile Ala Arg
50 55 60
Ser Tyr Lys Ala Lys Ser Arg Phe Gly Glu Ile Phe Asp Pro Leu Ala
65 70 75 80
Asp Lys Ile Leu Ile Leu Ser Ala Phe Leu Gly Leu Val Tyr Leu Asp
85 90 95
Arg Val Asn Ala Trp Ile Pro Phe Val Ile Leu Gly Arg Glu Phe Phe
100 105 110
Ile Ser Gly Leu Arg Val Leu Ala Ala Asn Glu Lys Lys Asp Ile Pro
115 120 125
Val Asn Ala Leu Gly Lys Tyr Lys Thr Val Ser Gln Val Val Ala Ile
130 135 140
Gly Ala Leu Leu Ala Asp Val Thr Tyr Ser Tyr Ala Leu Val Ala Ile
145 150 155 160
Ala Val Phe Leu Thr Leu Tyr Ser Gly Ile Asp Tyr Thr Ile Lys Tyr
165 170 175
Tyr Lys Ser

<210> 215
 <211> 913
 <212> DNA
 <213> Helicobacter pylori

<220>

<221> CDS
 <222> (19)...(879)

<400> 215

atagaagaag agtgagaa	atg	caa	gat	ttt	att	aag	att	ttt	att	caa	gag	51
	Met	Gln	Asp	Phe	Ile	Lys	Ile	Phe	Ile	Gln	Glu	
	1				5					10		
gtt gtc tct act tta gaa ggg tta gtg ggt aag gct cca agc gtg gga	99											
Val Val Ser Thr Leu Glu Gly Leu Val Gly Lys Ala Pro Ser Val Gly												
	15	20	25									
tta gaa aaa gaa att tct agt agc gac gaa tct ttt ttg aaa tta atc	147											
Leu Glu Lys Glu Ile Ser Ser Ser Asp Glu Ser Phe Leu Lys Leu Ile												
	30	35	40									
agc acg cct tat gca aga gtt gtg ata agc gcg att gaa aaa gaa gag	195											
Ser Thr Pro Tyr Ala Arg Val Val Ile Ser Ala Ile Glu Lys Glu Glu												
	45	50	55									
agc tct att gaa tta ctg gct ccg gta gtt tta gtt acc tct tta agc	243											
Ser Ser Ile Glu Leu Leu Ala Pro Val Val Leu Val Thr Ser Leu Ser												
	60	65	70	75								
gat ttg atg cta gga ggt gag gga gcg agt aag gaa gaa atg gat aat	291											
Asp Leu Met Leu Gly Gly Glu Gly Ala Ser Lys Glu Glu Met Asp Asn												
	80	85	90									
gac gat tta gac gct ttt aaa gaa atg gct tct aat att ttt ggc gcg	339											
Asp Asp Leu Asp Ala Phe Lys Glu Met Ala Ser Asn Ile Phe Gly Ala												
	95	100	105									
atc gct aca agc ttg aag tct caa gaa ttg ctc cct aaa ctc aat ttc	387											
Ile Ala Thr Ser Leu Lys Ser Gln Glu Leu Leu Pro Lys Leu Asn Phe												
	110	115	120									
acc act ata aac gct gaa atc gct aaa gag ctt cct aaa aaa gaa gat	435											
Thr Thr Ile Asn Ala Glu Ile Ala Lys Glu Leu Pro Lys Lys Glu Asp												
	125	130	135									
tac gct aaa gcg atg gtg ttt tct ttt aaa atg gaa gcc atc aaa gaa	483											
Tyr Ala Lys Ala Met Val Phe Ser Phe Lys Met Glu Ala Ile Lys Glu												
	140	145	150	155								
agc caa atc att tta ttg act acg gcg gct ttt gag ggc caa ttt gaa	531											
Ser Gln Ile Ile Leu Leu Thr Thr Ala Ala Phe Glu Gly Gln Phe Glu												
	160	165	170									
aaa acg cat aaa gaa gaa aaa gaa gaa acg aca gag ggc gtt gct gaa	579											
Lys Thr His Lys Glu Glu Lys Glu Glu Thr Thr Glu Gly Val Ala Glu												
	175	180	185									
gag gtt aaa acc cat gat gcg tct tta gaa aac ata gaa atc cgc aat	627											
Glu Val Lys Thr His Asp Ala Ser Leu Glu Asn Ile Glu Ile Arg Asn												
	190	195	200									
atc agc atg ctt tta gac gtg aaa ttg aac gtt aag gtg cgc atc ggg	675											
Ile Ser Met Leu Leu Asp Val Lys Leu Asn Val Lys Val Arg Ile Gly												
	205	210	215									

caa aaa aaa atg att tta aaa gac gtg gtc tct atg gat ata ggg agc	723
Gln Lys Lys Met Ile Leu Lys Asp Val Val Ser Met Asp Ile Gly Ser	
220 225 230 235	
gtg gta gag ctg gat caa ttg gtg aat gac cct ttg gaa att ctt gta	771
Val Val Glu Leu Asp Gln Leu Val Asn Asp Pro Leu Glu Ile Leu Val	
240 245 250	
gat gac aag gtg atc gct aag ggc gaa gtg gtg att gtg gat ggg aat	819
Asp Asp Lys Val Ile Ala Lys Gly Glu Val Val Ile Val Asp Gly Asn	
255 260 265	
ttt ggc att caa atc acg gat att ggc act aaa aaa gaa cgc tta gaa	867
Phe Gly Ile Gln Ile Thr Asp Ile Gly Thr Lys Lys Glu Arg Leu Glu	
270 275 280	
caa ttg aaa cat taaatctttt tatcataaaaa aggaaaggga tatg	913
Gln Leu Lys His	
285	

<210> 216
 <211> 287
 <212> PRT
 <213> *Helicobacter pylori*

<400> 216

Met Gln Asp Phe Ile Lys Ile Phe Ile Gln Glu Val Val Ser Thr Leu	
1 5 10 15	
Glu Gly Leu Val Gly Lys Ala Pro Ser Val Gly Leu Glu Lys Glu Ile	
20 25 30	
Ser Ser Ser Asp Glu Ser Phe Leu Lys Leu Ile Ser Thr Pro Tyr Ala	
35 40 45	
Arg Val Val Ile Ser Ala Ile Glu Lys Glu Glu Ser Ser Ile Glu Leu	
50 55 60	
Leu Ala Pro Val Val Leu Val Thr Ser Leu Ser Asp Leu Met Leu Gly	
65 70 75 80	
Gly Glu Gly Ala Ser Lys Glu Glu Met Asp Asn Asp Asp Leu Asp Ala	
85 90 95	
Phe Lys Glu Met Ala Ser Asn Ile Phe Gly Ala Ile Ala Thr Ser Leu	
100 105 110	
Lys Ser Gln Glu Leu Leu Pro Lys Leu Asn Phe Thr Thr Ile Asn Ala	
115 120 125	
Glu Ile Ala Lys Glu Leu Pro Lys Lys Glu Asp Tyr Ala Lys Ala Met	
130 135 140	
Val Phe Ser Phe Lys Met Glu Ala Ile Lys Glu Ser Gln Ile Ile Leu	
145 150 155 160	
Leu Thr Thr Ala Ala Phe Glu Gly Gln Phe Glu Lys Thr His Lys Glu	
165 170 175	
Glu Lys Glu Glu Thr Thr Glu Gly Val Ala Glu Glu Val Lys Thr His	
180 185 190	
Asp Ala Ser Leu Glu Asn Ile Glu Ile Arg Asn Ile Ser Met Leu Leu	
195 200 205	
Asp Val Lys Leu Asn Val Lys Val Arg Ile Gly Gln Lys Lys Met Ile	
210 215 220	
Leu Lys Asp Val Val Ser Met Asp Ile Gly Ser Val Val Glu Leu Asp	
225 230 235 240	
Gln Leu Val Asn Asp Pro Leu Glu Ile Leu Val Asp Asp Lys Val Ile	

Ala	Lys	Gly	Glu	Val	Val	Ile	Val	Asp	Gly	Asn	Phe	Gly	Ile	Gln	Ile
			260					265					270		
Thr	Asp	Ile	Gly	Thr	Lys	Lys	Glu	Arg	Leu	Glu	Gln	Leu	Lys	His	
		275					280					285			

<210> 217
 <211> 1111
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (13)...(1056)

<400> 217
 taaaaaagga ga atg atg caa gtt tac cac ctt tca cac att gat tta gac 51
 Met Met Gln Val Tyr His Leu Ser His Ile Asp Leu Asp
 1 5 10

ggc tat gca tgc cag ctt gtt tca aaa caa ttt ttt aaa aat atc caa 99
 Gly Tyr Ala Cys Gln Leu Val Ser Lys Gln Phe Phe Lys Asn Ile Gln
 15 20 25

tgc tat aac gct aat tac ggg cgt gaa gtc tca gcg aga att tat gag 147
 Cys Tyr Asn Ala Asn Tyr Gly Arg Glu Val Ser Ala Arg Ile Tyr Glu
 30 35 40 45

att tta aac gca atc gct cag tct aaa gag agt gaa ttc ctt att ttg 195
 Ile Leu Asn Ala Ile Ala Gln Ser Lys Glu Ser Glu Phe Leu Ile Leu
 50 55 60

gtt agc gat ttg aat ctg aat ttg aat gaa gca gag tat ttg cag gat 243
 Val Ser Asp Leu Asn Leu Asn Leu Asn Glu Ala Glu Tyr Leu Gln Asp
 65 70 75

aag atc caa gaa cac cgc ttg caa aat aaa aac att caa atc cag ctt 291
 Lys Ile Gln Glu His Arg Leu Gln Asn Lys Asn Ile Gln Ile Gln Leu
 80 85 90

tta gat cac cat atc agc ggt aag gaa gtg gct gag agt ttc cat tgg 339
 Leu Asp His His Ile Ser Gly Lys Glu Val Ala Glu Ser Phe His Trp
 95 100 105

tat ttt tta gac att aac cgt tgc gcg act aaa atc gtg tat gaa ttt 387
 Tyr Phe Leu Asp Ile Asn Arg Cys Ala Thr Lys Ile Val Tyr Glu Phe
 110 115 120 125

ttg aaa aag cat tac gct att tta gag cca aaa aac aca aca tgg cta 435
 Leu Lys Lys His Tyr Ala Ile Leu Glu Pro Lys Asn Thr Thr Trp Leu
 130 135 140

gag cct tta gtg gaa atg gtc aat tct gtg gat att tgg gac acg caa 483
 Glu Pro Leu Val Glu Met Val Asn Ser Val Asp Ile Trp Asp Thr Gln
 145 150 155

ggt tat ggc ttt gaa tta ggc aag gtg tgc atg cgc atg att aac caa 531
 Gly Tyr Gly Phe Glu Leu Gly Lys Val Cys Met Arg Met Ile Asn Gln

160	165	170	
agc tct gaa ttg aat cgt ttc atg ttt gat gat gaa aac cgc aac tat			579
Ser Ser Glu Leu Asn Arg Phe Met Phe Asp Asp Glu Asn Arg Asn Tyr			
175	180	185	
aaa tta aag ctt tta gaa gaa gtt aaa aac tat ttg ttt tta gaa aat			627
Lys Leu Lys Leu Leu Glu Glu Val Lys Asn Tyr Leu Phe Leu Glu Asn			
190	195	200	205
gcc cct gta gcc tat gat aac gat ttg ttc aaa ctc aaa aaa atc gct			675
Ala Pro Val Ala Tyr Asp Asn Asp Leu Phe Lys Leu Lys Lys Ile Ala			
	210	215	220
tta ggg ggc gac cct gat gca gaa acg atg gac aat atc tct tca aac			723
Leu Gly Gly Asp Pro Asp Ala Glu Thr Met Asp Asn Ile Ser Asn			
	225	230	235
gcg caa acg cat ttg ctc tct tta aaa aag cat gat tgc agc gtt tat			771
Ala Gln Thr His Leu Leu Ser Leu Lys Lys His Asp Cys Ser Val Tyr			
	240	245	250
tac cag gat aaa aaa ggg ttt tta agt tat tct atg ggg ggc att agc			819
Tyr Gln Asp Lys Lys Gly Phe Leu Ser Tyr Ser Met Gly Gly Ile Ser			
	255	260	265
gtg ttg gct aac ctt ttt tta acg caa aat ccg gat ttt gat ttt tat			867
Val Leu Ala Asn Leu Phe Leu Thr Gln Asn Pro Asp Phe Asp Phe Tyr			
	270	275	280
atg gat gtg aac gct aaa ggg aat gtg agc tta agg gcg aat ggg aat			915
Met Asp Val Asn Ala Lys Gly Asn Val Ser Leu Arg Ala Asn Gly Asn			
	290	295	300
tgc gat gtg tgc gaa ctc agt caa atg tgt ttt aat ggg ggt ggg cat			963
Cys Asp Val Cys Glu Leu Ser Gln Met Cys Phe Asn Gly Gly Gly His			
	305	310	315
agg aat gcg agc gga ggc aag att gat ggt ttt agg gag agt ttc aat			1011
Arg Asn Ala Ser Gly Gly Lys Ile Asp Gly Phe Arg Glu Ser Phe Asn			
	320	325	330
tat agg gat att aaa gaa caa att gaa gaa atc ttc aac aac gct			1056
Tyr Arg Asp Ile Lys Glu Gln Ile Glu Glu Ile Phe Asn Asn Ala			
	335	340	345
taaaactaag ctgttttagaa aaaactaaca aaaactgaaa agagtttaaaa agctc			1111

<210> 218

<211> 348

<212> PRT

<213> Helicobacter pylori

<400> 218

Met Met Gln Val Tyr His Leu Ser His Ile Asp Leu Asp Gly Tyr Ala	
1 5 10 15	
Cys Gln Leu Val Ser Lys Gln Phe Phe Lys Asn Ile Gln Cys Tyr Asn	
20 25 30	
Ala Asn Tyr Gly Arg Glu Val Ser Ala Arg Ile Tyr Glu Ile Leu Asn	

caa gcc agg att aaa aac atg tgc gaa tat aaa gat tta gtg cat gaa	152
Gln Ala Arg Ile Lys Asn Met Cys Glu Tyr Lys Asp Leu Val His Glu	
25 30 35	
gcc aat gaa gat tat gaa cat ttt tgg ggc gat tta gcc aag cag aaa	200
Ala Asn Glu Asp Tyr Glu His Phe Trp Gly Asp Leu Ala Lys Gln Lys	
40 45 50	
ctc aca tgg ttt aaa cct ttt gat aag gtt tta aac agc gat aac gcc	248
Leu Thr Trp Phe Lys Pro Phe Asp Lys Val Leu Asn Ser Asp Asn Ala	
55 60 65 70	
cct ttt ttc aaa tgg ttt gaa aac ggc aaa atc aat gtt tct tac aat	296
Pro Phe Phe Lys Trp Phe Glu Asn Gly Lys Ile Asn Val Ser Tyr Asn	
75 80 85	
tgc ata gac agg cat tta aaa gac aaa aaa aat aaa gtg gcg atc att	344
Cys Ile Asp Arg His Leu Lys Asp Lys Lys Asn Lys Val Ala Ile Ile	
90 95 100	
ttt gaa ggg gaa atg ggg gat tat aat gtc atc act tac aga aaa ctc	392
Phe Glu Gly Glu Met Gly Asp Tyr Asn Val Ile Thr Tyr Arg Lys Leu	
105 110 115	
cac tct gaa gtc aat aaa aca gcc aac ctt tta aaa aac gaa ttc aat	440
His Ser Glu Val Asn Lys Thr Ala Asn Leu Leu Lys Asn Glu Phe Asn	
120 125 130	
gtc aaa aaa ggc gat agg gtc att atc tat atg ccc atg att gta gaa	488
Val Lys Lys Gly Asp Arg Val Ile Ile Tyr Met Pro Met Ile Val Glu	
135 140 145 150	
agc gtt tat atg atg ctc gca tgc act agg att gga gcg atc cat agc	536
Ser Val Tyr Met Met Leu Ala Cys Thr Arg Ile Gly Ala Ile His Ser	
155 160 165	
atc gtt ttt gct ggg ttt agc cct gaa gcc tta agg gat agg atc aac	584
Ile Val Phe Ala Gly Phe Ser Pro Glu Ala Leu Arg Asp Arg Ile Asn	
170 175 180	
gac gct caa gct aaa tta gtt atc aca gcg gat ggg act ttt aga aaa	632
Asp Ala Gln Ala Lys Leu Val Ile Thr Ala Asp Gly Thr Phe Arg Lys	
185 190 195	
ggc aaa cct tac atg ctc aag cca gcc ctt gac aag gct cta gaa aat	680
Gly Lys Pro Tyr Met Leu Lys Pro Ala Leu Asp Lys Ala Leu Glu Asn	
200 205 210	
aac gcc tgc cct agc gtg gaa aaa gcg ctc att gtg ata cga aac gcc	728
Asn Ala Cys Pro Ser Val Glu Lys Ala Leu Ile Val Ile Arg Asn Ala	
215 220 225 230	
aaa gag att gac tat gtg aga ggg cgc gat ttt gtc tat aat gaa atg	776
Lys Glu Ile Asp Tyr Val Arg Gly Arg Asp Phe Val Tyr Asn Glu Met	
235 240 245	
gtc aat tac caa tcc gac aaa tgc gaa cct gaa atg atg gac tct gaa	824
Val Asn Tyr Gln Ser Asp Lys Cys Glu Pro Glu Met Met Asp Ser Glu	
250 255 260	

gat cct tta ttc ttg ctc tat aca agc gga tca acc gga aag cct aaa	872
Asp Pro Leu Phe Leu Leu Tyr Thr Ser Gly Ser Thr Gly Lys Pro Lys	
265 270 275	
ggc gtt caa cac agc agt gcg ggg tat ttg tta tgg gcg caa atg acg	920
Gly Val Gln His Ser Ser Ala Gly Tyr Leu Leu Trp Ala Gln Met Thr	
280 285 290	
atg gag tgg gtt ttt gat att aga gat aac gat aat ttt tgg tgc acc	968
Met Glu Trp Val Phe Asp Ile Arg Asp Asn Asp Asn Phe Trp Cys Thr	
295 300 305 310	
gcc gat att ggc tgg atc aca ggg cac act tat gtg gtt tat gga cct	1016
Ala Asp Ile Gly Trp Ile Thr Gly His Thr Tyr Val Val Tyr Gly Pro	
315 320 325	
tta gct tgt ggg gcg acg act ttg ata cta gaa ggc acg atg tct tat	1064
Leu Ala Cys Gly Ala Thr Thr Leu Ile Leu Glu Gly Thr Met Ser Tyr	
330 335 340	
ccg gat tat ggg aga tgg tgg agg atg ata gaa gaa tac cgt gtg gat	1112
Pro Asp Tyr Gly Arg Trp Trp Arg Met Ile Glu Glu Tyr Arg Val Asp	
345 350 355	
aaa ttc tac act tcc cct acc gct ata aga atg ttg cat gcc aaa ggt	1160
Lys Phe Tyr Thr Ser Pro Thr Ala Ile Arg Met Leu His Ala Lys Gly	
360 365 370	
gaa aac gaa ccc tca aag tat aat tta gag tcg ctc aaa gtt tta gga	1208
Glu Asn Glu Pro Ser Lys Tyr Asn Leu Glu Ser Leu Lys Val Leu Gly	
375 380 385 390	
acg gtg gga gag ccc att aac cct aca gca tgg aaa tgg ttt tat gaa	1256
Thr Val Gly Glu Pro Ile Asn Pro Thr Ala Trp Lys Trp Phe Tyr Glu	
395 400 405	
aaa atc ggc aac tca aaa tgc agc atc gtg gat act tgg tgg cag aca	1304
Lys Ile Gly Asn Ser Lys Cys Ser Ile Val Asp Thr Trp Trp Gln Thr	
410 415 420	
gaa aca ggc ggg cac atc atc agc cct tta ccg gga gct acg cct ata	1352
Glu Thr Gly Gly His Ile Ile Ser Pro Leu Pro Gly Ala Thr Pro Ile	
425 430 435	
agg gcc agt tgc gcg act tta cct ttg cct gga atc cat gcg gaa gtt	1400
Arg Ala Ser Cys Ala Thr Leu Pro Leu Pro Gly Ile His Ala Glu Val	
440 445 450	
tta aac gaa gac ggc act aaa aca aag cct gga gag caa ggg ttt tta	1448
Leu Asn Glu Asp Gly Thr Lys Thr Lys Pro Gly Glu Gln Gly Phe Leu	
455 460 465 470	
tgc atc act aag cca tgg cct tct atg ata aga aac att tgg ggc gat	1496
Cys Ile Thr Lys Pro Trp Pro Ser Met Ile Arg Asn Ile Trp Gly Asp	
475 480 485	
gaa aaa cga tac att gat agc tat ttt tct cag atc aag ttg aat ggg	1544
Glu Lys Arg Tyr Ile Asp Ser Tyr Phe Ser Gln Ile Lys Leu Asn Gly	

490	495	500	
gaa tat gtc tac ctc tct gga gat ggc gct atc gtg gat gaa aac gga Glu Tyr Val Tyr Leu Ser Gly Asp Gly Ala Ile Val Asp Glu Asn Gly 505 510 515			1592
tac att act att att ggg cgc aca gat gat att gtg aat gtg agt ggg Tyr Ile Thr Ile Ile Gly Arg Thr Asp Asp Ile Val Asn Val Ser Gly 520 525 530			1640
cat agg att ggc acg gct gaa gtg gag agc gct att tcc aag cat gaa His Arg Ile Gly Thr Ala Glu Val Glu Ser Ala Ile Ser Lys His Glu 535 540 545 550			1688
atg gtg gct gaa tgc gcg gtg gtg ggt atc cct gat gcg att aaa gga Met Val Ala Glu Cys Ala Val Val Gly Ile Pro Asp Ala Ile Lys Gly 555 560 565			1736
gag ggc ttg ttt gcg ttt gtg gtg ctg tgc gat ggg gct aaa tgc aat Glu Gly Leu Phe Ala Phe Val Val Leu Cys Asp Gly Ala Lys Cys Asn 570 575 580			1784
ctt ggc gag agt tta gaa ttg cta aaa gaa atg aac cat atc tta tcc Leu Gly Glu Ser Leu Glu Leu Leu Lys Glu Met Asn His Ile Leu Ser 585 590 595			1832
att gag att gga aag atc gcg aaa tta gac aat gtc atg tat gtg cca Ile Glu Ile Gly Lys Ile Ala Lys Leu Asp Asn Val Met Tyr Val Pro 600 605 610			1880
ggt ttg cct aaa acc agg agc ggg aaa atc atg aga agg ctt ttg aaa Gly Leu Pro Lys Thr Arg Ser Gly Lys Ile Met Arg Arg Leu Leu Lys 615 620 625 630			1928
tcc atc gcc aaa aaa gag cct atc act caa gat tta agc acg cta gaa Ser Ile Ala Lys Lys Glu Pro Ile Thr Gln Asp Leu Ser Thr Leu Glu 635 640 645			1976
gat gtg aat gtg gtt aaa gaa ata atg agc atc gct caa atg gag gag Asp Val Asn Val Val Lys Glu Ile Met Ser Ile Ala Gln Met Glu Glu 650 655 660			2024
taaaatctaa aaaatgcttt ttagcgtttt ttagccaaat aataag			2070

<210> 220

<211> 662

<212> PRT

<213> Helicobacter pylori

<400> 220

Met	Gln	Leu	Asp	Glu	Asp	Leu	Glu	Phe	Ala	Lys	Lys	Ile	Phe	Asn	Pro
1				5				10					15		
Asn	Arg	Ala	Phe	Ala	Lys	Gln	Ala	Arg	Ile	Lys	Asn	Met	Cys	Glu	Tyr
		20					25					30			
Lys	Asp	Leu	Val	His	Glu	Ala	Asn	Glu	Asp	Tyr	Glu	His	Phe	Trp	Gly
		35				40					45				
Asp	Leu	Ala	Lys	Gln	Lys	Leu	Thr	Trp	Phe	Lys	Pro	Phe	Asp	Lys	Val
	50				55					60					
Leu	Asn	Ser	Asp	Asn	Ala	Pro	Phe	Phe	Lys	Trp	Phe	Glu	Asn	Gly	Lys

65					70					75					80
Ile	Asn	Val	Ser	Tyr	Asn	Cys	Ile	Asp	Arg	His	Leu	Lys	Asp	Lys	Lys
				85					90					95	
Asn	Lys	Val	Ala	Ile	Ile	Phe	Glu	Gly	Glu	Met	Gly	Asp	Tyr	Asn	Val
			100					105					110		
Ile	Thr	Tyr	Arg	Lys	Leu	His	Ser	Glu	Val	Asn	Lys	Thr	Ala	Asn	Leu
			115				120					125			
Leu	Lys	Asn	Glu	Phe	Asn	Val	Lys	Lys	Gly	Asp	Arg	Val	Ile	Ile	Tyr
			130			135					140				
Met	Pro	Met	Ile	Val	Glu	Ser	Val	Tyr	Met	Met	Leu	Ala	Cys	Thr	Arg
145					150				155						160
Ile	Gly	Ala	Ile	His	Ser	Ile	Val	Phe	Ala	Gly	Phe	Ser	Pro	Glu	Ala
				165				170						175	
Leu	Arg	Asp	Arg	Ile	Asn	Asp	Ala	Gln	Ala	Lys	Leu	Val	Ile	Thr	Ala
			180					185					190		
Asp	Gly	Thr	Phe	Arg	Lys	Gly	Lys	Pro	Tyr	Met	Leu	Lys	Pro	Ala	Leu
			195				200					205			
Asp	Lys	Ala	Leu	Glu	Asn	Asn	Ala	Cys	Pro	Ser	Val	Glu	Lys	Ala	Leu
			210			215					220				
Ile	Val	Ile	Arg	Asn	Ala	Lys	Glu	Ile	Asp	Tyr	Val	Arg	Gly	Arg	Asp
225				230					235						240
Phe	Val	Tyr	Asn	Glu	Met	Val	Asn	Tyr	Gln	Ser	Asp	Lys	Cys	Glu	Pro
			245						250					255	
Glu	Met	Met	Asp	Ser	Glu	Asp	Pro	Leu	Phe	Leu	Leu	Tyr	Thr	Ser	Gly
			260					265					270		
Ser	Thr	Gly	Lys	Pro	Lys	Gly	Val	Gln	His	Ser	Ser	Ala	Gly	Tyr	Leu
			275				280					285			
Leu	Trp	Ala	Gln	Met	Thr	Met	Glu	Trp	Val	Phe	Asp	Ile	Arg	Asp	Asn
			290			295					300				
Asp	Asn	Phe	Trp	Cys	Thr	Ala	Asp	Ile	Gly	Trp	Ile	Thr	Gly	His	Thr
305				310					315						320
Tyr	Val	Val	Tyr	Gly	Pro	Leu	Ala	Cys	Gly	Ala	Thr	Thr	Leu	Ile	Leu
			325						330					335	
Glu	Gly	Thr	Met	Ser	Tyr	Pro	Asp	Tyr	Gly	Arg	Trp	Trp	Arg	Met	Ile
			340					345					350		
Glu	Glu	Tyr	Arg	Val	Asp	Lys	Phe	Tyr	Thr	Ser	Pro	Thr	Ala	Ile	Arg
			355				360					365			
Met	Leu	His	Ala	Lys	Gly	Glu	Asn	Glu	Pro	Ser	Lys	Tyr	Asn	Leu	Glu
			370			375					380				
Ser	Leu	Lys	Val	Leu	Gly	Thr	Val	Gly	Glu	Pro	Ile	Asn	Pro	Thr	Ala
385				390					395						400
Trp	Lys	Trp	Phe	Tyr	Glu	Lys	Ile	Gly	Asn	Ser	Lys	Cys	Ser	Ile	Val
			405					410						415	
Asp	Thr	Trp	Trp	Gln	Thr	Glu	Thr	Gly	Gly	His	Ile	Ile	Ser	Pro	Leu
			420					425					430		
Pro	Gly	Ala	Thr	Pro	Ile	Arg	Ala	Ser	Cys	Ala	Thr	Leu	Pro	Leu	Pro
			435				440					445			
Gly	Ile	His	Ala	Glu	Val	Leu	Asn	Glu	Asp	Gly	Thr	Lys	Thr	Lys	Pro
			450			455					460				
Gly	Glu	Gln	Gly	Phe	Leu	Cys	Ile	Thr	Lys	Pro	Trp	Pro	Ser	Met	Ile
465				470					475						480
Arg	Asn	Ile	Trp	Gly	Asp	Glu	Lys	Arg	Tyr	Ile	Asp	Ser	Tyr	Phe	Ser
			485					490						495	
Gln	Ile	Lys	Leu	Asn	Gly	Glu	Tyr	Val	Tyr	Leu	Ser	Gly	Asp	Gly	Ala
			500					505					510		
Ile	Val	Asp	Glu	Asn	Gly	Tyr	Ile	Thr	Ile	Ile	Gly	Arg	Thr	Asp	Asp
			515				520					525			
Ile	Val	Asn	Val	Ser	Gly	His	Arg	Ile	Gly	Thr	Ala	Glu	Val	Glu	Ser
			530			535					540				

Ala	Ile	Ser	Lys	His	Glu	Met	Val	Ala	Glu	Cys	Ala	Val	Val	Gly	Ile
545					550					555					560
Pro	Asp	Ala	Ile	Lys	Gly	Glu	Gly	Leu	Phe	Ala	Phe	Val	Val	Leu	Cys
				565					570						575
Asp	Gly	Ala	Lys	Cys	Asn	Leu	Gly	Glu	Ser	Leu	Glu	Leu	Leu	Lys	Glu
			580					585					590		
Met	Asn	His	Ile	Leu	Ser	Ile	Glu	Ile	Gly	Lys	Ile	Ala	Lys	Leu	Asp
		595				600						605			
Asn	Val	Met	Tyr	Val	Pro	Gly	Leu	Pro	Lys	Thr	Arg	Ser	Gly	Lys	Ile
	610					615					620				
Met	Arg	Arg	Leu	Leu	Lys	Ser	Ile	Ala	Lys	Lys	Glu	Pro	Ile	Thr	Gln
625					630					635					640
Asp	Leu	Ser	Thr	Leu	Glu	Asp	Val	Asn	Val	Val	Lys	Glu	Ile	Met	Ser
				645				650						655	
Ile	Ala	Gln	Met	Glu	Glu										
			660												

<210> 221
 <211> 725
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (19)...(669)

<400> 221	
tgaatggctt aatgagca atg gat aaa aac caa tat cac cgc ccc cat aga	51
Met Asp Lys Asn Gln Tyr His Arg Pro His Arg	
1 5 10	
gca agc caa acg gct ttt aat gaa agg ata gtc atg tta aaa acg aat	99
Ala Ser Gln Thr Ala Phe Asn Glu Arg Ile Val Met Leu Lys Thr Asn	
15 20 25	
caa aaa aat gtg cat gcg ttt gaa att gaa aag caa gag cct gaa gcg	147
Gln Lys Asn Val His Ala Phe Glu Ile Glu Lys Gln Glu Pro Glu Ala	
30 35 40	
gtc ata ggg ttt tta gaa aaa aac cat gcc ctt ttg caa tat ttt ctt	195
Val Ile Gly Phe Leu Glu Lys Asn His Ala Leu Leu Gln Tyr Phe Leu	
45 50 55	
att att ttt aaa tac gat att gaa tca gaa gtc aaa gcc gtt ttg cgc	243
Ile Ile Phe Lys Tyr Asp Ile Glu Ser Glu Val Lys Ala Val Leu Arg	
60 65 70 75	
aaa cac cag ctt ttg ttt tta gaa acg aat cgc gtt tta aac gga cgc	291
Lys His Gln Leu Leu Phe Leu Glu Thr Asn Arg Val Leu Asn Gly Arg	
80 85 90	
cat atc aaa acc atg cct tta aaa gac gaa acc gat cat cca aaa ccc	339
His Ile Lys Thr Met Pro Leu Lys Asp Glu Thr Asp His Pro Lys Pro	
95 100 105	
aat cat tct aaa aca gaa cct aaa aca acg att tat gag cgc cat atc	387
Asn His Ser Lys Thr Glu Pro Lys Thr Thr Ile Tyr Glu Arg His Ile	
110 115 120	

agg agt ggg gaa gag att tat agc act aat cac ctt att ttt ttg ggt	435
Arg Ser Gly Glu Glu Ile Tyr Ser Thr Asn His Leu Ile Phe Leu Gly	
125 130 135	
aat atc cat aat gga gcc aag att att tca gag ggc tgt gtg tct gtt	483
Asn Ile His Asn Gly Ala Lys Ile Ile Ser Glu Gly Cys Val Ser Val	
140 145 150 155	
tat ggg gtt tgc gaa ggg gcg att gtg tgc ttt gga gag tgt ttg atc	531
Tyr Gly Val Cys Glu Gly Ala Ile Val Cys Phe Gly Glu Cys Leu Ile	
160 165 170	
tta aaa gaa gtc aag agc gct caa atc gtt ttt caa aac aaa att ttg	579
Leu Lys Glu Val Lys Ser Ala Gln Ile Val Phe Gln Asn Lys Ile Leu	
175 180 185	
tct cta aaa gag gtt gaa ccg ctt ttg gta aat aaa aat att aaa ata	627
Ser Leu Lys Glu Val Glu Pro Leu Leu Val Asn Lys Asn Ile Lys Ile	
190 195 200	
atc act aaa aat gac gat ata cta gac ata aag gaa gta tta	669
Ile Thr Lys Asn Asp Asp Ile Leu Asp Ile Lys Glu Val Leu	
205 210 215	
tgaaacaaac aaccattaac cactctgtgg aattagtagg gataggcttg cacaag	725

<210> 222

<211> 217

<212> PRT

<213> Helicobacter pylori

<400> 222

Met Asp Lys Asn Gln Tyr His Arg Pro His Arg Ala Ser Gln Thr Ala	
1 5 10 15	
Phe Asn Glu Arg Ile Val Met Leu Lys Thr Asn Gln Lys Asn Val His	
20 25 30	
Ala Phe Glu Ile Glu Lys Gln Glu Pro Glu Ala Val Ile Gly Phe Leu	
35 40 45	
Glu Lys Asn His Ala Leu Leu Gln Tyr Phe Leu Ile Ile Phe Lys Tyr	
50 55 60	
Asp Ile Glu Ser Glu Val Lys Ala Val Leu Arg Lys His Gln Leu Leu	
65 70 75 80	
Phe Leu Glu Thr Asn Arg Val Leu Asn Gly Arg His Ile Lys Thr Met	
85 90 95	
Pro Leu Lys Asp Glu Thr Asp His Pro Lys Pro Asn His Ser Lys Thr	
100 105 110	
Glu Pro Lys Thr Thr Ile Tyr Glu Arg His Ile Arg Ser Gly Glu Glu	
115 120 125	
Ile Tyr Ser Thr Asn His Leu Ile Phe Leu Gly Asn Ile His Asn Gly	
130 135 140	
Ala Lys Ile Ile Ser Glu Gly Cys Val Ser Val Tyr Gly Val Cys Glu	
145 150 155 160	
Gly Ala Ile Val Cys Phe Gly Glu Cys Leu Ile Leu Lys Glu Val Lys	
165 170 175	
Ser Ala Gln Ile Val Phe Gln Asn Lys Ile Leu Ser Leu Lys Glu Val	
180 185 190	
Glu Pro Leu Leu Val Asn Lys Asn Ile Lys Ile Ile Thr Lys Asn Asp	
195 200 205	

Asp Ile Leu Asp Ile Lys Glu Val Leu
 210 215

<210> 223
 <211> 1121
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (64)...(1068)

<400> 223
 aaagaaaatc tgggtattgga taaacccaag tcttttagaag tgcctttgac taggcccga 60
 atc atg ggg cta gaa gac aag tgc ctt tta tat gaa att aaa gct aat 108
 Met Gly Leu Glu Asp Lys Cys Leu Leu Tyr Glu Ile Lys Ala Asn
 1 5 10 15
 gat tgg agt tat gct aat ttt ttc aat ggc aat aaa gcg tct ttc aaa 156
 Asp Trp Ser Tyr Ala Asn Phe Phe Asn Gly Asn Lys Ala Ser Phe Lys
 20 25 30
 caa gaa gtg tgt gtt gat acg ata aaa ccc tca atc act att tta tct 204
 Gln Glu Val Cys Val Asp Thr Ile Lys Pro Ser Ile Thr Ile Leu Ser
 35 40 45
 cga tcc cca agc atc gct tat ggg ggg agc gcg ata gtc gtt ttt gaa 252
 Arg Ser Pro Ser Ile Ala Tyr Gly Gly Ser Ala Ile Val Val Phe Glu
 50 55 60
 gct ttg gat aag aat ttg tct caa gcg ttt gtg cgc gtc aaa aaa aag 300
 Ala Leu Asp Lys Asn Leu Ser Gln Ala Phe Val Arg Val Lys Lys Lys
 65 70 75
 gat ttt gaa gct ttc agg ctt tta gaa ttc aaa cag cgt aat gtt ttt 348
 Asp Phe Glu Ala Phe Arg Leu Leu Glu Phe Lys Gln Arg Asn Val Phe
 80 85 90 95
 atc gct cta gtg cct tgg tct tat aaa aat aag gat ttt aag gcg ttc 396
 Ile Ala Leu Val Pro Trp Ser Tyr Lys Asn Lys Asp Phe Lys Ala Phe
 100 105 110
 att gtc gct aaa gat aaa gcc tat aac ttt aat acc gcc cct tta ttg 444
 Ile Val Ala Lys Asp Lys Ala Tyr Asn Phe Asn Thr Ala Pro Leu Leu
 115 120 125
 ttc aag cga aaa atc cat cgt ttg agg gaa aaa gat ata gac tta agc 492
 Phe Lys Arg Lys Ile His Arg Leu Arg Glu Lys Asp Ile Asp Leu Ser
 130 135 140
 gcc tta aaa gat aag att gca aag caa gaa aaa ttt caa aac gac act 540
 Ala Leu Lys Asp Lys Ile Ala Lys Gln Glu Lys Phe Gln Asn Asp Thr
 145 150 155
 gaa caa gct tta tta gaa aga ttt tcc aat gcg cgc cca aaa gat tta 588
 Glu Gln Ala Leu Leu Glu Arg Phe Ser Asn Ala Arg Pro Lys Asp Leu
 160 165 170 175

gaa aaa atc caa aag atc gct tta gag caa ggg gat ttt tat aag gat	636
Glu Lys Ile Gln Lys Ile Ala Leu Glu Gln Gly Asp Phe Tyr Lys Asp	
180 185 190	
ttt tct cat ttt caa gcg cta aaa ccc ttg aac ggg cct ttt aaa atg	684
Phe Ser His Phe Gln Ala Leu Lys Pro Leu Asn Gly Pro Phe Lys Met	
195 200 205	
gca agc aat ttt tta gaa aat cgg cgt atc tta aag aat aat cag gtg	732
Ala Ser Asn Phe Leu Glu Asn Arg Arg Ile Leu Lys Asn Asn Gln Val	
210 215 220	
ttg ttt aaa ttc ttg cat tta ggg gtg gat ttg ata cct ggc aag gat	780
Leu Phe Lys Phe Leu His Leu Gly Val Asp Leu Ile Pro Gly Lys Asp	
225 230 235	
tta tct tta gcg ttt gat ttg tct gtg aag agg gtt ttt aag ggg gag	828
Leu Ser Leu Ala Phe Asp Leu Ser Val Lys Arg Val Phe Lys Gly Glu	
240 245 250 255	
ttc gat ttt tat ggt aat agt tta atc cat tgc tat ggg tta ggt ttg	876
Phe Asp Phe Tyr Gly Asn Ser Leu Ile His Cys Tyr Gly Leu Gly Leu	
260 265 270	
tgc gtt ttt tta gcc cat tta aaa gat gat aaa agc gtg ggg agt agt	924
Cys Val Phe Leu Ala His Leu Lys Asp Asp Lys Ser Val Gly Ser Ser	
275 280 285	
ggt ttg aaa tta ggg agc ggg ttg cat tta ggg atg ctt ttg caa ggg	972
Gly Leu Lys Leu Gly Ser Gly Leu His Leu Gly Met Leu Leu Gln Gly	
290 295 300	
gtt ttt gtc cgg ccc aat gaa tgg ctt aat gag caa tgg ata aaa acc	1020
Val Phe Val Arg Pro Asn Glu Trp Leu Asn Glu Gln Trp Ile Lys Thr	
305 310 315	
aat atc acc gcc ccc ata gag caa gcc aaa cgg ctt tta atg aaa gga	1068
Asn Ile Thr Ala Pro Ile Glu Gln Ala Lys Arg Leu Leu Met Lys Gly	
320 325 330 335	
tagtcatgtt aaaaacgaat caaaaaaatg tgcattgcgtt tgaaattgaa aag	1121

<210> 224

<211> 335

<212> PRT

<213> *Helicobacter pylori*

<400> 224

Met Gly Leu Glu Asp Lys Cys Leu Leu Tyr Glu Ile Lys Ala Asn Asp	
1 5 10 15	
Trp Ser Tyr Ala Asn Phe Phe Asn Gly Asn Lys Ala Ser Phe Lys Gln	
20 25 30	
Glu Val Cys Val Asp Thr Ile Lys Pro Ser Ile Thr Ile Leu Ser Arg	
35 40 45	
Ser Pro Ser Ile Ala Tyr Gly Gly Ser Ala Ile Val Val Phe Glu Ala	
50 55 60	
Leu Asp Lys Asn Leu Ser Gln Ala Phe Val Arg Val Lys Lys Lys Asp	
65 70 75 80	
Phe Glu Ala Phe Arg Leu Leu Glu Phe Lys Gln Arg Asn Val Phe Ile	

ttt gaa gaa gaa tac atc aat cga tct tat cct aaa att tct tcc aag	246
Phe Glu Glu Glu Tyr Ile Asn Arg Ser Tyr Pro Lys Ile Ser Ser Lys	
60 65 70	
aaa aaa gag aaa ttg ctc aaa tct ttt tcc ata gcc gat gat aag agt	294
Lys Lys Glu Lys Leu Leu Lys Ser Phe Ser Ile Ala Asp Asp Lys Ser	
75 80 85	
ggg gtt ttt tta ggg ggt ggg tat gct tat ggg gaa ctt aac ttg tct	342
Gly Val Phe Leu Gly Gly Gly Tyr Ala Tyr Gly Glu Leu Asn Leu Ser	
90 95 100 105	
tat caa ggg gaa atg tta gac aga tac ggc gcg aat gcc cct agc gcg	390
Tyr Gln Gly Glu Met Leu Asp Arg Tyr Gly Ala Asn Ala Pro Ser Ala	
110 115 120	
ttt aaa aac aat atc aat att aac gct cct gtt tct atg att agc gct	438
Phe Lys Asn Asn Ile Asn Ile Asn Ala Pro Val Ser Met Ile Ser Ala	
125 130 135	
aaa ttt ggg tat caa aaa tac ttt gtg tct tat ttt ggg aca cga ttt	486
Lys Phe Gly Tyr Gln Lys Tyr Phe Val Ser Tyr Phe Gly Thr Arg Phe	
140 145 150	
tat ggg gat tta ttg ctt ggg ggt ggg gca tta aaa gag gat gca atc	534
Tyr Gly Asp Leu Leu Leu Gly Gly Gly Ala Leu Lys Glu Asp Ala Ile	
155 160 165	
aag cag cct gta ggc tcg ttt att tat gtt tta ggg gct gtc aat acc	582
Lys Gln Pro Val Gly Ser Phe Ile Tyr Val Leu Gly Ala Val Asn Thr	
170 175 180 185	
gat tta ttg ttt gat atg cct tta gat ttt aaa act aaa aag cat ttt	630
Asp Leu Leu Phe Asp Met Pro Leu Asp Phe Lys Thr Lys Lys His Phe	
190 195 200	
tta ggc gtt tat gcg ggt ttt ggg ata ggg ctt atg ctc tat caa gac	678
Leu Gly Val Tyr Ala Gly Phe Gly Ile Gly Leu Met Leu Tyr Gln Asp	
205 210 215	
agg cct aat caa aac ggg agg aat tta gta gtg ggg ggc tat tca agc	726
Arg Pro Asn Gln Asn Gly Arg Asn Leu Val Val Gly Gly Tyr Ser Ser	
220 225 230	
cct aat ttt tta tgg aaa tct ttg att gaa gtg gat tac act ttt aat	774
Pro Asn Phe Leu Trp Lys Ser Leu Ile Glu Val Asp Tyr Thr Phe Asn	
235 240 245	
gtg ggc gtg agt tta acg ctt tat agg aaa cac cgt tta gag att ggc	822
Val Gly Val Ser Leu Thr Leu Tyr Arg Lys His Arg Leu Glu Ile Gly	
250 255 260 265	
aca aaa ttg ccg att agc tat ttg aga atg gga gtg gaa gag gga gcg	870
Thr Lys Leu Pro Ile Ser Tyr Leu Arg Met Gly Val Glu Glu Gly Ala	
270 275 280	
att tat caa aat aaa gaa gat gat gag cgt ttg ttg gtt tcg gct aac	918
Ile Tyr Gln Asn Lys Glu Asp Asp Glu Arg Leu Leu Val Ser Ala Asn	
285 290 295	

aac cag ttc aag cga tcc agt ttt tta tta gtg aat tat gcg ttt att 966
 Asn Gln Phe Lys Arg Ser Ser Phe Leu Leu Val Asn Tyr Ala Phe Ile
 300 305 310

ttt taaggcttga tcttgagatt aagggttaaaa atttt 1004
 Phe

<210> 226
 <211> 314
 <212> PRT
 <213> *Helicobacter pylori*

<400> 226
 Met Leu Lys Phe Lys Tyr Gly Leu Ile Tyr Ile Ala Leu Ile Leu Gly
 1 5 10 15
 Leu Gln Ala Thr Asp Tyr Asp Asn Leu Glu Glu Glu Asn Gln Gln Leu
 20 25 30
 Asp Glu Lys Ile Asn His Leu Lys Gln Gln Leu Thr Glu Lys Gly Val
 35 40 45
 Ser Pro Lys Glu Met Asp Lys Asp Lys Phe Glu Glu Tyr Ile Asn
 50 55 60
 Arg Ser Tyr Pro Lys Ile Ser Ser Lys Lys Lys Glu Lys Leu Leu Lys
 65 70 75 80
 Ser Phe Ser Ile Ala Asp Asp Lys Ser Gly Val Phe Leu Gly Gly Gly
 85 90 95
 Tyr Ala Tyr Gly Glu Leu Asn Leu Ser Tyr Gln Gly Glu Met Leu Asp
 100 105 110
 Arg Tyr Gly Ala Asn Ala Pro Ser Ala Phe Lys Asn Asn Ile Asn Ile
 115 120 125
 Asn Ala Pro Val Ser Met Ile Ser Ala Lys Phe Gly Tyr Gln Lys Tyr
 130 135 140
 Phe Val Ser Tyr Phe Gly Thr Arg Phe Tyr Gly Asp Leu Leu Leu Gly
 145 150 155 160
 Gly Gly Ala Leu Lys Glu Asp Ala Ile Lys Gln Pro Val Gly Ser Phe
 165 170 175
 Ile Tyr Val Leu Gly Ala Val Asn Thr Asp Leu Leu Phe Asp Met Pro
 180 185 190
 Leu Asp Phe Lys Thr Lys Lys His Phe Leu Gly Val Tyr Ala Gly Phe
 195 200 205
 Gly Ile Gly Leu Met Leu Tyr Gln Asp Arg Pro Asn Gln Asn Gly Arg
 210 215 220
 Asn Leu Val Val Gly Gly Tyr Ser Ser Pro Asn Phe Leu Trp Lys Ser
 225 230 235 240
 Leu Ile Glu Val Asp Tyr Thr Phe Asn Val Gly Val Ser Leu Thr Leu
 245 250 255
 Tyr Arg Lys His Arg Leu Glu Ile Gly Thr Lys Leu Pro Ile Ser Tyr
 260 265 270
 Leu Arg Met Gly Val Glu Glu Gly Ala Ile Tyr Gln Asn Lys Glu Asp
 275 280 285
 Asp Glu Arg Leu Leu Val Ser Ala Asn Asn Gln Phe Lys Arg Ser Ser
 290 295 300
 Phe Leu Leu Val Asn Tyr Ala Phe Ile Phe
 305 310

<210> 227

<211> 874
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (18)...(827)

```

<400> 227
aacacttagg attttta atg agc atg caa acc gcc cca att aaa aag atc      50
                    Met Ser Met Gln Thr Ala Pro Ile Lys Lys Ile
                    1          5          10

act ctc aac cac ctc caa gct aaa aaa aat caa gaa aaa atc atc gct      98
Thr Leu Asn His Leu Gln Ala Lys Lys Asn Gln Glu Lys Ile Ile Ala
                    15          20          25

att acc gct tat gat gcg ctg ttc gct caa ata ttt gat ccg cta gtg     146
Ile Thr Ala Tyr Asp Ala Leu Phe Ala Gln Ile Phe Asp Pro Leu Val
                    30          35          40

gat gtg att tta gtg ggc gat agt ttg aat atg agt ttt ttc aat caa     194
Asp Val Ile Leu Val Gly Asp Ser Leu Asn Met Ser Phe Phe Asn Gln
                    45          50          55

aac gac act tta agc gcg agt gtg gaa atg atg ctc tat cac acc aaa     242
Asn Asp Thr Leu Ser Ala Ser Val Glu Met Met Leu Tyr His Thr Lys
                    60          65          70          75

gcc gtg tgc gcg ggc gct aag act cct ttt atc atc aca gac atg cct     290
Ala Val Cys Ala Gly Ala Lys Thr Pro Phe Ile Ile Thr Asp Met Pro
                    80          85          90

ttt gga agc tat aaa gat gaa aaa aca gcc cta aaa aac gcc att agg     338
Phe Gly Ser Tyr Lys Asp Glu Lys Thr Ala Leu Lys Asn Ala Ile Arg
                    95          100          105

gtt tat aaa gaa acc caa gcg agc gca atc aaa tta gag ggg ggg aaa     386
Val Tyr Lys Glu Thr Gln Ala Ser Ala Ile Lys Leu Glu Gly Gly Lys
                    110          115          120

gaa aaa gcg aaa ctg gtt aaa acg ctc act aat gag ggc gtt att gtg     434
Glu Lys Ala Lys Leu Val Lys Thr Leu Thr Asn Glu Gly Val Ile Val
                    125          130          135

gta ggg cat att ggc ttg atg ccc caa ttc gtg cgc ctt gat gga ggt     482
Val Gly His Ile Gly Leu Met Pro Gln Phe Val Arg Leu Asp Gly Gly
                    140          145          150          155

tat aag att aag ggc aaa aat gaa gaa caa caa aaa aag ctt tta gaa     530
Tyr Lys Ile Lys Gly Lys Asn Glu Glu Gln Gln Lys Lys Leu Leu Glu
                    160          165          170

gac gcc ttg agt tta gaa gaa gct ggg gtg ggt ttg ttg gtt tta gag     578
Asp Ala Leu Ser Leu Glu Glu Ala Gly Val Gly Leu Leu Val Leu Glu
                    175          180          185

ggg ata acc acc cct atc gct caa aaa atc acg caa aaa atc aaa atc     626
Gly Ile Thr Thr Pro Ile Ala Gln Lys Ile Thr Gln Lys Ile Lys Ile

```

190	195	200	
ccc acg atc ggc ata ggg agc ggt aaa gat tgc gat ggg cag att tta			674
Pro Thr Ile Gly Ile Gly Ser Gly Lys Asp Cys Asp Gly Gln Ile Leu			
205	210	215	
gtg tgg agc gat atg tta ggc ttt ttt gat agc ttt aag cct aaa ttc			722
Val Trp Ser Asp Met Leu Gly Phe Phe Asp Ser Phe Lys Pro Lys Phe			
220	225	230	235
gtg cga gaa tac ctt aag ggg aaa gaa ttg att caa aac gct atc aaa			770
Val Arg Glu Tyr Leu Lys Gly Lys Glu Leu Ile Gln Asn Ala Ile Lys			
	240	245	250
caa tac gct gat gat gtg aaa aag gga aac ttc cct aac gaa tta gaa			818
Gln Tyr Ala Asp Asp Val Lys Lys Gly Asn Phe Pro Asn Glu Leu Glu			
	255	260	265
agt tat cat taatgaaaga acggatagtc aatttagaaa ctttggattt			867
Ser Tyr His			
270			
tgaaatt			874
<210> 228			
<211> 270			
<212> PRT			
<213> Helicobacter pylori			

<400> 228

Met Ser Met Gln Thr Ala Pro Ile Lys Lys Ile Thr Leu Asn His Leu	
1 5 10 15	
Gln Ala Lys Lys Asn Gln Glu Lys Ile Ala Ile Thr Ala Tyr Asp	
20 25 30	
Ala Leu Phe Ala Gln Ile Phe Asp Pro Leu Val Asp Val Ile Leu Val	
35 40 45	
Gly Asp Ser Leu Asn Met Ser Phe Phe Asn Gln Asn Asp Thr Leu Ser	
50 55 60	
Ala Ser Val Glu Met Met Leu Tyr His Thr Lys Ala Val Cys Ala Gly	
65 70 75 80	
Ala Lys Thr Pro Phe Ile Ile Thr Asp Met Pro Phe Gly Ser Tyr Lys	
85 90 95	
Asp Glu Lys Thr Ala Leu Lys Asn Ala Ile Arg Val Tyr Lys Glu Thr	
100 105 110	
Gln Ala Ser Ala Ile Lys Leu Glu Gly Gly Lys Glu Lys Ala Lys Leu	
115 120 125	
Val Lys Thr Leu Thr Asn Glu Gly Val Ile Val Val Gly His Ile Gly	
130 135 140	
Leu Met Pro Gln Phe Val Arg Leu Asp Gly Gly Tyr Lys Ile Lys Gly	
145 150 155 160	
Lys Asn Glu Glu Gln Lys Lys Leu Leu Glu Asp Ala Leu Ser Leu	
165 170 175	
Glu Glu Ala Gly Val Gly Leu Leu Val Leu Glu Gly Ile Thr Thr Pro	
180 185 190	
Ile Ala Gln Lys Ile Thr Gln Lys Ile Lys Ile Pro Thr Ile Gly Ile	
195 200 205	
Gly Ser Gly Lys Asp Cys Asp Gly Gln Ile Leu Val Trp Ser Asp Met	
210 215 220	
Leu Gly Phe Phe Asp Ser Phe Lys Pro Lys Phe Val Arg Glu Tyr Leu	

<400> 229																
aataacgata	aaatttttaa	gggtgtaaaa	gtagattggt	atg	ttt	ggc	atg	ggc								55
				Met	Phe	Gly	Met	Gly								
				1				5								
ttt	ttt	gaa	atc	ctt	gtg	gtg	ttg	ggt	gta	gcg	att	att	ttt	tta	ggg	103
Phe	Phe	Glu	Ile	Leu	Val	Val	Leu	Val	Val	Ala	Ile	Ile	Phe	Leu	Gly	
				10					15					20		
cca	gaa	aaa	ttc	ccc	cag	gct	gtc	gtg	gat	gtg	gtg	aag	ttt	ttt	cgc	151
Pro	Glu	Lys	Phe	Pro	Gln	Ala	Val	Val	Asp	Val	Val	Lys	Phe	Phe	Arg	
			25					30					35			
gcg	ggt	aaa	aaa	acg	ctc	aat	gac	gct	aag	gac	act	tta	gat	aaa	gaa	199
Ala	Val	Lys	Lys	Thr	Leu	Asn	Asp	Ala	Lys	Asp	Thr	Leu	Asp	Lys	Glu	
		40					45					50				
atc	aat	att	gaa	gaa	atc	aaa	aaa	gaa	acc	cta	gag	tat	caa	aag	ctc	247
Ile	Asn	Ile	Glu	Glu	Ile	Lys	Lys	Glu	Thr	Leu	Glu	Tyr	Gln	Lys	Leu	
	55					60					65					
ttt	gaa	aac	aaa	gtg	gag	agt	ctt	aag	ggc	ggt	aag	att	gaa	gaa	tta	295
Phe	Glu	Asn	Lys	Val	Glu	Ser	Leu	Lys	Gly	Val	Lys	Ile	Glu	Glu	Leu	
70					75					80					85	
gaa	gac	gct	aaa	gtg	act	gca	gaa	aat	gag	att	aaa	agc	att	cag	gat	343
Glu	Asp	Ala	Lys	Val	Thr	Ala	Glu	Asn	Glu	Ile	Lys	Ser	Ile	Gln	Asp	
				90					95					100		
ttg	atg	caa	gat	tac	caa	aaa	agc	tta	gaa	acc	aac	aca	atc	cct	aac	391
Leu	Met	Gln	Asp	Tyr	Gln	Lys	Ser	Leu	Glu	Thr	Asn	Thr	Ile	Pro	Asn	
			105					110					115			
cat	tta	aac	gaa	gaa	ggt	tcc	aat	gaa	gaa	gcc	tta	aac	aaa	gaa	ggt	439
His	Leu	Asn	Glu	Glu	Val	Ser	Asn	Glu	Glu	Ala	Leu	Asn	Lys	Glu	Val	
		120					125					130				
tca	agc	gat	gaa	tcc	cct	aaa	gaa	gtc	caa	tta	gca	acc	gat	aac	aac	487
Ser	Ser	Asp	Glu	Ser	Pro	Lys	Glu	Val	Gln	Leu	Ala	Thr	Asp	Asn	Asn	
	135					140					145					
acc	aaa	gaa	cac	gac	aaa	gaa	aaa	gag	aat	ggt	tgaagattta	aaaccgcatt				540
Thr	Lys	Glu	His	Asp	Lys	Glu	Lys	Glu	Asn	Val						

tacaggaatt aaqaaqcgt ttgatggt 568

```
<210> 230
<211> 160
<212> PRT
<213> Helicobacter pylori
```

<400> 230															
Met	Phe	Gly	Met	Gly	Phe	Phe	Glu	Ile	Leu	Val	Val	Leu	Val	Val	Ala
1				5					10					15	
Ile	Ile	Phe	Leu	Gly	Pro	Glu	Lys	Phe	Pro	Gln	Ala	Val	Val	Asp	Val
			20					25					30		
Val	Lys	Phe	Phe	Arg	Ala	Val	Lys	Lys	Thr	Leu	Asn	Asp	Ala	Lys	Asp
		35					40					45			
Thr	Leu	Asp	Lys	Glu	Ile	Asn	Ile	Glu	Glu	Ile	Lys	Lys	Glu	Thr	Leu
	50					55					60				
Glu	Tyr	Gln	Lys	Leu	Phe	Glu	Asn	Lys	Val	Glu	Ser	Leu	Lys	Gly	Val
65				70					75					80	
Lys	Ile	Glu	Glu	Leu	Glu	Asp	Ala	Lys	Val	Thr	Ala	Glu	Asn	Glu	Ile
				85					90					95	
Lys	Ser	Ile	Gln	Asp	Leu	Met	Gln	Asp	Tyr	Gln	Lys	Ser	Leu	Glu	Thr
			100					105					110		
Asn	Thr	Ile	Pro	Asn	His	Leu	Asn	Glu	Glu	Val	Ser	Asn	Glu	Glu	Ala
			115				120					125			
Leu	Asn	Lys	Glu	Val	Ser	Ser	Asp	Glu	Ser	Pro	Lys	Glu	Val	Gln	Leu
	130					135					140				
Ala	Thr	Asp	Asn	Asn	Thr	Lys	Glu	His	Asp	Lys	Glu	Lys	Glu	Asn	Val
145				150					155					160	

```
<210> 231
<211> 359
<212> DNA
<213> Helicobacter pylori
```

```
<220>
<221> CDS
<222> (46) ... (324)
```

```
<400> 231
taaaggcgag cagttaaaag atgaaatcgc ttgtaaagac actga atg ctt tat gca 57
                               Met Leu Tyr Ala
                               1
```

tca aaa acg agt tta ttt tta caa atc aaa gga aag ttt atg tta aga 105
Ser Lys Thr Ser Leu Phe Leu Gln Ile Lys Gly Lys Phe Met Leu Arg
5 10 15 20

att tta atc ccc ttg ctc att att gtg tgg gtt tta tgg cgt ttg ttt 153
Ile Leu Ile Pro Leu Leu Ile Ile Val Trp Val Leu Trp Arg Leu Phe
25 30 35

ttg agg caa aaa ccc cct aaa gac aac cac tct tac acg caa caa acc 201
Leu Arg Gln Lys Pro Pro Lys Asp Asn His Ser Tyr Thr Gln Gln Thr
40 45 50

cct aaa gaa tta gaa gat cac atg att qta tgc tct aaa tgc caa acc 249

Pro Lys Glu Leu Glu Asp His Met Ile Val Cys Ser Lys Cys Gln Thr
55 60 65
tat gtc tct agc aaa gac gct att tat agc ggg gcg gtg gcg tat tgc 297
Tyr Val Ser Ser Lys Asp Ala Ile Tyr Ser Gly Ala Val Ala Tyr Cys
70 75 80
agt gaa acc tgt ttg aag gat aag agg taaatatgct tatttttagga 344
Ser Glu Thr Cys Leu Lys Asp Lys Arg
85 90
caccctttaa tccct 359

<210> 232
<211> 93
<212> PRT
<213> Helicobacter pylori

<400> 232
Met Leu Tyr Ala Ser Lys Thr Ser Leu Phe Leu Gln Ile Lys Gly Lys
1 5 10 15
Phe Met Leu Arg Ile Leu Ile Pro Leu Leu Ile Ile Val Trp Val Leu
20 25 30
Trp Arg Leu Phe Leu Arg Gln Lys Pro Pro Lys Asp Asn His Ser Tyr
35 40 45
Thr Gln Gln Thr Pro Lys Glu Leu Glu Asp His Met Ile Val Cys Ser
50 55 60
Lys Cys Gln Thr Tyr Val Ser Ser Lys Asp Ala Ile Tyr Ser Gly Ala
65 70 75 80
Val Ala Tyr Cys Ser Glu Thr Cys Leu Lys Asp Lys Arg
85 90

<210> 233
<211> 814
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (31)...(765)

<400> 233
taaaaaaaca ccaataaatt aaggattata atg aaa cca acg aac gaa cct aaa 54
Met Lys Pro Thr Asn Glu Pro Lys
1 5
aaa cct ttt ttt caa agt ccc att atc ctt gcg gtt ctt gga ggg att 102
Lys Pro Phe Phe Gln Ser Pro Ile Ile Leu Ala Val Leu Gly Gly Ile
10 15 20
tta ctc atc ttt ttt cta cgc tct ttc aat tct gat ggc agt ttt tcg 150
Leu Leu Ile Phe Phe Leu Arg Ser Phe Asn Ser Asp Gly Ser Phe Ser
25 30 35 40
gac aat ttc tta gct tct agc act aaa aat gtg agc tac cat gaa atc 198
Asp Asn Phe Leu Ala Ser Ser Thr Lys Asn Val Ser Tyr His Glu Ile
45 50 55

aaa cag ctc atc agc aat aat gaa gtg gaa aat gtg agt atc ggt caa 246
 Lys Gln Leu Ile Ser Asn Asn Glu Val Glu Asn Val Ser Ile Gly Gln
 60 65 70

act ttg atc aaa gcc agc cat aaa gag ggc aac aat cgt gtg atc tat 294
 Thr Leu Ile Lys Ala Ser His Lys Glu Gly Asn Asn Arg Val Ile Tyr
 75 80 85

atc gct aaa cgg gtg cct gat ttg acc tta gtg cct ttg tta gac gag 342
 Ile Ala Lys Arg Val Pro Asp Leu Thr Leu Val Pro Leu Leu Asp Glu
 90 95 100

aaa aaa atc aat tat tct ggt ttt agc gag tct aac ttt ttt acg gac 390
 Lys Lys Ile Asn Tyr Ser Gly Phe Ser Glu Ser Asn Phe Phe Thr Asp
 105 110 115 120

atg cta ggg tgg ctc atg cct att tta gtg att tta ggg cta tgg atg 438
 Met Leu Gly Trp Leu Met Pro Ile Leu Val Ile Leu Gly Leu Trp Met
 125 130 135

ttt atg gcg aac cgc atg caa aaa aat atg ggt ggg ggt att ttt ggc 486
 Phe Met Ala Asn Arg Met Gln Lys Asn Met Gly Gly Gly Ile Phe Gly
 140 145 150

atg ggg agc gcg aaa aaa ctc att aac gct gaa aaa ccc aat gtg cgt 534
 Met Gly Ser Ala Lys Lys Leu Ile Asn Ala Glu Lys Pro Asn Val Arg
 155 160 165

ttt aat gac atg gca ggc aat gaa gaa gcc aaa gaa gaa gtg gta gaa 582
 Phe Asn Asp Met Ala Gly Asn Glu Glu Ala Lys Glu Glu Val Val Glu
 170 175 180

atc gta gat ttc tta aaa tac cct gaa cga tac gcc aat tta ggg gct 630
 Ile Val Asp Phe Leu Lys Tyr Pro Glu Arg Tyr Ala Asn Leu Gly Ala
 185 190 195 200

aaa atc cct aaa ggc gtg tta tta gta ggg cct cca gga acc ggt aaa 678
 Lys Ile Pro Lys Gly Val Leu Leu Val Gly Pro Pro Gly Thr Gly Lys
 205 210 215

acc ctt tta gcc aaa gcg gta gcc ggc gaa cgc atg tgc cgt ttt tct 726
 Thr Leu Leu Ala Lys Ala Val Ala Gly Glu Arg Met Cys Arg Phe Ser
 220 225 230

cta tgg gag gga gca gtt tca ttg aaa tgt ttg tgg gct taggggcaag 775
 Leu Trp Glu Gly Ala Val Ser Leu Lys Cys Leu Trp Ala
 235 240 245

cagggttagg gatttatttg aaaccgctaa aaaacaagc 814

<210> 234
 <211> 245
 <212> PRT
 <213> Helicobacter pylori

<400> 234
 Met Lys Pro Thr Asn Glu Pro Lys Lys Pro Phe Phe Gln Ser Pro Ile
 1 5 10 15
 Ile Leu Ala Val Leu Gly Gly Ile Leu Leu Ile Phe Phe Leu Arg Ser

			20					25					30				
Phe	Asn	Ser	Asp	Gly	Ser	Phe	Ser	Asp	Asn	Phe	Leu	Ala	Ser	Ser	Thr		
		35						40				45					
Lys	Asn	Val	Ser	Tyr	His	Glu	Ile	Lys	Gln	Leu	Ile	Ser	Asn	Asn	Glu		
	50					55					60						
Val	Glu	Asn	Val	Ser	Ile	Gly	Gln	Thr	Leu	Ile	Lys	Ala	Ser	His	Lys		
65					70					75					80		
Glu	Gly	Asn	Asn	Arg	Val	Ile	Tyr	Ile	Ala	Lys	Arg	Val	Pro	Asp	Leu		
				85					90					95			
Thr	Leu	Val	Pro	Leu	Leu	Asp	Glu	Lys	Lys	Ile	Asn	Tyr	Ser	Gly	Phe		
			100					105					110				
Ser	Glu	Ser	Asn	Phe	Phe	Thr	Asp	Met	Leu	Gly	Trp	Leu	Met	Pro	Ile		
	115						120					125					
Leu	Val	Ile	Leu	Gly	Leu	Trp	Met	Phe	Met	Ala	Asn	Arg	Met	Gln	Lys		
	130					135					140						
Asn	Met	Gly	Gly	Gly	Ile	Phe	Gly	Met	Gly	Ser	Ala	Lys	Lys	Leu	Ile		
145					150				155						160		
Asn	Ala	Glu	Lys	Pro	Asn	Val	Arg	Phe	Asn	Asp	Met	Ala	Gly	Asn	Glu		
				165					170					175			
Glu	Ala	Lys	Glu	Glu	Val	Val	Glu	Ile	Val	Asp	Phe	Leu	Lys	Tyr	Pro		
			180					185					190				
Glu	Arg	Tyr	Ala	Asn	Leu	Gly	Ala	Lys	Ile	Pro	Lys	Gly	Val	Leu	Leu		
	195					200					205						
Val	Gly	Pro	Pro	Gly	Thr	Gly	Lys	Thr	Leu	Leu	Ala	Lys	Ala	Val	Ala		
	210					215					220						
Gly	Glu	Arg	Met	Cys	Arg	Phe	Ser	Leu	Trp	Glu	Gly	Ala	Val	Ser	Leu		
225				230					235						240		
Lys	Cys	Leu	Trp	Ala													
				245													

<210> 235
 <211> 1137
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (59)...(1093)

<400> 235																
aagtgtttgt	atcggtttta	gtgatttctt	gcccttg	gcgc	tttaggattg	ctacgcct										58
atg	agc	att	tta	gta	gcg	aac	cag	aaa	gcg	agt	tct	tta	ggg	tta	ttt	106
Met	Ser	Ile	Leu	Val	Ala	Asn	Gln	Lys	Ala	Ser	Ser	Leu	Gly	Leu	Phe	
1				5					10					15		
ttt	aaa	gac	gct	aaa	agt	tta	gaa	aaa	gca	agg	cta	gtc	aat	acg	atc	154
Phe	Lys	Asp	Ala	Lys	Ser	Leu	Glu	Lys	Ala	Arg	Leu	Val	Asn	Thr	Ile	
			20					25					30			
gtt	ttt	gat	aaa	acc	ggc	acg	ctc	act	aac	ggc	aag	cct	gtc	gtt	aaa	202
Val	Phe	Asp	Lys	Thr	Gly	Thr	Leu	Thr	Asn	Gly	Lys	Pro	Val	Val	Lys	
		35					40					45				
agc	gtt	cat	tct	aag	ata	gaa	tta	tta	gag	tta	ttg	agt	tta	gcg	ctc	250
Ser	Val	His	Ser	Lys	Ile	Glu	Leu	Leu	Glu	Leu	Leu	Ser	Leu	Ala	Leu	
	50					55					60					
agt	att	gaa	aag	agt	agc	gaa	cat	gtc	atc	gct	aaa	ggg	att	gta	gaa	298

Ser 65	Ile	Glu	Lys	Ser	Ser 70	Glu	His	Val	Ile	Ala 75	Lys	Gly	Ile	Val	Glu 80	
tac	gca	aaa	gag	cat	aac	gct	ccc	tta	aaa	gaa	atg	agc	ggg	gtt	aaa	346
Tyr	Ala	Lys	Glu	His 85	Asn	Ala	Pro	Leu	Lys 90	Glu	Met	Ser	Gly	Val 95	Lys	
gtg	aaa	acg	ggt	ttt	ggc	att	agt	gct	aaa	aca	gat	tat	caa	ggc	act	394
Val	Lys	Thr	Gly 100	Phe	Gly	Ile	Ser	Ala 105	Lys	Thr	Asp	Tyr	Gln 110	Gly	Thr	
aaa	gag	att	att	aaa	gta	ggc	aac	agc	gag	ttt	ttt	aac	cct	att	aac	442
Lys	Glu	Ile 115	Ile	Lys	Val	Gly	Asn 120	Ser	Glu	Phe	Phe	Asn 125	Pro	Ile	Asn	
acg	cta	gaa	att	aaa	gaa	aac	ggg	att	tta	gtg	ttt	gtt	ggt	aga	gcg	490
Thr	Leu	Glu	Ile	Lys	Glu	Asn 135	Gly	Ile	Leu	Val 140	Phe	Val	Gly	Arg	Ala	
atc	agt	gaa	aaa	gaa	gac	gag	ctt	tta	ggg	gcg	ttt	gtt	tta	gaa	gat	538
Ile	Ser	Glu	Lys	Glu	Asp 150	Glu	Leu	Leu	Gly	Ala 155	Phe	Val	Leu	Glu	Asp 160	
ttg	ccc	aaa	aaa	ggc	gtg	aaa	gag	cat	atc	gct	caa	atc	aaa	aat	tta	586
Leu	Pro	Lys	Lys 165	Gly	Val	Lys	Glu	His 170	Ile	Ala	Gln	Ile	Lys	Asn 175	Leu	
ggc	att	aac	acc	ttt	ctt	tta	agc	gga	gac	aat	agg	gag	aat	gtc	caa	634
Gly	Ile	Asn 180	Thr	Phe	Leu	Leu	Ser	Gly 185	Asp	Asn	Arg	Glu	Asn 190	Val	Gln	
aaa	tgc	gcg	ttt	gaa	tta	ggg	att	gat	ggt	tat	atc	agc	aac	gct	aaa	682
Lys	Cys	Ala 195	Phe	Glu	Leu	Gly	Ile 200	Asp	Gly	Tyr	Ile	Ser 205	Asn	Ala	Lys	
cca	caa	gac	aag	ctc	aat	aag	atc	aaa	gag	ctt	aag	gaa	aaa	ggg	cag	730
Pro	Gln	Asp 210	Lys	Leu	Asn	Lys 215	Ile	Lys	Glu	Leu	Lys 220	Glu	Lys	Gly	Gln	
atc	gtt	atg	atg	gtg	ggc	gat	ggc	ttg	aat	gac	gct	cct	agt	ctt	gct	778
Ile	Val	Met 225	Met	Val	Gly 230	Asp	Gly	Leu	Asn	Asp 235	Ala	Pro	Ser	Leu	Ala 240	
atg	agc	gat	gtg	gcg	gtg	gtg	atg	gct	aaa	ggg	agc	gat	gtg	agc	gtg	826
Met	Ser	Asp 245	Val	Ala	Val	Val	Met	Ala 250	Lys	Gly	Ser	Asp	Val	Ser 255	Val	
caa	gca	gcg	gac	att	gtg	agt	ttt	aat	aac	gat	att	aaa	tcg	gtt	tat	874
Gln	Ala	Ala 260	Asp	Ile	Val	Ser	Phe 265	Asn	Asn	Asp	Ile	Lys 270	Ser	Val	Tyr	
agc	gcg	att	aaa	tta	agc	cag	gcg	aca	att	aaa	aat	atc	aaa	gaa	aat	922
Ser	Ala	Ile 275	Lys	Leu	Ser	Gln	Ala 280	Thr	Ile	Lys	Asn	Ile 285	Lys	Glu	Asn	
ttg	ttt	tgg	gct	ttt	tgt	tat	aat	agc	gtg	ttc	atc	cct	tta	gct	tgt	970
Leu	Phe	Trp 290	Ala	Phe	Cys	Tyr 295	Asn	Ser	Val	Phe	Ile 300	Pro	Leu	Ala	Cys	

ggg gtt ctt tat aag gct aat ctc atg tta agc ccg gcg att gcg ggt 1018
 Gly Val Leu Tyr Lys Ala Asn Leu Met Leu Ser Pro Ala Ile Ala Gly
 305 310 315 320

tta gcg atg agt tta agc tct gtg agt gtg gtc tta aac tcc caa agg 1066
 Leu Ala Met Ser Leu Ser Ser Val Ser Val Val Leu Asn Ser Gln Arg
 325 330 335

cta agg aat ttt aaa att aag gat cat tgaatgaaag caacttttca 1113
 Leu Arg Asn Phe Lys Ile Lys Asp His
 340 345

agtgccaagc attacttgca acca 1137

<210> 236

<211> 345

<212> PRT

<213> Helicobacter pylori

<400> 236

Met Ser Ile Leu Val Ala Asn Gln Lys Ala Ser Ser Leu Gly Leu Phe
 1 5 10 15
 Phe Lys Asp Ala Lys Ser Leu Glu Lys Ala Arg Leu Val Asn Thr Ile
 20 25 30
 Val Phe Asp Lys Thr Gly Thr Leu Thr Asn Gly Lys Pro Val Val Lys
 35 40 45
 Ser Val His Ser Lys Ile Glu Leu Leu Glu Leu Leu Ser Leu Ala Leu
 50 55 60
 Ser Ile Glu Lys Ser Ser Glu His Val Ile Ala Lys Gly Ile Val Glu
 65 70 75 80
 Tyr Ala Lys Glu His Asn Ala Pro Leu Lys Glu Met Ser Gly Val Lys
 85 90 95
 Val Lys Thr Gly Phe Gly Ile Ser Ala Lys Thr Asp Tyr Gln Gly Thr
 100 105 110
 Lys Glu Ile Ile Lys Val Gly Asn Ser Glu Phe Phe Asn Pro Ile Asn
 115 120 125
 Thr Leu Glu Ile Lys Glu Asn Gly Ile Leu Val Phe Val Gly Arg Ala
 130 135 140
 Ile Ser Glu Lys Glu Asp Glu Leu Leu Gly Ala Phe Val Leu Glu Asp
 145 150 155 160
 Leu Pro Lys Lys Gly Val Lys Glu His Ile Ala Gln Ile Lys Asn Leu
 165 170 175
 Gly Ile Asn Thr Phe Leu Leu Ser Gly Asp Asn Arg Glu Asn Val Gln
 180 185 190
 Lys Cys Ala Phe Glu Leu Gly Ile Asp Gly Tyr Ile Ser Asn Ala Lys
 195 200 205
 Pro Gln Asp Lys Leu Asn Lys Ile Lys Glu Leu Lys Glu Lys Gly Gln
 210 215 220
 Ile Val Met Met Val Gly Asp Gly Leu Asn Asp Ala Pro Ser Leu Ala
 225 230 235 240
 Met Ser Asp Val Ala Val Val Met Ala Lys Gly Ser Asp Val Ser Val
 245 250 255
 Gln Ala Ala Asp Ile Val Ser Phe Asn Asn Asp Ile Lys Ser Val Tyr
 260 265 270
 Ser Ala Ile Lys Leu Ser Gln Ala Thr Ile Lys Asn Ile Lys Glu Asn
 275 280 285
 Leu Phe Trp Ala Phe Cys Tyr Asn Ser Val Phe Ile Pro Leu Ala Cys
 290 295 300
 Gly Val Leu Tyr Lys Ala Asn Leu Met Leu Ser Pro Ala Ile Ala Gly

-260-

155 160 165 575
agg gct tagaattcag ctctctagtt tagaaaattt gattttcc
Arg Ala
170

<210> 238
<211> 171
<212> PRT
<213> Helicobacter pylori

<400> 238
Met Asp Ile Leu Lys Thr Leu Gln Lys His Leu Gly Asp Val Glu Thr
1 5 10 15
Ser Asp Phe Thr Thr Asn Ala Ile Glu Lys Ser Gln Gln Ile Ala Lys
20 25 30
Phe Ser Arg Asp Met Lys Asn Ile Asn Glu Ser Val Gly Ala Leu Gln
35 40 45
Val Leu Gln Ile Ala Cys Lys Lys Leu Phe Asn Lys Ser Met Gly Leu
50 55 60
Glu Asp Lys Asp Ala Leu Gln Ala Ser Ile Ile Lys Gln Glu Leu Arg
65 70 75 80
Glu Ile Val Glu Asn Cys Gln Phe Leu Ala Ser Pro Leu Phe Asp Thr
85 90 95
Gln Leu Asn Ile Ala Ile Asn Asp Glu Ile Phe Ser Met Ile Val Val
100 105 110
Asn Pro Leu Asp Leu Leu Glu Asn Val Gly Glu Phe Gln Ala Tyr Leu
115 120 125
Glu Glu Lys Leu Asn Glu Ile Lys Glu Leu Leu Gly Tyr Leu Ser Glu
130 135 140
Ser Leu Ser Asn Pro Lys Ala Phe Met Pro Ser Phe Ser Asn Gln Ser
145 150 155 160
Leu Lys Asp Leu Leu Ser Asp Asn Leu Arg Ala
165 170

<210> 239
<211> 1025
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (49)...(972)

<400> 239
tttttagcga ttgtgttctt gcatgcattg ggtttagcgt tgctcttt atg gcc aat 57
Met Ala Asn
1
aac gct tcg ttt tat gcg gcg gcg tct atg gcc tac atg cta ggg gca 105
Asn Ala Ser Phe Tyr Ala Ala Ala Ser Met Ala Tyr Met Leu Gly Ala
5 10 15
aag cat gcg ttt gat gcg gat cac atc gct tgc ata gat aac acc att 153
Lys His Ala Phe Asp Ala Asp His Ile Ala Cys Ile Asp Asn Thr Ile
20 25 30 35

aga aag ctc acc caa caa ggc aaa aac gcc tat ggt gtg ggg ttt tac	201
Arg Lys Leu Thr Gln Gln Gly Lys Asn Ala Tyr Gly Val Gly Phe Tyr	
40 45 50	
ttt tct atg ggg cat tca agc gtg gtg att tta atg acc atc atc agc	249
Phe Ser Met Gly His Ser Ser Val Val Ile Leu Met Thr Ile Ile Ser	
55 60 65	
gcg ttt gcg atc gct tgg gct aaa gaa cac acg ccg atg cta gaa gaa	297
Ala Phe Ala Ile Ala Trp Ala Lys Glu His Thr Pro Met Leu Glu Glu	
70 75 80	
ata ggg ggg gta gtg ggg act tta gtt tct ggg ctt ttt ttg ctc att	345
Ile Gly Gly Val Val Gly Thr Leu Val Ser Gly Leu Phe Leu Leu Ile	
85 90 95	
ata ggg cta ttg aat gcg att att ctc ttg gat tta tta aaa ata ttc	393
Ile Gly Leu Leu Asn Ala Ile Ile Leu Leu Asp Leu Leu Lys Ile Phe	
100 105 110 115	
aaa aaa tcg cac tct aat gaa agc cta agc cag caa caa aat gaa gag	441
Lys Lys Ser His Ser Asn Glu Ser Leu Ser Gln Gln Gln Asn Glu Glu	
120 125 130	
atc gag cgg ctc tta acg agt agg ggc ttg ctc aac cgc ttt ttt aaa	489
Ile Glu Arg Leu Leu Thr Ser Arg Gly Leu Leu Asn Arg Phe Phe Lys	
135 140 145	
ccc ttg ttt aat ttt gtc tcc aag tcg tgg cat att tat cct atc ggt	537
Pro Leu Phe Asn Phe Val Ser Lys Ser Trp His Ile Tyr Pro Ile Gly	
150 155 160	
ttt ctt ttt ggg ctg ggt ttt gat acc gct agt gaa atc gcg ctt ttg	585
Phe Leu Phe Gly Leu Gly Phe Asp Thr Ala Ser Glu Ile Ala Leu Leu	
165 170 175	
gcc ctc tct agc agc gcg att aaa gtg agt atg gtg ggc atg ctc tct	633
Ala Leu Ser Ser Ser Ala Ile Lys Val Ser Met Val Gly Met Leu Ser	
180 185 190 195	
tta ccc att ctt ttt gcc gct ggc atg agt ttg ttt gac act tta gat	681
Leu Pro Ile Leu Phe Ala Ala Gly Met Ser Leu Phe Asp Thr Leu Asp	
200 205 210	
ggg gcg ttc atg ctc aag gcg tat gac tgg gcg ttc aaa acc cct tta	729
Gly Ala Phe Met Leu Lys Ala Tyr Asp Trp Ala Phe Lys Thr Pro Leu	
215 220 225	
aga aaa atc tat tac aat atc tct atc acg gcc tta agc gtg ttt atc	777
Arg Lys Ile Tyr Tyr Asn Ile Ser Ile Thr Ala Leu Ser Val Phe Ile	
230 235 240	
gcg ctc ttt att ggc ttg att gag ctt ttt caa gtc gtt agc gag aaa	825
Ala Leu Phe Ile Gly Leu Ile Glu Leu Phe Gln Val Val Ser Glu Lys	
245 250 255	
ctc cat tta aaa ttt gaa aac cgc ctt tta aga gcc tta caa agc ctg	873
Leu His Leu Lys Phe Glu Asn Arg Leu Leu Arg Ala Leu Gln Ser Leu	
260 265 270 275	

gaa ttt aca gac ttg ggc tat tac ttg gtg ggc tta ttt gta ata gcg	921
Glu Phe Thr Asp Leu Gly Tyr Tyr Leu Val Gly Leu Phe Val Ile Ala	
280 285 290	

ttt cta gga tcg ttc ttt tta tgg aaa atc aaa ttt tct aaa cta gag	969
Phe Leu Gly Ser Phe Phe Leu Trp Lys Ile Lys Phe Ser Lys Leu Glu	
295 300 305	

agc tgaattctaa gccctcaaat tatcgcttaa taaatcttta aggctttgat	1022
Ser	

ttg	1025
-----	------

<210> 240
 <211> 308
 <212> PRT
 <213> Helicobacter pylori

<400> 240

Met Ala Asn Asn Ala Ser Phe Tyr Ala Ala Ala Ser Met Ala Tyr Met	
1 5 10 15	
Leu Gly Ala Lys His Ala Phe Asp Ala Asp His Ile Ala Cys Ile Asp	
20 25 30	
Asn Thr Ile Arg Lys Leu Thr Gln Gln Gly Lys Asn Ala Tyr Gly Val	
35 40 45	
Gly Phe Tyr Phe Ser Met Gly His Ser Ser Val Val Ile Leu Met Thr	
50 55 60	
Ile Ile Ser Ala Phe Ala Ile Ala Trp Ala Lys Glu His Thr Pro Met	
65 70 75 80	
Leu Glu Glu Ile Gly Gly Val Val Gly Thr Leu Val Ser Gly Leu Phe	
85 90 95	
Leu Leu Ile Ile Gly Leu Leu Asn Ala Ile Ile Leu Leu Asp Leu Leu	
100 105 110	
Lys Ile Phe Lys Lys Ser His Ser Asn Glu Ser Leu Ser Gln Gln Gln	
115 120 125	
Asn Glu Glu Ile Glu Arg Leu Leu Thr Ser Arg Gly Leu Leu Asn Arg	
130 135 140	
Phe Phe Lys Pro Leu Phe Asn Phe Val Ser Lys Ser Trp His Ile Tyr	
145 150 155 160	
Pro Ile Gly Phe Leu Phe Gly Leu Gly Phe Asp Thr Ala Ser Glu Ile	
165 170 175	
Ala Leu Leu Ala Leu Ser Ser Ser Ala Ile Lys Val Ser Met Val Gly	
180 185 190	
Met Leu Ser Leu Pro Ile Leu Phe Ala Ala Gly Met Ser Leu Phe Asp	
195 200 205	
Thr Leu Asp Gly Ala Phe Met Leu Lys Ala Tyr Asp Trp Ala Phe Lys	
210 215 220	
Thr Pro Leu Arg Lys Ile Tyr Tyr Asn Ile Ser Ile Thr Ala Leu Ser	
225 230 235 240	
Val Phe Ile Ala Leu Phe Ile Gly Leu Ile Glu Leu Phe Gln Val Val	
245 250 255	
Ser Glu Lys Leu His Leu Lys Phe Glu Asn Arg Leu Leu Arg Ala Leu	
260 265 270	
Gln Ser Leu Glu Phe Thr Asp Leu Gly Tyr Tyr Leu Val Gly Leu Phe	
275 280 285	
Val Ile Ala Phe Leu Gly Ser Phe Phe Leu Trp Lys Ile Lys Phe Ser	
290 295 300	

Lys Leu Glu Ser
305

<210> 241
<211> 1034
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (75)...(989)

```

<400> 241
ttgtgaaaga aaatgaagcg ttttttaaaaa tcggtatcaa aaacatcgcc gtggctgaaa 60
tttcttcgcc tttta atg gag ttt tta ggt tca atc gct ata gcg cta gtg 110
          Met Glu Phe Leu Gly Ser Ile Ala Ile Ala Leu Val
                1                5                10

att tat tta ggg ggg aat gaa gtg att aga ggc cat att agc gtg ggg 158
Ile Tyr Leu Gly Gly Asn Glu Val Ile Arg Gly His Ile Ser Val Gly
          15                20                25

gcg ttt ttt tct ttc att acg gcc ctt ttt atg ctc tat acg ccg att 206
Ala Phe Phe Ser Phe Ile Thr Ala Leu Phe Met Leu Tyr Thr Pro Ile
          30                35                40

aaa cgc tta act agg att gtt tct aat ttt caa gaa gcc tta gtc gct 254
Lys Arg Leu Thr Arg Ile Val Ser Asn Phe Gln Glu Ala Leu Val Ala
          45                50                55                60

agc gac agg atc cat gag att tta gaa aga gag ccg gct att gtt gat 302
Ser Asp Arg Ile His Glu Ile Leu Glu Arg Glu Pro Ala Ile Val Asp
          65                70                75

ggg gaa ttg acg cta aat aac gcc ata cac acc ata gaa ttt aaa aag 350
Gly Glu Leu Thr Leu Asn Asn Ala Ile His Thr Ile Glu Phe Lys Lys
          80                85                90

gta tgg ctg gct tat acg cta gac aat caa gag cgt tat gtt tta aac 398
Val Trp Leu Ala Tyr Thr Leu Asp Asn Gln Glu Arg Tyr Val Leu Asn
          95                100                105

gat att agt ttg aag ttc caa caa aat gaa atc atc gct tta aag ggc 446
Asp Ile Ser Leu Lys Phe Gln Gln Asn Glu Ile Ile Ala Leu Lys Gly
          110                115                120

gaa agc ggg agc ggt aaa agc tca tta gtg aat ctg atc tta cgc ctt 494
Glu Ser Gly Ser Gly Lys Ser Ser Leu Val Asn Leu Ile Leu Arg Leu
          125                130                135                140

tat gag cca agc aaa ggc gaa att ttc atc aac gat caa aaa ata gag 542
Tyr Glu Pro Ser Lys Gly Glu Ile Phe Ile Asn Asp Gln Lys Ile Glu
          145                150                155

agc atc act caa aaa tcc tta aga gaa aag att agc gtt gtc act caa 590
Ser Ile Thr Gln Lys Ser Leu Arg Glu Lys Ile Ser Val Val Thr Gln
          160                165                170

```

agg gtg ttt att ttt aac ggg agc gtg gct gaa aat gtg gcg tat ggt	638
Arg Val Phe Ile Phe Asn Gly Ser Val Ala Glu Asn Val Ala Tyr Gly	
175 180 185	
tta gaa att gat gag gta aaa atc aaa gaa tgc cta aaa aaa gct caa	686
Leu Glu Ile Asp Glu Val Lys Ile Lys Glu Cys Leu Lys Lys Ala Gln	
190 195 200	
gcc tta gat ttt gtt gaa aaa atg cct cat ggg ata gag agc gtt tta	734
Ala Leu Asp Phe Val Glu Lys Met Pro His Gly Ile Glu Ser Val Leu	
205 210 215 220	
gat gaa ttt ggc gct aat ctt agc ggc ggc caa cgc caa aga atc gcc	782
Asp Glu Phe Gly Ala Asn Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala	
225 230 235	
att gca aga gct ttg tat aaa gac gtt caa gtt tta atc ttt gat gaa	830
Ile Ala Arg Ala Leu Tyr Lys Asp Val Gln Val Leu Ile Phe Asp Glu	
240 245 250	
gcc act tcc gct tta gac aat aac aca gaa gag agc gtt aaa caa agc	878
Ala Thr Ser Ala Leu Asp Asn Asn Thr Glu Glu Ser Val Lys Gln Ser	
255 260 265	
att tta gaa ttg aaa caa aac cgc ttg atc att ctt att tcg cac aac	926
Ile Leu Glu Leu Lys Gln Asn Arg Leu Ile Ile Leu Ile Ser His Asn	
270 275 280	
cca agc acg cta aaa tta gcc act aag cat gtg aaa tta gag cat ggg	974
Pro Ser Thr Leu Lys Leu Ala Thr Lys His Val Lys Leu Glu His Gly	
285 290 295 300	
cgt ttg aca gaa tgc taagggtttt aagcggttggt gttgctttta ttttactagg	1029
Arg Leu Thr Glu Cys	
305	
gtgtc	1034
<210> 242	
<211> 305	
<212> PRT	
<213> Helicobacter pylori	
<400> 242	
Met Glu Phe Leu Gly Ser Ile Ala Ile Ala Leu Val Ile Tyr Leu Gly	
1 5 10 15	
Gly Asn Glu Val Ile Arg Gly His Ile Ser Val Gly Ala Phe Phe Ser	
20 25 30	
Phe Ile Thr Ala Leu Phe Met Leu Tyr Thr Pro Ile Lys Arg Leu Thr	
35 40 45	
Arg Ile Val Ser Asn Phe Gln Glu Ala Leu Val Ala Ser Asp Arg Ile	
50 55 60	
His Glu Ile Leu Glu Arg Glu Pro Ala Ile Val Asp Gly Glu Leu Thr	
65 70 75 80	
Leu Asn Asn Ala Ile His Thr Ile Glu Phe Lys Lys Val Trp Leu Ala	
85 90 95	
Tyr Thr Leu Asp Asn Gln Glu Arg Tyr Val Leu Asn Asp Ile Ser Leu	
100 105 110	
Lys Phe Gln Gln Asn Glu Ile Ile Ala Leu Lys Gly Glu Ser Gly Ser	

		115					120				125					
Gly	Lys	Ser	Ser	Leu	Val	Asn	Leu	Ile	Leu	Arg	Leu	Tyr	Glu	Pro	Ser	
	130					135					140					
Lys	Gly	Glu	Ile	Phe	Ile	Asn	Asp	Gln	Lys	Ile	Glu	Ser	Ile	Thr	Gln	
145					150					155					160	
Lys	Ser	Leu	Arg	Glu	Lys	Ile	Ser	Val	Val	Thr	Gln	Arg	Val	Phe	Ile	
				165					170						175	
Phe	Asn	Gly	Ser	Val	Ala	Glu	Asn	Val	Ala	Tyr	Gly	Leu	Glu	Ile	Asp	
			180					185					190			
Glu	Val	Lys	Ile	Lys	Glu	Cys	Leu	Lys	Lys	Ala	Gln	Ala	Leu	Asp	Phe	
	195					200					205					
Val	Glu	Lys	Met	Pro	His	Gly	Ile	Glu	Ser	Val	Leu	Asp	Glu	Phe	Gly	
	210					215					220					
Ala	Asn	Leu	Ser	Gly	Gly	Gln	Arg	Gln	Arg	Ile	Ala	Ile	Ala	Arg	Ala	
225				230						235					240	
Leu	Tyr	Lys	Asp	Val	Gln	Val	Leu	Ile	Phe	Asp	Glu	Ala	Thr	Ser	Ala	
				245					250					255		
Leu	Asp	Asn	Asn	Thr	Glu	Glu	Ser	Val	Lys	Gln	Ser	Ile	Leu	Glu	Leu	
		260					265					270				
Lys	Gln	Asn	Arg	Leu	Ile	Ile	Leu	Ile	Ser	His	Asn	Pro	Ser	Thr	Leu	
	275					280					285					
Lys	Leu	Ala	Thr	Lys	His	Val	Lys	Leu	Glu	His	Gly	Arg	Leu	Thr	Glu	
	290					295					300					

Cys
305

<210> 243
 <211> 604
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (99)...(563)

<400> 243
 ttttatttttc ttcttttagtg gtggcctttaa gcacggcttg ggggacttat ttagtcaagc 60
 ccacttttaga tgaaattttt atcaataaag acactcac atg ctc aaa atc ctg cct 116
 Met Leu Lys Ile Leu Pro
 1 5

ttt tta gtg att ttg gcg tat ttg ggt aag agt ggg ggc atg tat tta 164
 Phe Leu Val Ile Leu Ala Tyr Leu Gly Lys Ser Gly Gly Met Tyr Leu
 10 15 20

ggc act tat ttc acc aac ttc att ggg ctt gat att gtc aaa aaa ata 212
 Gly Thr Tyr Phe Thr Asn Phe Ile Gly Leu Asp Ile Val Lys Lys Ile
 25 30 35

cgc aac act atg cta gaa agc ctt ctt aaa atg gaa atg gat ttt ttt 260
 Arg Asn Thr Met Leu Glu Ser Leu Leu Lys Met Glu Met Asp Phe Phe
 40 45 50

aac agg acg aaa aag ggc gaa ttg atc gca agg atc acc aat gat ata 308
 Asn Arg Thr Lys Lys Gly Glu Leu Ile Ala Arg Ile Thr Asn Asp Ile
 55 60 65 70

ggg ttg att aga gcg agt ttg tcc aat tac ctt tca gag agc ata aga 356

Gly	Leu	Ile	Arg	Ala	Ser	Leu	Ser	Asn	Tyr	Leu	Ser	Glu	Ser	Ile	Arg		
				75					80					85			
gag	ggg	cta	acg	att	gtt	ggg	tta	gtg	ggg	gtg	gtg	atc	tat	caa	agc	404	
Glu	Gly	Leu	Thr	Ile	Val	Gly	Leu	Val	Gly	Val	Val	Ile	Tyr	Gln	Ser		
			90					95					100				
cct	aaa	tta	gcg	tta	gtg	ggg	tta	gtc	atc	atg	ccg	tta	gct	gct	att	452	
Pro	Lys	Leu	Ala	Leu	Val	Gly	Leu	Val	Ile	Met	Pro	Leu	Ala	Ala	Ile		
		105					110					115					
cct	atc	agt	aaa	atc	att	cgt	aag	gtt	aaa	aaa	ctc	gct	aaa	tcc	cat	500	
Pro	Ile	Ser	Lys	Ile	Ile	Arg	Lys	Val	Lys	Lys	Leu	Ala	Lys	Ser	His		
	120					125					130						
caa	gag	agt	aac	gcc	aaa	atc	acc	gct	cgt	ttg	agt	gaa	gtt	ttt	aac	548	
Gln	Glu	Ser	Asn	Ala	Lys	Ile	Thr	Ala	Arg	Leu	Ser	Glu	Val	Phe	Asn		
135					140					145					150		
aac	gtg	gga	agc	gat	taaaatctct	aatggcgaaa	aattagagca	taaggctttt	603								
Asn	Val	Gly	Ser	Asp													
				155													

g 604

<210> 244
 <211> 155
 <212> PRT
 <213> Helicobacter pylori

<400> 244

Met	Leu	Lys	Ile	Leu	Pro	Phe	Leu	Val	Ile	Leu	Ala	Tyr	Leu	Gly	Lys		
1				5					10					15			
Ser	Gly	Gly	Met	Tyr	Leu	Gly	Thr	Tyr	Phe	Thr	Asn	Phe	Ile	Gly	Leu		
			20					25					30				
Asp	Ile	Val	Lys	Lys	Ile	Arg	Asn	Thr	Met	Leu	Glu	Ser	Leu	Leu	Lys		
		35					40					45					
Met	Glu	Met	Asp	Phe	Phe	Asn	Arg	Thr	Lys	Lys	Gly	Glu	Leu	Ile	Ala		
	50					55					60						
Arg	Ile	Thr	Asn	Asp	Ile	Gly	Leu	Ile	Arg	Ala	Ser	Leu	Ser	Asn	Tyr		
65					70				75					80			
Leu	Ser	Glu	Ser	Ile	Arg	Glu	Gly	Leu	Thr	Ile	Val	Gly	Leu	Val	Gly		
				85				90						95			
Val	Val	Ile	Tyr	Gln	Ser	Pro	Lys	Leu	Ala	Leu	Val	Gly	Leu	Val	Ile		
			100					105					110				
Met	Pro	Leu	Ala	Ala	Ile	Pro	Ile	Ser	Lys	Ile	Ile	Arg	Lys	Val	Lys		
		115					120					125					
Lys	Leu	Ala	Lys	Ser	His	Gln	Glu	Ser	Asn	Ala	Lys	Ile	Thr	Ala	Arg		
	130					135					140						
Leu	Ser	Glu	Val	Phe	Asn	Asn	Val	Gly	Ser	Asp							
145					150					155							

<210> 245
 <211> 789
 <212> DNA
 <213> Helicobacter pylori

<220>

<221> CDS
 <222> (34)...(738)

<400> 245

```

tttcgcttat caagtcccc tacctcaatt tta atg cgc tta gat tac gcc tta 54
                                Met Arg Leu Asp Tyr Ala Leu
                                1           5

ttc agt cag cat tta gta aat agc aga gaa aaa gct aaa gcg ttg gtt 102
Phe Ser Gln His Leu Val Asn Ser Arg Glu Lys Ala Lys Ala Leu Val
          10           15           20

tta aaa aat cag gtt tta gtc aat aaa atg gtg gtt tcc aaa ccc tct 150
Leu Lys Asn Gln Val Leu Val Asn Lys Met Val Val Ser Lys Pro Ser
          25           30           35

ttt ata gtg aaa gag aac gat aaa att gaa ctc atc gct gaa aaa ctt 198
Phe Ile Val Lys Glu Asn Asp Lys Ile Glu Leu Ile Ala Glu Lys Leu
          40           45           50           55

ttc gtt agc agg gct ggg gaa aaa tta ggg gct ttt tta gaa acc cat 246
Phe Val Ser Arg Ala Gly Glu Lys Leu Gly Ala Phe Leu Glu Thr His
          60           65           70

ttc gtg gat ttt aag gga aag gtg gtt tta gat gtg gga gcg agc aaa 294
Phe Val Asp Phe Lys Gly Lys Val Val Leu Asp Val Gly Ala Ser Lys
          75           80           85

ggg ggc ttt agt caa gtg gct ctt tta aaa ggg gct aaa aga gtg ctt 342
Gly Gly Phe Ser Gln Val Ala Leu Leu Lys Gly Ala Lys Arg Val Leu
          90           95           100

tgc gtg gat gtg ggg aaa atg caa tta gat gaa agt ttg aaa caa gac 390
Cys Val Asp Val Gly Lys Met Gln Leu Asp Glu Ser Leu Lys Gln Asp
          105           110           115

aag cgc ata gaa tgt tac gaa gaa tgc gat att aga ggg ttt aaa acg 438
Lys Arg Ile Glu Cys Tyr Glu Glu Cys Asp Ile Arg Gly Phe Lys Thr
          120           125           130           135

cca gaa aca att gat tta gcg ctt tgc gat gtg agc ttt att tct tta 486
Pro Glu Thr Ile Asp Leu Ala Leu Cys Asp Val Ser Phe Ile Ser Leu
          140           145           150

tat tat att tta gaa gcg att ttg cct tta agc gat gaa ttt tta aca 534
Tyr Tyr Ile Leu Glu Ala Ile Leu Pro Leu Ser Asp Glu Phe Leu Thr
          155           160           165

ctt ttc aaa ccg caa ttt gaa gtg ggc aga gga ata aaa cgc aat aaa 582
Leu Phe Lys Pro Gln Phe Glu Val Gly Arg Gly Ile Lys Arg Asn Lys
          170           175           180

aaa ggg gtg gtg gtg gat aaa gaa gcc att ttg aac gct tta gaa aac 630
Lys Gly Val Val Val Asp Lys Glu Ala Ile Leu Asn Ala Leu Glu Asn
          185           190           195

ttt aaa aac cat tta aaa aca aag gat ttt caa atc tta aag atc caa 678
Phe Lys Asn His Leu Lys Thr Lys Asp Phe Gln Ile Leu Lys Ile Gln
          200           205           210           215

```


gaa agc tta gtg aaa ggg aaa aac ggg aat gtt gaa ttt ttt atc cat 726
 Glu Ser Leu Val Lys Gly Lys Asn Gly Asn Val Glu Phe Phe Ile His
 220 225 230

ttc aag cga gcc taaaattaaa agcctagcta tcggttaaatt tgacggcttg 778
 Phe Lys Arg Ala
 235

catttagggc a 789

<210> 246
 <211> 235
 <212> PRT
 <213> *Helicobacter pylori*

<400> 246
 Met Arg Leu Asp Tyr Ala Leu Phe Ser Gln His Leu Val Asn Ser Arg
 1 5 10 15
 Glu Lys Ala Lys Ala Leu Val Leu Lys Asn Gln Val Leu Val Asn Lys
 20 25 30
 Met Val Val Ser Lys Pro Ser Phe Ile Val Lys Glu Asn Asp Lys Ile
 35 40 45
 Glu Leu Ile Ala Glu Lys Leu Phe Val Ser Arg Ala Gly Glu Lys Leu
 50 55 60
 Gly Ala Phe Leu Glu Thr His Phe Val Asp Phe Lys Gly Lys Val Val
 65 70 75 80
 Leu Asp Val Gly Ala Ser Lys Gly Gly Phe Ser Gln Val Ala Leu Leu
 85 90 95
 Lys Gly Ala Lys Arg Val Leu Cys Val Asp Val Gly Lys Met Gln Leu
 100 105 110
 Asp Glu Ser Leu Lys Gln Asp Lys Arg Ile Glu Cys Tyr Glu Glu Cys
 115 120 125
 Asp Ile Arg Gly Phe Lys Thr Pro Glu Thr Ile Asp Leu Ala Leu Cys
 130 135 140
 Asp Val Ser Phe Ile Ser Leu Tyr Tyr Ile Leu Glu Ala Ile Leu Pro
 145 150 155 160
 Leu Ser Asp Glu Phe Leu Thr Leu Phe Lys Pro Gln Phe Glu Val Gly
 165 170 175
 Arg Gly Ile Lys Arg Asn Lys Lys Gly Val Val Val Asp Lys Glu Ala
 180 185 190
 Ile Leu Asn Ala Leu Glu Asn Phe Lys Asn His Leu Lys Thr Lys Asp
 195 200 205
 Phe Gln Ile Leu Lys Ile Gln Glu Ser Leu Val Lys Gly Lys Asn Gly
 210 215 220
 Asn Val Glu Phe Phe Ile His Phe Lys Arg Ala
 225 230 235

<210> 247
 <211> 906
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (19) ... (858)

<400> 247

tgaaagggaa aaacggga atg ttg aat ttt tta tcc att tca agc gag cct	51
Met Leu Asn Phe Leu Ser Ile Ser Ser Glu Pro	
1 5 10	
aaa att aaa agc cta gct atc ggt aaa ttt gac ggc ttg cat tta ggg	99
Lys Ile Lys Ser Leu Ala Ile Gly Lys Phe Asp Gly Leu His Leu Gly	
15 20 25	
cat caa gcc ctt ttt aaa gag tta aaa gat ccc aaa gcc ctt tta atc	147
His Gln Ala Leu Phe Lys Glu Leu Lys Asp Pro Lys Ala Leu Leu Ile	
30 35 40	
ata gaa aaa aaa cat tac act aaa ggc tat tta acc ccc cta aaa tac	195
Ile Glu Lys Lys His Tyr Thr Lys Gly Tyr Leu Thr Pro Leu Lys Tyr	
45 50 55	
cgc gct aaa ctc gtg ggc atg cct tta ttt ttt gtg tat tta gaa gag	243
Arg Ala Lys Leu Val Gly Met Pro Leu Phe Phe Val Tyr Leu Glu Glu	
60 65 70 75	
att tca caa tta aac gcc cta gat ttt tta gat ctt tta aaa aag aaa	291
Ile Ser Gln Leu Asn Ala Leu Asp Phe Leu Asp Leu Leu Lys Lys Lys	
80 85 90	
ttt ccc cat tta gaa cgc ctg gtc gtg ggc tat gat ttc agg ttt ggg	339
Phe Pro His Leu Glu Arg Leu Val Val Gly Tyr Asp Phe Arg Phe Gly	
95 100 105	
cat gag agg caa aat gac gct tta ttt tta aaa gag cgt ttt gaa aaa	387
His Glu Arg Gln Asn Asp Ala Leu Phe Leu Lys Glu Arg Phe Glu Lys	
110 115 120	
acc att att gtg cct gaa gtg aaa gtc caa gag att agc gtg cat tct	435
Thr Ile Ile Val Pro Glu Val Lys Val Gln Glu Ile Ser Val His Ser	
125 130 135	
aag atg atc aaa cta gcc cta agt cat ggc gac tta tct tta gct aac	483
Lys Met Ile Lys Leu Ala Leu Ser His Gly Asp Leu Ser Leu Ala Asn	
140 145 150 155	
aag ctc tta ggc aga cct tat gaa gtg tgt ggg gaa gtc att agt gat	531
Lys Leu Leu Gly Arg Pro Tyr Glu Val Cys Gly Glu Val Ile Ser Asp	
160 165 170	
caa ggt ttg ggg cat aaa gaa tta gca ccc act tta aat ata aaa act	579
Gln Gly Leu Gly His Lys Glu Leu Ala Pro Thr Leu Asn Ile Lys Thr	
175 180 185	
aaa gat ttt atc ctc cct agt ttt ggg gtg tat gcg agt tta gtg aaa	627
Lys Asp Phe Ile Leu Pro Ser Phe Gly Val Tyr Ala Ser Leu Val Lys	
190 195 200	
ata aaa gat cca att tat caa aaa agc gtg agt ttt ata ggc aat cgc	675
Ile Lys Asp Pro Ile Tyr Gln Lys Ser Val Ser Phe Ile Gly Asn Arg	
205 210 215	
tta agc acg gat caa aat ttc gcc ata gaa tgc cat gtc ctt gat acc	723
Leu Ser Thr Asp Gln Asn Phe Ala Ile Glu Cys His Val Leu Asp Thr	
220 225 230 235	

atc	ata	gaa	aac	ccg	ccc	caa	gaa	atc	gct	ttg	cgt	tggt	gtt	caa	aaa	771
Ile	Ile	Glu	Asn	Pro	Pro	Gln	Glu	Ile	Ala	Leu	Arg	Trp	Val	Gln	Lys	
			240						245					250		

ata	cga	gac	aac	atg	cgt	ttt	tct	tct	tta	aaa	gag	ctt	aaa	aat	cag	819
Ile	Arg	Asp	Asn	Met	Arg	Phe	Ser	Ser	Leu	Lys	Glu	Leu	Lys	Asn	Gln	
			255					260					265			

atc	caa	caa	gac	atc	tta	aga	gcc	aaa	gag	att	ttg	aga	taattttgtgt	868		
Ile	Gln	Gln	Asp	Ile	Leu	Arg	Ala	Lys	Glu	Ile	Leu	Arg				
		270					275					280				

taaaatgact	ctcaaaaacc	ttaaaaatgg	aaaaattt	906
------------	------------	------------	----------	-----

<210> 248
 <211> 280
 <212> PRT
 <213> Helicobacter pylori

<400> 248															
Met	Leu	Asn	Phe	Leu	Ser	Ile	Ser	Ser	Glu	Pro	Lys	Ile	Lys	Ser	Leu
1				5					10					15	
Ala	Ile	Gly	Lys	Phe	Asp	Gly	Leu	His	Leu	Gly	His	Gln	Ala	Leu	Phe
			20					25					30		
Lys	Glu	Leu	Lys	Asp	Pro	Lys	Ala	Leu	Leu	Ile	Ile	Glu	Lys	Lys	His
		35					40					45			
Tyr	Thr	Lys	Gly	Tyr	Leu	Thr	Pro	Leu	Lys	Tyr	Arg	Ala	Lys	Leu	Val
	50					55					60				
Gly	Met	Pro	Leu	Phe	Phe	Val	Tyr	Leu	Glu	Glu	Ile	Ser	Gln	Leu	Asn
65					70					75					80
Ala	Leu	Asp	Phe	Leu	Asp	Leu	Leu	Lys	Lys	Lys	Phe	Pro	His	Leu	Glu
				85					90					95	
Arg	Leu	Val	Val	Gly	Tyr	Asp	Phe	Arg	Phe	Gly	His	Glu	Arg	Gln	Asn
			100					105					110		
Asp	Ala	Leu	Phe	Leu	Lys	Glu	Arg	Phe	Glu	Lys	Thr	Ile	Ile	Val	Pro
		115					120					125			
Glu	Val	Lys	Val	Gln	Glu	Ile	Ser	Val	His	Ser	Lys	Met	Ile	Lys	Leu
	130					135					140				
Ala	Leu	Ser	His	Gly	Asp	Leu	Ser	Leu	Ala	Asn	Lys	Leu	Leu	Gly	Arg
145					150					155					160
Pro	Tyr	Glu	Val	Cys	Gly	Glu	Val	Ile	Ser	Asp	Gln	Gly	Leu	Gly	His
				165					170					175	
Lys	Glu	Leu	Ala	Pro	Thr	Leu	Asn	Ile	Lys	Thr	Lys	Asp	Phe	Ile	Leu
			180					185					190		
Pro	Ser	Phe	Gly	Val	Tyr	Ala	Ser	Leu	Val	Lys	Ile	Lys	Asp	Pro	Ile
		195					200					205			
Tyr	Gln	Lys	Ser	Val	Ser	Phe	Ile	Gly	Asn	Arg	Leu	Ser	Thr	Asp	Gln
	210					215					220				
Asn	Phe	Ala	Ile	Glu	Cys	His	Val	Leu	Asp	Thr	Ile	Ile	Glu	Asn	Pro
225					230					235					240
Pro	Gln	Glu	Ile	Ala	Leu	Arg	Trp	Val	Gln	Lys	Ile	Arg	Asp	Asn	Met
				245					250					255	
Arg	Phe	Ser	Ser	Leu	Lys	Glu	Leu	Lys	Asn	Gln	Ile	Gln	Gln	Asp	Ile
			260					265					270		
Leu	Arg	Ala	Lys	Glu	Ile	Leu	Arg								
		275					280								

<210> 249
 <211> 2627
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (18)...(2582)

```

<400> 249
aaagacatgt gcaaccg atg aaa tct aaa aaa ctt tat ttg gct tta atc      50
                Met Lys Ser Lys Lys Leu Tyr Leu Ala Leu Ile
                  1                5                10

ata ggg gtt tta tta gcg ttt tta acc cta tct tca tgg ctg ggt aat      98
Ile Gly Val Leu Leu Ala Phe Leu Thr Leu Ser Ser Trp Leu Gly Asn
              15                20                25

agc ggt tta gtg ggg cgt ttt ggg gtg tgg ttt gcc gca ctc aat aaa     146
Ser Gly Leu Val Gly Arg Phe Gly Val Trp Phe Ala Ala Leu Asn Lys
              30                35                40

aaa tat ttt ggg cat ctt tca ttc att aat tta ccc tat tta gca tgg     194
Lys Tyr Phe Gly His Leu Ser Phe Ile Asn Leu Pro Tyr Leu Ala Trp
              45                50                55

gtt tta ttc ctt tta tac aag act aaa aac cct ttt aca gaa atc gtt     242
Val Leu Phe Leu Leu Tyr Lys Thr Lys Asn Pro Phe Thr Glu Ile Val
              60                65                70                75

tta gaa aaa act tta ggg cat cta tta ggc att tta tct ttg ctc ttt     290
Leu Glu Lys Thr Leu Gly His Leu Leu Gly Ile Leu Ser Leu Leu Phe
              80                85                90

tta caa tct agc cta tta aat caa ggg gaa atc ggc aac agc gcg cgt     338
Leu Gln Ser Ser Leu Leu Asn Gln Gly Glu Ile Gly Asn Ser Ala Arg
              95                100                105

ttg ttt tta cgc cct ttt ata ggg gat ttt ggg ctt tat gcg ctg ata     386
Leu Phe Leu Arg Pro Phe Ile Gly Asp Phe Gly Leu Tyr Ala Leu Ile
              110                115                120

acg ctt atg gta gtt att tct tat ttg att cta ttc aaa cta ccc cct     434
Thr Leu Met Val Val Ile Ser Tyr Leu Ile Leu Phe Lys Leu Pro Pro
              125                130                135

aaa agc gtt ttt tat cct tat atg aac aaa aca caa aac ctt tta aaa     482
Lys Ser Val Phe Tyr Pro Tyr Met Asn Lys Thr Gln Asn Leu Leu Lys
              140                145                150                155

gag att tac aaa caa tgc tta caa gcc ttt agc cct aat ttt agc cca     530
Glu Ile Tyr Lys Gln Cys Leu Gln Ala Phe Ser Pro Asn Phe Ser Pro
              160                165                170

aaa aaa gag ggt ttt gaa aac acc cca tca gat att caa aaa aaa gaa     578
Lys Lys Glu Gly Phe Glu Asn Thr Pro Ser Asp Ile Gln Lys Lys Glu
              175                180                185

acc aaa aac gac aaa gaa aaa gaa aac cgc aaa gaa aac cct att aat     626

```

Thr	Lys	Asn	Asp	Lys	Glu	Lys	Glu	Asn	Arg	Lys	Glu	Asn	Pro	Ile	Asn		
		190					195					200					
gaa	aac	cac	aaa	acc	cct	aac	gaa	gaa	ccg	ttt	tta	gcg	atc	cct	acc	674	
Glu	Asn	His	Lys	Thr	Pro	Asn	Glu	Glu	Pro	Phe	Leu	Ala	Ile	Pro	Thr		
	205					210				215							
ccc	tat	aac	acg	act	tta	aat	gat	tca	gag	ccg	caa	gaa	ggc	tta	gtc	722	
Pro	Tyr	Asn	Thr	Thr	Leu	Asn	Asp	Ser	Glu	Pro	Gln	Glu	Gly	Leu	Val		
220					225					230					235		
caa	att	tcc	tcc	cac	ccc	cct	acc	cat	tac	acc	att	tac	cct	aaa	aga	770	
Gln	Ile	Ser	Ser	His	Pro	Pro	Thr	His	Tyr	Thr	Ile	Tyr	Pro	Lys	Arg		
				240					245					250			
aac	cga	ttt	gat	gat	ttg	act	aac	ccc	act	aac	ccc	cct	tta	aaa	gaa	818	
Asn	Arg	Phe	Asp	Asp	Leu	Thr	Asn	Pro	Thr	Asn	Pro	Pro	Leu	Lys	Glu		
			255					260					265				
att	aaa	caa	gaa	act	aaa	gaa	aga	gaa	ccc	acg	cct	aca	aaa	gaa	act	866	
Ile	Lys	Gln	Glu	Thr	Lys	Glu	Arg	Glu	Pro	Thr	Pro	Thr	Lys	Glu	Thr		
	270						275					280					
ctt	acg	ccc	acc	acg	ccc	aaa	cct	atc	atg	ccc	aca	ctt	gca	ccc	ata	914	
Leu	Thr	Pro	Thr	Thr	Pro	Lys	Pro	Ile	Met	Pro	Thr	Leu	Ala	Pro	Ile		
	285					290					295						
ata	gaa	aat	gac	aac	aaa	aca	gaa	aac	caa	aaa	acc	ccc	aac	cac	cct	962	
Ile	Glu	Asn	Asp	Asn	Lys	Thr	Glu	Asn	Gln	Lys	Thr	Pro	Asn	His	Pro		
300					305					310					315		
aaa	aaa	gaa	gaa	aac	cca	caa	gaa	aac	acg	caa	gaa	gaa	atg	ata	gaa	1010	
Lys	Lys	Glu	Glu	Asn	Pro	Gln	Glu	Asn	Thr	Gln	Glu	Glu	Met	Ile	Glu		
				320					325					330			
gga	agg	ata	gaa	gaa	atg	ata	aag	gaa	aat	cta	aaa	aaa	gaa	gaa	aaa	1058	
Gly	Arg	Ile	Glu	Glu	Met	Ile	Lys	Glu	Asn	Leu	Lys	Lys	Glu	Glu	Lys		
			335					340					345				
gaa	gtg	caa	aac	gct	cca	aac	ttt	agc	cca	gta	acc	ccc	aca	agc	gct	1106	
Glu	Val	Gln	Asn	Ala	Pro	Asn	Phe	Ser	Pro	Val	Thr	Pro	Thr	Ser	Ala		
		350					355					360					
aaa	aaa	ccc	gtt	atg	gtt	aaa	gaa	ttg	agc	gaa	aat	aaa	gag	ata	tta	1154	
Lys	Lys	Pro	Val	Met	Val	Lys	Glu	Leu	Ser	Glu	Asn	Lys	Glu	Ile	Leu		
	365					370					375						
gac	gga	ttg	gat	tat	ggc	gaa	gtg	caa	aaa	ccc	aaa	gat	tat	gag	ctt	1202	
Asp	Gly	Leu	Asp	Tyr	Gly	Glu	Val	Gln	Lys	Pro	Lys	Asp	Tyr	Glu	Leu		
380					385					390					395		
ccc	acc	acg	caa	tta	ttg	aat	gcg	gtt	tgt	ttg	aaa	gac	act	tct	tta	1250	
Pro	Thr	Thr	Gln	Leu	Leu	Asn	Ala	Val	Cys	Leu	Lys	Asp	Thr	Ser	Leu		
				400					405					410			
gac	gaa	aac	gag	att	gac	caa	aaa	atc	cag	gat	cta	ttg	agc	aaa	ctg	1298	
Asp	Glu	Asn	Glu	Ile	Asp	Gln	Lys	Ile	Gln	Asp	Leu	Leu	Ser	Lys	Leu		
			415					420					425				

cgc acc ttt aaa att gat ggc gat att atc cgc act tat tca ggc cct	1346
Arg Thr Phe Lys Ile Asp Gly Asp Ile Ile Arg Thr Tyr Ser Gly Pro	
430 435 440	
att gta acc act ttt gaa ttc cgc cca gcc cct aac gtt aag gtg agt	1394
Ile Val Thr Thr Phe Glu Phe Arg Pro Ala Pro Asn Val Lys Val Ser	
445 450 455	
cgt att tta ggc ttg agc gat gat tta gcg atg act tta tgc gct gaa	1442
Arg Ile Leu Gly Leu Ser Asp Asp Leu Ala Met Thr Leu Cys Ala Glu	
460 465 470 475	
tcc atc cgc att caa gcc cct att aag ggt aaa gat gtc gtt ggc att	1490
Ser Ile Arg Ile Gln Ala Pro Ile Lys Gly Lys Asp Val Val Gly Ile	
480 485 490	
gaa atc cct aac agc caa agc caa att att tat tta aga gaa att cta	1538
Glu Ile Pro Asn Ser Gln Ser Gln Ile Ile Tyr Leu Arg Glu Ile Leu	
495 500 505	
gag agc gaa ttg ttt caa aaa tcc agc tcg ccc tta act cta gct tta	1586
Glu Ser Glu Leu Phe Gln Lys Ser Ser Ser Pro Leu Thr Leu Ala Leu	
510 515 520	
ggc aaa gac att gtg ggt aac cct ttc atc acg gat tta aaa aag ctc	1634
Gly Lys Asp Ile Val Gly Asn Pro Phe Ile Thr Asp Leu Lys Lys Leu	
525 530 535	
ccc cat ttg ctc atc gct ggc acg aca gga agc ggt aag agc gtg ggc	1682
Pro His Leu Leu Ile Ala Gly Thr Thr Gly Ser Gly Lys Ser Val Gly	
540 545 550 555	
gtg aat gcg atg att tta tcc tta ctt tat aaa aac cct ccc gat caa	1730
Val Asn Ala Met Ile Leu Ser Leu Leu Tyr Lys Asn Pro Pro Asp Gln	
560 565 570	
ctc aaa tta gtg atg atc gat ccc aaa atg gta gaa ttt agt att tat	1778
Leu Lys Leu Val Met Ile Asp Pro Lys Met Val Glu Phe Ser Ile Tyr	
575 580 585	
gcg gat atc cct cat ttg ctc acg ccc att atc acc gac cct aaa aaa	1826
Ala Asp Ile Pro His Leu Leu Thr Pro Ile Ile Thr Asp Pro Lys Lys	
590 595 600	
gct att ggg gct ttg caa agc gtg gct aaa gaa atg gaa cgc cgg tat	1874
Ala Ile Gly Ala Leu Gln Ser Val Ala Lys Glu Met Glu Arg Arg Tyr	
605 610 615	
tct tta atg agc gaa tac aag gtt aaa acc att gat tct tat aat gaa	1922
Ser Leu Met Ser Glu Tyr Lys Val Lys Thr Ile Asp Ser Tyr Asn Glu	
620 625 630 635	
caa gcc cca agt aac ggc gtt gaa gcg ttc ccc tat ttg att gtg gtg	1970
Gln Ala Pro Ser Asn Gly Val Glu Ala Phe Pro Tyr Leu Ile Val Val	
640 645 650	
att gat gaa tta gcg gat tta atg atg aca ggg ggc aaa gaa gcg gag	2018
Ile Asp Glu Leu Ala Asp Leu Met Met Thr Gly Gly Lys Glu Ala Glu	
655 660 665	

ttt cct atc gct aga atc gct caa atg ggg cgc gcg agc ggc tta cac	2066
Phe Pro Ile Ala Arg Ile Ala Gln Met Gly Arg Ala Ser Gly Leu His	
670 675 680	
ctc att gta gcg acc caa cgc cca agc gtg gat gtc gta acc ggc ttg	2114
Leu Ile Val Ala Thr Gln Arg Pro Ser Val Asp Val Val Thr Gly Leu	
685 690 695	
att aaa acc aac ttg cct tca agg gtg agt ttt agg gta ggc act aag	2162
Ile Lys Thr Asn Leu Pro Ser Arg Val Ser Phe Arg Val Gly Thr Lys	
700 705 710 715	
att gat tct aaa gtg att tta gac act gat ggg gcg caa agc ttg tta	2210
Ile Asp Ser Lys Val Ile Leu Asp Thr Asp Gly Ala Gln Ser Leu Leu	
720 725 730	
gga aga ggc gat atg ctc ttt acc ccc cca gga gcg aac ggg tta gtg	2258
Gly Arg Gly Asp Met Leu Phe Thr Pro Pro Gly Ala Asn Gly Leu Val	
735 740 745	
cgc ttg cat gcc ccc ttt gcc act gaa gat gaa atc aaa aaa atc gtg	2306
Arg Leu His Ala Pro Phe Ala Thr Glu Asp Glu Ile Lys Lys Ile Val	
750 755 760	
gat ttt att aaa gcc caa aaa gaa gta caa tac gat aaa gat ttc ttg	2354
Asp Phe Ile Lys Ala Gln Lys Glu Val Gln Tyr Asp Lys Asp Phe Leu	
765 770 775	
cta gaa gaa tca cgc atg cct tta gac acc cct aat tat caa ggc gat	2402
Leu Glu Glu Ser Arg Met Pro Leu Asp Thr Pro Asn Tyr Gln Gly Asp	
780 785 790 795	
gac att tta gaa agg gct aaa gcg gtg att tta gaa aaa aag atc act	2450
Asp Ile Leu Glu Arg Ala Lys Ala Val Ile Leu Glu Lys Lys Ile Thr	
800 805 810	
tct acg agt ttt tta caa cgc caa tta aaa atc ggc tac aac caa gcc	2498
Ser Thr Ser Phe Leu Gln Arg Gln Leu Lys Ile Gly Tyr Asn Gln Ala	
815 820 825	
gct acc att act gac gaa tta gaa gct caa ggc ttt tta tcc cca aga	2546
Ala Thr Ile Thr Asp Glu Leu Glu Ala Gln Gly Phe Leu Ser Pro Arg	
830 835 840	
aac gct aaa ggc aac aga gag att ttg caa aac ttt taggcctttgt	2592
Asn Ala Lys Gly Asn Arg Glu Ile Leu Gln Asn Phe	
845 850 855	
tttcattgga tattggcaaa cattatTTTT gattt	2627
<210> 250	
<211> 855	
<212> PRT	
<213> Helicobacter pylori	
<400> 250	
Met Lys Ser Lys Lys Leu Tyr Leu Ala Leu Ile Ile Gly Val Leu Leu	
1 5 10 15	

Ala	Phe	Leu	Thr	Leu	Ser	Ser	Trp	Leu	Gly	Asn	Ser	Gly	Leu	Val	Gly
			20					25					30		
Arg	Phe	Gly	Val	Trp	Phe	Ala	Ala	Leu	Asn	Lys	Lys	Tyr	Phe	Gly	His
		35				40						45			
Leu	Ser	Phe	Ile	Asn	Leu	Pro	Tyr	Leu	Ala	Trp	Val	Leu	Phe	Leu	Leu
	50				55						60				
Tyr	Lys	Thr	Lys	Asn	Pro	Phe	Thr	Glu	Ile	Val	Leu	Glu	Lys	Thr	Leu
65				70					75						80
Gly	His	Leu	Leu	Gly	Ile	Leu	Ser	Leu	Leu	Phe	Leu	Gln	Ser	Ser	Leu
				85				90						95	
Leu	Asn	Gln	Gly	Glu	Ile	Gly	Asn	Ser	Ala	Arg	Leu	Phe	Leu	Arg	Pro
			100				105						110		
Phe	Ile	Gly	Asp	Phe	Gly	Leu	Tyr	Ala	Leu	Ile	Thr	Leu	Met	Val	Val
		115				120						125			
Ile	Ser	Tyr	Leu	Ile	Leu	Phe	Lys	Leu	Pro	Pro	Lys	Ser	Val	Phe	Tyr
	130				135						140				
Pro	Tyr	Met	Asn	Lys	Thr	Gln	Asn	Leu	Leu	Lys	Glu	Ile	Tyr	Lys	Gln
145				150						155					160
Cys	Leu	Gln	Ala	Phe	Ser	Pro	Asn	Phe	Ser	Pro	Lys	Lys	Glu	Gly	Phe
			165					170						175	
Glu	Asn	Thr	Pro	Ser	Asp	Ile	Gln	Lys	Lys	Glu	Thr	Lys	Asn	Asp	Lys
			180					185					190		
Glu	Lys	Glu	Asn	Arg	Lys	Glu	Asn	Pro	Ile	Asn	Glu	Asn	His	Lys	Thr
		195				200						205			
Pro	Asn	Glu	Glu	Pro	Phe	Leu	Ala	Ile	Pro	Thr	Pro	Tyr	Asn	Thr	Thr
	210				215						220				
Leu	Asn	Asp	Ser	Glu	Pro	Gln	Glu	Gly	Leu	Val	Gln	Ile	Ser	Ser	His
225				230					235						240
Pro	Pro	Thr	His	Tyr	Thr	Ile	Tyr	Pro	Lys	Arg	Asn	Arg	Phe	Asp	Asp
			245					250						255	
Leu	Thr	Asn	Pro	Thr	Asn	Pro	Pro	Leu	Lys	Glu	Ile	Lys	Gln	Glu	Thr
		260				265							270		
Lys	Glu	Arg	Glu	Pro	Thr	Pro	Thr	Lys	Glu	Thr	Leu	Thr	Pro	Thr	Thr
		275				280						285			
Pro	Lys	Pro	Ile	Met	Pro	Thr	Leu	Ala	Pro	Ile	Ile	Glu	Asn	Asp	Asn
	290				295						300				
Lys	Thr	Glu	Asn	Gln	Lys	Thr	Pro	Asn	His	Pro	Lys	Lys	Glu	Glu	Asn
305				310					315						320
Pro	Gln	Glu	Asn	Thr	Gln	Glu	Glu	Met	Ile	Glu	Gly	Arg	Ile	Glu	Glu
			325					330						335	
Met	Ile	Lys	Glu	Asn	Leu	Lys	Lys	Glu	Glu	Lys	Glu	Val	Gln	Asn	Ala
		340						345					350		
Pro	Asn	Phe	Ser	Pro	Val	Thr	Pro	Thr	Ser	Ala	Lys	Lys	Pro	Val	Met
		355				360						365			
Val	Lys	Glu	Leu	Ser	Glu	Asn	Lys	Glu	Ile	Leu	Asp	Gly	Leu	Asp	Tyr
	370				375						380				
Gly	Glu	Val	Gln	Lys	Pro	Lys	Asp	Tyr	Glu	Leu	Pro	Thr	Thr	Gln	Leu
385				390					395						400
Leu	Asn	Ala	Val	Cys	Leu	Lys	Asp	Thr	Ser	Leu	Asp	Glu	Asn	Glu	Ile
			405					410						415	
Asp	Gln	Lys	Ile	Gln	Asp	Leu	Leu	Ser	Lys	Leu	Arg	Thr	Phe	Lys	Ile
			420					425					430		
Asp	Gly	Asp	Ile	Ile	Arg	Thr	Tyr	Ser	Gly	Pro	Ile	Val	Thr	Thr	Phe
		435				440						445			
Glu	Phe	Arg	Pro	Ala	Pro	Asn	Val	Lys	Val	Ser	Arg	Ile	Leu	Gly	Leu
	450				455					460					
Ser	Asp	Asp	Leu	Ala	Met	Thr	Leu	Cys	Ala	Glu	Ser	Ile	Arg	Ile	Gln
465				470					475						480
Ala	Pro	Ile	Lys	Gly	Lys	Asp	Val	Val	Gly	Ile	Glu	Ile	Pro	Asn	Ser

				485					490					495			
Gln	Ser	Gln	Ile	Ile	Tyr	Leu	Arg	Glu	Ile	Leu	Glu	Ser	Glu	Leu	Phe		
			500					505					510				
Gln	Lys	Ser	Ser	Ser	Pro	Leu	Thr	Leu	Ala	Leu	Gly	Lys	Asp	Ile	Val		
		515					520					525					
Gly	Asn	Pro	Phe	Ile	Thr	Asp	Leu	Lys	Lys	Leu	Pro	His	Leu	Leu	Ile		
	530					535					540						
Ala	Gly	Thr	Thr	Gly	Ser	Gly	Lys	Ser	Val	Gly	Val	Asn	Ala	Met	Ile		
545					550					555					560		
Leu	Ser	Leu	Leu	Tyr	Lys	Asn	Pro	Pro	Asp	Gln	Leu	Lys	Leu	Val	Met		
				565					570					575			
Ile	Asp	Pro	Lys	Met	Val	Glu	Phe	Ser	Ile	Tyr	Ala	Asp	Ile	Pro	His		
		580						585					590				
Leu	Leu	Thr	Pro	Ile	Ile	Thr	Asp	Pro	Lys	Lys	Ala	Ile	Gly	Ala	Leu		
		595					600					605					
Gln	Ser	Val	Ala	Lys	Glu	Met	Glu	Arg	Arg	Tyr	Ser	Leu	Met	Ser	Glu		
	610					615					620						
Tyr	Lys	Val	Lys	Thr	Ile	Asp	Ser	Tyr	Asn	Glu	Gln	Ala	Pro	Ser	Asn		
625					630					635					640		
Gly	Val	Glu	Ala	Phe	Pro	Tyr	Leu	Ile	Val	Val	Ile	Asp	Glu	Leu	Ala		
				645					650					655			
Asp	Leu	Met	Met	Thr	Gly	Gly	Lys	Glu	Ala	Glu	Phe	Pro	Ile	Ala	Arg		
		660						665					670				
Ile	Ala	Gln	Met	Gly	Arg	Ala	Ser	Gly	Leu	His	Leu	Ile	Val	Ala	Thr		
		675					680					685					
Gln	Arg	Pro	Ser	Val	Asp	Val	Val	Thr	Gly	Leu	Ile	Lys	Thr	Asn	Leu		
	690					695					700						
Pro	Ser	Arg	Val	Ser	Phe	Arg	Val	Gly	Thr	Lys	Ile	Asp	Ser	Lys	Val		
705					710					715					720		
Ile	Leu	Asp	Thr	Asp	Gly	Ala	Gln	Ser	Leu	Leu	Gly	Arg	Gly	Asp	Met		
			725					730						735			
Leu	Phe	Thr	Pro	Pro	Gly	Ala	Asn	Gly	Leu	Val	Arg	Leu	His	Ala	Pro		
			740					745					750				
Phe	Ala	Thr	Glu	Asp	Glu	Ile	Lys	Lys	Ile	Val	Asp	Phe	Ile	Lys	Ala		
		755					760					765					
Gln	Lys	Glu	Val	Gln	Tyr	Asp	Lys	Asp	Phe	Leu	Leu	Glu	Glu	Ser	Arg		
	770					775					780						
Met	Pro	Leu	Asp	Thr	Pro	Asn	Tyr	Gln	Gly	Asp	Asp	Ile	Leu	Glu	Arg		
785					790					795					800		
Ala	Lys	Ala	Val	Ile	Leu	Glu	Lys	Lys	Ile	Thr	Ser	Thr	Ser	Phe	Leu		
				805					810					815			
Gln	Arg	Gln	Leu	Lys	Ile	Gly	Tyr	Asn	Gln	Ala	Ala	Thr	Ile	Thr	Asp		
			820					825					830				
Glu	Leu	Glu	Ala	Gln	Gly	Phe	Leu	Ser	Pro	Arg	Asn	Ala	Lys	Gly	Asn		
		835					840					845					
Arg	Glu	Ile	Leu	Gln	Asn	Phe											
	850					855											

<210> 251
 <211> 1136
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (51)...(1094)

<400> 251

aaccataaaa acgatacaat agcgggtat	ttt taataaaaaca aggagtttta atg aga	56
	Met Arg	
	1	
ggt caa tct aaa ggt ttt gct att ttt tct aaa gac ggg cat ttc aaa	104	
Val Gln Ser Lys Gly Phe Ala Ile Phe Ser Lys Asp Gly His Phe Lys		
5	10	15
ccc cat gat ttt agc cgc cat gct gta ggc cct aaa gat gtg ttg att	152	
Pro His Asp Phe Ser Arg His Ala Val Gly Pro Lys Asp Val Leu Ile		
20	25	30
gac att ctt tat gca ggg att tgt cat agc gat att cat agc gct tat	200	
Asp Ile Leu Tyr Ala Gly Ile Cys His Ser Asp Ile His Ser Ala Tyr		
35	40	45
agc gaa tgg aaa gaa ggc att tac cct atg gtt cct ggg cat gaa att	248	
Ser Glu Trp Lys Glu Gly Ile Tyr Pro Met Val Pro Gly His Glu Ile		
55	60	65
gct ggg gcc atc aaa gaa gtg ggt aag gaa gtt aag aaa ttt aag gtt	296	
Ala Gly Ala Ile Lys Glu Val Gly Lys Glu Val Lys Lys Phe Lys Val		
70	75	80
ggc gat gtg gtg ggc gtg ggc tgt ttt gtc aat tca tgc aaa gcg tgt	344	
Gly Asp Val Val Gly Val Gly Cys Phe Val Asn Ser Cys Lys Ala Cys		
85	90	95
aag ccc tgt aaa gaa cac caa gag caa ttt tgc gcc aaa gtg gta ttc	392	
Lys Pro Cys Lys Glu His Gln Glu Gln Phe Cys Ala Lys Val Val Phe		
100	105	110
act tac gat tgt ttg gat tat ttc cat gac aac gaa ccc cac atg ggc	440	
Thr Tyr Asp Cys Leu Asp Tyr Phe His Asp Asn Glu Pro His Met Gly		
115	120	125
gga tac tct aat aat att gta gtg gat gaa aac tat gtg att agc gtg	488	
Gly Tyr Ser Asn Asn Ile Val Val Asp Glu Asn Tyr Val Ile Ser Val		
135	140	145
gat aaa aac gct cct tta gaa aaa gta gcc ccc ttg ctt tgt gcg ggc	536	
Asp Lys Asn Ala Pro Leu Glu Lys Val Ala Pro Leu Leu Cys Ala Gly		
150	155	160
atc acc act tat tcg ccc tta aaa ttt tct aag gtt act aaa ggc aca	584	
Ile Thr Thr Tyr Ser Pro Leu Lys Phe Ser Lys Val Thr Lys Gly Thr		
165	170	175
aaa gtt ggc gtc gct ggg ttt ggc ggg cta gga agc atg gcg gtt aaa	632	
Lys Val Gly Val Ala Gly Phe Gly Gly Leu Gly Ser Met Ala Val Lys		
180	185	190
tac gct gtg gct atg ggg gct gaa gtg agc gtt ttt gca aga aac gaa	680	
Tyr Ala Val Ala Met Gly Ala Glu Val Ser Val Phe Ala Arg Asn Glu		
195	200	205
cac aaa aag caa gac gct ttg agc atg ggg gtt aaa cat ttc tac act	728	
His Lys Lys Gln Asp Ala Leu Ser Met Gly Val Lys His Phe Tyr Thr		
215	220	225

gac ccc aaa caa tgc aaa gag gaa ttg gac ttt atc att tca acc att 776
Asp Pro Lys Gln Cys Lys Glu Glu Leu Asp Phe Ile Ile Ser Thr Ile
230 235 240
cct acc cat tat gat tta aaa gac tac ctc aag ctc tta act tat aat 824
Pro Thr His Tyr Asp Leu Lys Asp Tyr Leu Lys Leu Thr Tyr Asn
245 250 255
ggc gat cta gcc ctt gtg gga ctc ccc cct gta gaa atc gct cca gcg 872
Gly Asp Leu Ala Leu Val Gly Leu Pro Pro Val Glu Ile Ala Pro Ala
260 265 270
ctt agc gtt ttt gat ttt atc cat tta ggc aat cgc aag gtt tat ggc 920
Leu Ser Val Phe Asp Phe Ile His Leu Gly Asn Arg Lys Val Tyr Gly
275 280 285 290
tca ttg att ggg ggc att aaa gaa acc caa gaa atg atg gat ttt tct 968
Ser Leu Ile Gly Gly Ile Lys Glu Thr Gln Glu Met Met Asp Phe Ser
295 300 305
atc aaa cac aat att tac cct gaa ata gat ttg atc tta ggc aag gat 1016
Ile Lys His Asn Ile Tyr Pro Glu Ile Asp Leu Ile Leu Gly Lys Asp
310 315 320
att gac acc gct tat cat aat cta acc cat ggg aaa gcg aaa ttc cgc 1064
Ile Asp Thr Ala Tyr His Asn Leu Thr His Gly Lys Ala Lys Phe Arg
325 330 335
tat gtg att gat atg aaa aaa tcg ttt gat taaaagt ttt ggctctagct 1114
Tyr Val Ile Asp Met Lys Lys Ser Phe Asp
340 345
cttttttaag agcttgagtt gg 1136

<210> 252

<211> 348

<212> PRT

<213> *Helicobacter pylori*

<400> 252

Met Arg Val Gln Ser Lys Gly Phe Ala Ile Phe Ser Lys Asp Gly His
1 5 10 15
Phe Lys Pro His Asp Phe Ser Arg His Ala Val Gly Pro Lys Asp Val
20 25 30
Leu Ile Asp Ile Leu Tyr Ala Gly Ile Cys His Ser Asp Ile His Ser
35 40 45
Ala Tyr Ser Glu Trp Lys Glu Gly Ile Tyr Pro Met Val Pro Gly His
50 55 60
Glu Ile Ala Gly Ala Ile Lys Glu Val Gly Lys Glu Val Lys Lys Phe
65 70 75 80
Lys Val Gly Asp Val Val Gly Val Gly Cys Phe Val Asn Ser Cys Lys
85 90 95
Ala Cys Lys Pro Cys Lys Glu His Gln Glu Gln Phe Cys Ala Lys Val
100 105 110
Val Phe Thr Tyr Asp Cys Leu Asp Tyr Phe His Asp Asn Glu Pro His
115 120 125
Met Gly Gly Tyr Ser Asn Asn Ile Val Val Asp Glu Asn Tyr Val Ile
130 135 140

Ser	Val	Asp	Lys	Asn	Ala	Pro	Leu	Glu	Lys	Val	Ala	Pro	Leu	Leu	Cys
145					150					155					160
Ala	Gly	Ile	Thr	Thr	Tyr	Ser	Pro	Leu	Lys	Phe	Ser	Lys	Val	Thr	Lys
				165					170						175
Gly	Thr	Lys	Val	Gly	Val	Ala	Gly	Phe	Gly	Gly	Leu	Gly	Ser	Met	Ala
			180					185					190		
Val	Lys	Tyr	Ala	Val	Ala	Met	Gly	Ala	Glu	Val	Ser	Val	Phe	Ala	Arg
		195					200					205			
Asn	Glu	His	Lys	Lys	Gln	Asp	Ala	Leu	Ser	Met	Gly	Val	Lys	His	Phe
	210					215					220				
Tyr	Thr	Asp	Pro	Lys	Gln	Cys	Lys	Glu	Glu	Leu	Asp	Phe	Ile	Ile	Ser
225					230					235					240
Thr	Ile	Pro	Thr	His	Tyr	Asp	Leu	Lys	Asp	Tyr	Leu	Lys	Leu	Leu	Thr
				245					250					255	
Tyr	Asn	Gly	Asp	Leu	Ala	Leu	Val	Gly	Leu	Pro	Pro	Val	Glu	Ile	Ala
			260					265					270		
Pro	Ala	Leu	Ser	Val	Phe	Asp	Phe	Ile	His	Leu	Gly	Asn	Arg	Lys	Val
		275					280					285			
Tyr	Gly	Ser	Leu	Ile	Gly	Gly	Ile	Lys	Glu	Thr	Gln	Glu	Met	Met	Asp
	290					295					300				
Phe	Ser	Ile	Lys	His	Asn	Ile	Tyr	Pro	Glu	Ile	Asp	Leu	Ile	Leu	Gly
305					310					315					320
Lys	Asp	Ile	Asp	Thr	Ala	Tyr	His	Asn	Leu	Thr	His	Gly	Lys	Ala	Lys
				325					330					335	
Phe	Arg	Tyr	Val	Ile	Asp	Met	Lys	Lys	Ser	Phe	Asp				
			340					345							

<210> 253
 <211> 1378
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (25)...(1317)

<400> 253															
ttaaaaaagg	gtgtttaatt	tttt	atg	act	tca	gct	tca	agc	cat	tct	ttt				51
			Met	Thr	Ser	Ala	Ser	Ser	His	Ser	Phe				
			1				5								
aaa gaa caa gat ttt cat att cct atc gct ttt gct ttt gat aag aat															99
Lys Glu Gln Asp Phe His Ile Pro Ile Ala Phe Ala Phe Asp Lys Asn															
10				15			20							25	
tac ctc att cct gcg ggc gcg tgt ctt tat tcc ttg cta gaa agc atc															147
Tyr Leu Ile Pro Ala Gly Ala Cys Leu Tyr Ser Leu Leu Glu Ser Ile															
			30				35						40		
gct aaa gcc aat aaa aaa atc cgt tac acc cta cac gct tta gtg gta															195
Ala Lys Ala Asn Lys Lys Ile Arg Tyr Thr Leu His Ala Leu Val Val															
			45				50						55		
ggc ttg aat gaa gaa gat aaa gca aag ctt aat caa atc aca gag cct															243
Gly Leu Asn Glu Glu Asp Lys Ala Lys Leu Asn Gln Ile Thr Glu Pro															
			60				65						70		
ttt aaa gaa ttt gcc gct ttg gaa gtg aga gat att gag tct ttt tta															291

Phe	Lys	Glu	Phe	Ala	Ala	Leu	Glu	Val	Arg	Asp	Ile	Glu	Ser	Phe	Leu		
	75					80					85						
gac	act	atc	cct	aac	cct	ttt	gat	gag	gat	ttc	act	aag	cgt	ttt	tct	339	
Asp	Thr	Ile	Pro	Asn	Pro	Phe	Asp	Glu	Asp	Phe	Thr	Lys	Arg	Phe	Ser		
	90				95					100					105		
aaa	atg	gtg	tta	gtg	aag	tat	ttt	ttg	gcg	gat	ttg	ttc	ccc	aaa	tat	387	
Lys	Met	Val	Leu	Val	Lys	Tyr	Phe	Leu	Ala	Asp	Leu	Phe	Pro	Lys	Tyr		
				110					115					120			
tcc	aaa	atg	gtg	tgg	agc	gat	gtg	gat	gtc	atc	ttt	tgc	aat	gaa	ttt	435	
Ser	Lys	Met	Val	Trp	Ser	Asp	Val	Asp	Val	Ile	Phe	Cys	Asn	Glu	Phe		
			125					130					135				
agc	gct	gat	ttc	tta	aac	ctt	gaa	gaa	aat	gat	gag	aat	tat	ttt	tat	483	
Ser	Ala	Asp	Phe	Leu	Asn	Leu	Glu	Glu	Asn	Asp	Glu	Asn	Tyr	Phe	Tyr		
		140					145					150					
gga	gtt	tta	gaa	gtt	gaa	aag	cac	cac	atg	atg	gaa	ggg	ttt	ttg	ttt	531	
Gly	Val	Leu	Glu	Val	Glu	Lys	His	His	Met	Met	Glu	Gly	Phe	Leu	Phe		
	155					160					165						
tgc	aat	tta	gat	tac	cag	cgc	aag	aaa	aat	ttc	acc	tta	aga	atg	cat	579	
Cys	Asn	Leu	Asp	Tyr	Gln	Arg	Lys	Lys	Asn	Phe	Thr	Leu	Arg	Met	His		
	170				175					180					185		
gag	ctt	tta	agg	ggg	aat	gag	gct	aaa	ggg	gag	ttg	gat	ttc	acg	aaa	627	
Glu	Leu	Leu	Arg	Gly	Asn	Glu	Ala	Lys	Gly	Glu	Leu	Asp	Phe	Thr	Lys		
			190						195					200			
tgg	tgt	tgg	cct	aac	atg	aaa	gct	tta	ggg	att	gaa	tat	tgc	gtt	ttc	675	
Trp	Cys	Trp	Pro	Asn	Met	Lys	Ala	Leu	Gly	Ile	Glu	Tyr	Cys	Val	Phe		
			205					210					215				
cct	tat	tat	tac	acc	att	aaa	gat	ttt	tct	aac	gcg	tat	tta	aac	gag	723	
Pro	Tyr	Tyr	Tyr	Thr	Ile	Lys	Asp	Phe	Ser	Asn	Ala	Tyr	Leu	Asn	Glu		
		220					225					230					
aat	tac	aag	aaa	acc	att	tta	gag	gca	cga	gaa	aac	cct	acc	att	atc	771	
Asn	Tyr	Lys	Lys	Thr	Ile	Leu	Glu	Ala	Arg	Glu	Asn	Pro	Thr	Ile	Ile		
		235				240					245						
cac	tat	gac	gct	tgg	tgg	gga	gcg	gtg	aag	cct	tgg	gac	tat	cct	ttt	819	
His	Tyr	Asp	Ala	Trp	Trp	Gly	Ala	Val	Lys	Pro	Trp	Asp	Tyr	Pro	Phe		
					255					260					265		
ggt	tta	aaa	gcg	gat	tta	tgg	ctg	aac	gct	ttg	gct	aaa	acc	cct	ttt	867	
Gly	Leu	Lys	Ala	Asp	Leu	Trp	Leu	Asn	Ala	Leu	Ala	Lys	Thr	Pro	Phe		
				270					275					280			
atg	agc	gat	tgg	att	gat	tcg	atc	gct	agg	gtg	gaa	ata	ggc	agc	gaa	915	
Met	Ser	Asp	Trp	Ile	Asp	Ser	Ile	Ala	Arg	Val	Glu	Ile	Gly	Ser	Glu		
			285					290					295				
aaa	tgg	cat	cgt	tac	cac	agc	atc	gtt	gcc	tat	cac	tac	tac	ttt	ccc	963	
Lys	Trp	His	Arg	Tyr	His	Ser	Ile	Val	Ala	Tyr	His	Tyr	Tyr	Phe	Pro		
		300					305					310					

cta tgg aag act gaa gag cag atc gcc cat gac gca ctc aag acc ttt	1011
Leu Trp Lys Thr Glu Glu Gln Ile Ala His Asp Ala Leu Lys Thr Phe	
315 320 325	
tta gac cat tat ttt tcg tgc atc cat gcc gca atc aag caa gaa aat	1059
Leu Asp His Tyr Phe Ser Cys Ile His Ala Ala Ile Lys Gln Glu Asn	
330 335 340 345	
ctc gga atg ttc ttg aac cac tac ttc tcg cat gcc cat gca gag atc	1107
Leu Gly Met Phe Leu Asn His Tyr Phe Ser His Ala His Ala Glu Ile	
350 355 360	
aaa gaa aac tcc ctt gaa atg ttc ttg aac cac tac ttc tcg cat gtt	1155
Lys Glu Asn Ser Leu Glu Met Phe Leu Asn His Tyr Phe Ser His Val	
365 370 375	
tat agg ctc cct aaa aaa gca cgg aag aga ctc ttt agg gtg ttt gtc	1203
Tyr Arg Leu Pro Lys Lys Ala Arg Lys Arg Leu Phe Arg Val Phe Val	
380 385 390	
aaa cac tgc atc ctc ata cca ctc aag agc ctt gtg ggt aag act cta	1251
Lys His Cys Ile Leu Ile Pro Leu Lys Ser Leu Val Gly Lys Thr Leu	
395 400 405	
cga ctc tta aaa ctc cat gcg cta gct aaa aaa atc cta atc caa ctc	1299
Arg Leu Leu Lys Leu His Ala Leu Ala Lys Lys Ile Leu Ile Gln Leu	
410 415 420 425	
aag ctc tta aaa aag agc tagagccaaa acttttaatc aaacgatttt	1347
Lys Leu Leu Lys Lys Ser	
430	
ttcatatcaa tcacatagcg gaatttcgct t	1378
<210> 254	
<211> 431	
<212> PRT	
<213> Helicobacter pylori	
<400> 254	
Met Thr Ser Ala Ser Ser His Ser Phe Lys Glu Gln Asp Phe His Ile	
1 5 10 15	
Pro Ile Ala Phe Ala Phe Asp Lys Asn Tyr Leu Ile Pro Ala Gly Ala	
20 25 30	
Cys Leu Tyr Ser Leu Leu Glu Ser Ile Ala Lys Ala Asn Lys Lys Ile	
35 40 45	
Arg Tyr Thr Leu His Ala Leu Val Val Gly Leu Asn Glu Glu Asp Lys	
50 55 60	
Ala Lys Leu Asn Gln Ile Thr Glu Pro Phe Lys Glu Phe Ala Ala Leu	
65 70 75 80	
Glu Val Arg Asp Ile Glu Ser Phe Leu Asp Thr Ile Pro Asn Pro Phe	
85 90 95	
Asp Glu Asp Phe Thr Lys Arg Phe Ser Lys Met Val Leu Val Lys Tyr	
100 105 110	
Phe Leu Ala Asp Leu Phe Pro Lys Tyr Ser Lys Met Val Trp Ser Asp	
115 120 125	
Val Asp Val Ile Phe Cys Asn Glu Phe Ser Ala Asp Phe Leu Asn Leu	
130 135 140	
Glu Glu Asn Asp Glu Asn Tyr Phe Tyr Gly Val Leu Glu Val Glu Lys	

145					150					155					160
His	His	Met	Met	Glu	Gly	Phe	Leu	Phe	Cys	Asn	Leu	Asp	Tyr	Gln	Arg
				165					170					175	
Lys	Lys	Asn	Phe	Thr	Leu	Arg	Met	His	Glu	Leu	Leu	Arg	Gly	Asn	Glu
			180					185					190		
Ala	Lys	Gly	Glu	Leu	Asp	Phe	Thr	Lys	Trp	Cys	Trp	Pro	Asn	Met	Lys
		195					200					205			
Ala	Leu	Gly	Ile	Glu	Tyr	Cys	Val	Phe	Pro	Tyr	Tyr	Tyr	Thr	Ile	Lys
	210					215					220				
Asp	Phe	Ser	Asn	Ala	Tyr	Leu	Asn	Glu	Asn	Tyr	Lys	Lys	Thr	Ile	Leu
225					230					235					240
Glu	Ala	Arg	Glu	Asn	Pro	Thr	Ile	Ile	His	Tyr	Asp	Ala	Trp	Trp	Gly
				245					250					255	
Ala	Val	Lys	Pro	Trp	Asp	Tyr	Pro	Phe	Gly	Leu	Lys	Ala	Asp	Leu	Trp
			260					265					270		
Leu	Asn	Ala	Leu	Ala	Lys	Thr	Pro	Phe	Met	Ser	Asp	Trp	Ile	Asp	Ser
		275					280					285			
Ile	Ala	Arg	Val	Glu	Ile	Gly	Ser	Glu	Lys	Trp	His	Arg	Tyr	His	Ser
	290					295					300				
Ile	Val	Ala	Tyr	His	Tyr	Tyr	Phe	Pro	Leu	Trp	Lys	Thr	Glu	Glu	Gln
305					310					315					320
Ile	Ala	His	Asp	Ala	Leu	Lys	Thr	Phe	Leu	Asp	His	Tyr	Phe	Ser	Cys
			325					330						335	
Ile	His	Ala	Ala	Ile	Lys	Gln	Glu	Asn	Leu	Gly	Met	Phe	Leu	Asn	His
		340						345					350		
Tyr	Phe	Ser	His	Ala	His	Ala	Glu	Ile	Lys	Glu	Asn	Ser	Leu	Glu	Met
		355				360						365			
Phe	Leu	Asn	His	Tyr	Phe	Ser	His	Val	Tyr	Arg	Leu	Pro	Lys	Lys	Ala
	370				375						380				
Arg	Lys	Arg	Leu	Phe	Arg	Val	Phe	Val	Lys	His	Cys	Ile	Leu	Ile	Pro
385					390					395					400
Leu	Lys	Ser	Leu	Val	Gly	Lys	Thr	Leu	Arg	Leu	Leu	Lys	Leu	His	Ala
				405					410					415	
Leu	Ala	Lys	Lys	Ile	Leu	Ile	Gln	Leu	Lys	Leu	Leu	Lys	Lys	Ser	
			420					425					430		

<210> 255
 <211> 650
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (46)...(603)

<400> 255
 gctgaattca atttatttta tacgatatta aggagacata ttacc atg ttt caa att 57
 Met Phe Gln Ile
 1

aga	tgg	cat	gca	cga	gcg	ggt	caa	ggt	gca	atc	act	ggc	gct	aaa	ggg	105
Arg	Trp	His	Ala	Arg	Ala	Gly	Gln	Gly	Ala	Ile	Thr	Gly	Ala	Lys	Gly	
5					10				15					20		

ttg	gct	gat	gtg	att	tca	aaa	aca	ggc	aaa	gaa	gtg	caa	gcg	ttc	gct	153
Leu	Ala	Asp	Val	Ile	Ser	Lys	Thr	Gly	Lys	Glu	Val	Gln	Ala	Phe	Ala	
				25				30						35		

tct tat ggt tca gct aaa agg ggg gct gct atg atg gct tat aac cgc	201
Ser Tyr Gly Ser Ala Lys Arg Gly Ala Ala Met Met Ala Tyr Asn Arg	
40 45 50	
ggt gat gat gaa cct atc tta aac cat gaa cgc ttc atg cag cct gat	249
Val Asp Asp Glu Pro Ile Leu Asn His Glu Arg Phe Met Gln Pro Asp	
55 60 65	
tat gtg ctg gtg att gac cct ggt ttg gtt ttc att gaa aac atc ttc	297
Tyr Val Leu Val Ile Asp Pro Gly Leu Val Phe Ile Glu Asn Ile Phe	
70 75 80	
gcc aat gaa aaa gaa gac acg act tat att atc act agc tac ctt aac	345
Ala Asn Glu Lys Glu Asp Thr Thr Tyr Ile Ile Thr Ser Tyr Leu Asn	
85 90 95 100	
aaa gaa gaa ttg ttt gaa aaa aaa cct gaa tta aaa acc cgt aag gtg	393
Lys Glu Glu Leu Phe Glu Lys Lys Pro Glu Leu Lys Thr Arg Lys Val	
105 110 115	
ttt tta gtg gat tgt tta aaa atc tct atg gaa acc tta aaa cgc ccc	441
Phe Leu Val Asp Cys Leu Lys Ile Ser Met Glu Thr Leu Lys Arg Pro	
120 125 130	
atc cct aac acg ccc atg tta ggg gcg tta atg aaa gtg tct ggc atg	489
Ile Pro Asn Thr Pro Met Leu Gly Ala Leu Met Lys Val Ser Gly Met	
135 140 145	
ctt gaa att ggg gct ttt aaa gaa gct ttt aag aaa gtt tta ggc aaa	537
Leu Glu Ile Gly Ala Phe Lys Glu Ala Phe Lys Lys Val Leu Gly Lys	
150 155 160	
aaa ctc acg caa gaa gtc att gac gct aac atg ctc gct atc caa aga	585
Lys Leu Thr Gln Glu Val Ile Asp Ala Asn Met Leu Ala Ile Gln Arg	
165 170 175 180	
gct tat gaa gaa gtt caa taacattaag gaacaaagat gaaagattgg	633
Ala Tyr Glu Glu Val Gln	
185	
aacgaatttg aaatggg	650
<210> 256	
<211> 186	
<212> PRT	
<213> Helicobacter pylori	
<400> 256	
Met Phe Gln Ile Arg Trp His Ala Arg Ala Gly Gln Gly Ala Ile Thr	
1 5 10 15	
Gly Ala Lys Gly Leu Ala Asp Val Ile Ser Lys Thr Gly Lys Glu Val	
20 25 30	
Gln Ala Phe Ala Ser Tyr Gly Ser Ala Lys Arg Gly Ala Ala Met Met	
35 40 45	
Ala Tyr Asn Arg Val Asp Asp Glu Pro Ile Leu Asn His Glu Arg Phe	
50 55 60	
Met Gln Pro Asp Tyr Val Leu Val Ile Asp Pro Gly Leu Val Phe Ile	
65 70 75 80	
Glu Asn Ile Phe Ala Asn Glu Lys Glu Asp Thr Thr Tyr Ile Ile Thr	

				85					90					95			
Ser	Tyr	Leu	Asn	Lys	Glu	Glu	Leu	Phe	Glu	Lys	Lys	Pro	Glu	Leu	Lys		
			100					105					110				
Thr	Arg	Lys	Val	Phe	Leu	Val	Asp	Cys	Leu	Lys	Ile	Ser	Met	Glu	Thr		
		115					120					125					
Leu	Lys	Arg	Pro	Ile	Pro	Asn	Thr	Pro	Met	Leu	Gly	Ala	Leu	Met	Lys		
	130					135					140						
Val	Ser	Gly	Met	Leu	Glu	Ile	Gly	Ala	Phe	Lys	Glu	Ala	Phe	Lys	Lys		
145					150					155					160		
Val	Leu	Gly	Lys	Lys	Leu	Thr	Gln	Glu	Val	Ile	Asp	Ala	Asn	Met	Leu		
				165				170						175			
Ala	Ile	Gln	Arg	Ala	Tyr	Glu	Glu	Val	Gln								
			180					185									

<210> 257
 <211> 1008
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (19)...(954)

<400> 257																	
ttggggattt taactttt	atg	gat	ttt	tgc	tct	ggc	att	ggt	gga	ggc	cgt						51
	Met	Asp	Phe	Cys	Ser	Gly	Ile	Gly	Gly	Gly	Arg						
	1				5					10							
ttg ggc ttg gag caa tgc cat tta aaa tgc gta ggg cat gca gaa atc																	99
Leu Gly Leu Glu Gln Cys His Leu Lys Cys Val Gly His Ala Glu Ile																	
			15				20			25							
aat cat gaa gcc ctt agg act tat gaa tta ttt ttt aaa gat acc cat																	147
Asn His Glu Ala Leu Arg Thr Tyr Glu Leu Phe Phe Lys Asp Thr His																	
		30				35				40							
aat ttt ggg gat ttg atg cga atc aac cct aat gat tta ccc gat ttt																	195
Asn Phe Gly Asp Leu Met Arg Ile Asn Pro Asn Asp Leu Pro Asp Phe																	
	45				50			55									
gat gca ctc att agc ggg ttt cct tgt caa gct ttt tct atc aat ggc																	243
Asp Ala Leu Ile Ser Gly Phe Pro Cys Gln Ala Phe Ser Ile Asn Gly																	
	60				65			70								75	
aaa agg aag ggg ctt gaa gat gaa aga ggg acg att att tac ggg ctt																	291
Lys Arg Lys Gly Leu Glu Asp Glu Arg Gly Thr Ile Ile Tyr Gly Leu																	
			80				85						90				
att cgc att tta aaa gtt aaa cag cct gaa tgt ttc ttg ctt gaa aat																	339
Ile Arg Ile Leu Lys Val Lys Gln Pro Glu Cys Phe Leu Leu Glu Asn																	
		95				100							105				
gtt aag ggc ttg atc aat cat aat aaa aag gca act ttt aat att att																	387
Val Lys Gly Leu Ile Asn His Asn Lys Lys Ala Thr Phe Asn Ile Ile																	
	110					115					120						
atc aaa gcc cta caa gaa gtg ggt tat aca act tat tat aaa att tta																	435
Ile Lys Ala Leu Gln Glu Val Gly Tyr Thr Thr Tyr Tyr Lys Ile Leu																	

125	130	135	
aac agc gct gat ttt	caa tta gcc caa aat	aga gaa cgc ctt tat atc	483
Asn Ser Ala Asp Phe	Gln Leu Ala Gln Asn	Arg Glu Arg Leu Tyr Ile	
140	145	150 155	
gta ggg ttt agg aag	gat tta aaa cac cca	ttt aat ttc cct tta ggt	531
Val Gly Phe Arg Lys	Asp Leu Lys His Pro	Phe Asn Phe Pro Leu Gly	
	160	165 170	
tta gcc aat gat tat	tat ttc aag gat ttt	tta gac gct gat aat gaa	579
Leu Ala Asn Asp Tyr	Tyr Phe Lys Asp Phe	Leu Asp Ala Asp Asn Glu	
	175	180 185	
tgt tat ttg gat gtg	agt aac gct gca ttt	caa aga tac ttg cac aac	627
Cys Tyr Leu Asp Val	Ser Asn Ala Ala Phe	Gln Arg Tyr Leu His Asn	
	190	195 200	
cga tac aac cat aac	cgg gtt tct tta gag	gat ctc tta act tta gaa	675
Arg Tyr Asn His Asn	Arg Val Ser Leu Glu	Asp Leu Leu Thr Leu Glu	
	205	210 215	
aac gct gtt tta gac	aca aga caa tct gat	tta agg ttg tat tct aat	723
Asn Ala Val Leu Asp	Thr Arg Gln Ser Asp	Leu Arg Leu Tyr Ser Asn	
	220 225	230 235	
gtt ttt cct act tta	agg act tct cgg cat	ggc ctg ttt tat acc caa	771
Val Phe Pro Thr Leu	Arg Thr Ser Arg His	Gly Leu Phe Tyr Thr Gln	
	240	245 250	
aaa ggc aaa atc aaa	aga tta aac gct att	gaa agc ttg ctt ttg caa	819
Lys Gly Lys Ile Lys	Arg Leu Asn Ala Ile	Glu Ser Leu Leu Leu Gln	
	255	260 265	
gga ttt cct agg gat	ttg atc gct aag att	aaa gat aat cct aac ttt	867
Gly Phe Pro Arg Asp	Leu Ile Ala Lys Ile	Lys Asp Asn Pro Asn Phe	
	270	275 280	
aaa gca agc cat ttg	cta tcc caa gcg ggg	aat gcg atg agc gtg aat	915
Lys Ala Ser His Leu	Leu Ser Gln Ala Gly	Asn Ala Met Ser Val Asn	
	285	290 295	
gtg att gct gca atc	gct aaa caa atg tta	aag gcg att taataaggga	964
Val Ile Ala Ala Ile	Ala Lys Gln Met Leu	Lys Ala Ile	
	300	305 310	
gctttaagg gagaatgatt tcaaaatacc ccctatcccc ttaa			1008
<210> 258			
<211> 312			
<212> PRT			
<213> Helicobacter pylori			
<400> 258			
Met Asp Phe Cys Ser	Gly Ile Gly Gly Gly	Arg Leu Gly Leu Glu Gln	
1	5	10 15	
Cys His Leu Lys Cys	Val Gly His Ala Glu	Ile Asn His Glu Ala Leu	
	20	25 30	
Arg Thr Tyr Glu Leu	Phe Phe Lys Asp	Thr His Asn Phe Gly Asp Leu	

		35				40				45					
Met	Arg	Ile	Asn	Pro	Asn	Asp	Leu	Pro	Asp	Phe	Asp	Ala	Leu	Ile	Ser
	50					55					60				
Gly	Phe	Pro	Cys	Gln	Ala	Phe	Ser	Ile	Asn	Gly	Lys	Arg	Lys	Gly	Leu
65					70					75					80
Glu	Asp	Glu	Arg	Gly	Thr	Ile	Ile	Tyr	Gly	Leu	Ile	Arg	Ile	Leu	Lys
				85					90					95	
Val	Lys	Gln	Pro	Glu	Cys	Phe	Leu	Leu	Glu	Asn	Val	Lys	Gly	Leu	Ile
			100					105					110		
Asn	His	Asn	Lys	Lys	Ala	Thr	Phe	Asn	Ile	Ile	Ile	Lys	Ala	Leu	Gln
		115					120					125			
Glu	Val	Gly	Tyr	Thr	Thr	Tyr	Tyr	Lys	Ile	Leu	Asn	Ser	Ala	Asp	Phe
	130					135					140				
Gln	Leu	Ala	Gln	Asn	Arg	Glu	Arg	Leu	Tyr	Ile	Val	Gly	Phe	Arg	Lys
145					150					155					160
Asp	Leu	Lys	His	Pro	Phe	Asn	Phe	Pro	Leu	Gly	Leu	Ala	Asn	Asp	Tyr
				165					170					175	
Tyr	Phe	Lys	Asp	Phe	Leu	Asp	Ala	Asp	Asn	Glu	Cys	Tyr	Leu	Asp	Val
			180					185					190		
Ser	Asn	Ala	Ala	Phe	Gln	Arg	Tyr	Leu	His	Asn	Arg	Tyr	Asn	His	Asn
		195					200					205			
Arg	Val	Ser	Leu	Glu	Asp	Leu	Leu	Thr	Leu	Glu	Asn	Ala	Val	Leu	Asp
	210					215					220				
Thr	Arg	Gln	Ser	Asp	Leu	Arg	Leu	Tyr	Ser	Asn	Val	Phe	Pro	Thr	Leu
225					230					235					240
Arg	Thr	Ser	Arg	His	Gly	Leu	Phe	Tyr	Thr	Gln	Lys	Gly	Lys	Ile	Lys
				245					250					255	
Arg	Leu	Asn	Ala	Ile	Glu	Ser	Leu	Leu	Leu	Gln	Gly	Phe	Pro	Arg	Asp
			260					265					270		
Leu	Ile	Ala	Lys	Ile	Lys	Asp	Asn	Pro	Asn	Phe	Lys	Ala	Ser	His	Leu
	275						280					285			
Leu	Ser	Gln	Ala	Gly	Asn	Ala	Met	Ser	Val	Asn	Val	Ile	Ala	Ala	Ile
	290					295					300				
Ala	Lys	Gln	Met	Leu	Lys	Ala	Ile								
305					310										

<210> 259
 <211> 1468
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (30)...(1436)

<400> 259															
aaaataaaaa	ttatattaat	caaggagcgc	atg	aaa	gcg	atg	gaa	ggt	aaa	atc					53
			Met	Lys	Ala	Met	Glu	Gly	Lys	Ile					
			1				5								
att	cag	gtt	tta	ggc	cct	gtg	gta	gat	gtg	gag	ttt	gaa	tcc	tat	ctg
Ile	Gln	Val	Leu	Gly	Pro	Val	Val	Asp	Val	Glu	Phe	Glu	Ser	Tyr	Leu
	10					15				20					
ccg	gcg	att	ttt	gaa	gcg	tta	gac	att	aat	ttt	gaa	gtc	aat	ggt	gtt
Pro	Ala	Ile	Phe	Glu	Ala	Leu	Asp	Ile	Asn	Phe	Glu	Val	Asn	Gly	Val
	25				30					35				40	

caa aag tct tta gtt tta gag gtg gca gcc cat ttg ggc ggt aat cgg	197
Gln Lys Ser Leu Val Leu Glu Val Ala Ala His Leu Gly Gly Asn Arg	
45 50 55	
gtg cga gcg att gct atg gat atg aca gaa ggc tta gtg cgt aac caa	245
Val Arg Ala Ile Ala Met Asp Met Thr Glu Gly Leu Val Arg Asn Gln	
60 65 70	
gtg atc aag gct cgc ggc aaa atg att gaa gtg cct gtg ggc gaa gaa	293
Val Ile Lys Ala Arg Gly Lys Met Ile Glu Val Pro Val Gly Glu Glu	
75 80 85	
gta tta ggg cgt att ttt aat gtt gtg ggc gag agc att gac aat tta	341
Val Leu Gly Arg Ile Phe Asn Val Val Gly Glu Ser Ile Asp Asn Leu	
90 95 100	
gag ccg ctt aag ccg tcc tta act tgg ccc att cac aga aaa gcc cct	389
Glu Pro Leu Lys Pro Ser Leu Thr Trp Pro Ile His Arg Lys Ala Pro	
105 110 115 120	
agt ttt gag cag caa agc act aaa aca gaa atg ttt gaa act ggt att	437
Ser Phe Glu Gln Gln Ser Thr Lys Thr Glu Met Phe Glu Thr Gly Ile	
125 130 135	
aaa gtc att gac tta ctc gcg cct tat tct aag ggc ggt aaa gta ggc	485
Lys Val Ile Asp Leu Leu Ala Pro Tyr Ser Lys Gly Gly Lys Val Gly	
140 145 150	
ttg ttt ggt ggg gct ggc gta ggc aaa acg gtg atc att atg gag ctt	533
Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Ile Ile Met Glu Leu	
155 160 165	
atc cat aat gtg gct tat aag cat aac ggg tat tcg gtg ttt gca ggt	581
Ile His Asn Val Ala Tyr Lys His Asn Gly Tyr Ser Val Phe Ala Gly	
170 175 180	
gtg ggg gag cgc acc aga gag ggg aat gat ctg tat ttt gaa atg aaa	629
Val Gly Glu Arg Thr Arg Glu Gly Asn Asp Leu Tyr Phe Glu Met Lys	
185 190 195 200	
gaa ggg ggc gtt tta gac aaa gtc gca ctg tgt tat ggg caa atg aat	677
Glu Gly Gly Val Leu Asp Lys Val Ala Leu Cys Tyr Gly Gln Met Asn	
205 210 215	
gag cca cca ggc gcg agg aac cgc atc gca ttc acc ggc ttg acg atg	725
Glu Pro Pro Gly Ala Arg Asn Arg Ile Ala Phe Thr Gly Leu Thr Met	
220 225 230	
gcg gag tat ttt cgt gat gaa aag ggc tta gat gtg ttg atg ttt att	773
Ala Glu Tyr Phe Arg Asp Glu Lys Gly Leu Asp Val Leu Met Phe Ile	
235 240 245	
gac aac atc ttt aga tac gct caa agc ggt gcg gaa atg agc gcg cta	821
Asp Asn Ile Phe Arg Tyr Ala Gln Ser Gly Ala Glu Met Ser Ala Leu	
250 255 260	
tta ggc cgt atc cct tca gcg gtg ggg tat cag ccc acg cta gcc ggg	869
Leu Gly Arg Ile Pro Ser Ala Val Gly Tyr Gln Pro Thr Leu Ala Gly	
265 270 275 280	

gaa atg ggg aaa ctt caa gag cgt atc gct tcc act aaa aat ggc tct	917
Glu Met Gly Lys Leu Gln Glu Arg Ile Ala Ser Thr Lys Asn Gly Ser	
285 290 295	
atc act tcc gtt caa gcg gtg tat gtg cca gca gat gac ttg act gac	965
Ile Thr Ser Val Gln Ala Val Tyr Val Pro Ala Asp Asp Leu Thr Asp	
300 305 310	
cca gcc cct gct tcg gtg ttt gcg cat ttg gat gcg act acg gtg ttg	1013
Pro Ala Pro Ala Ser Val Phe Ala His Leu Asp Ala Thr Thr Val Leu	
315 320 325	
aat aga aag atc gct gaa aaa ggg att tat ccg gcg gtg gat cct ttg	1061
Asn Arg Lys Ile Ala Glu Lys Gly Ile Tyr Pro Ala Val Asp Pro Leu	
330 335 340	
gat tcc act tca agg att tta agc cct caa atg atc ggt gag aaa cac	1109
Asp Ser Thr Ser Arg Ile Leu Ser Pro Gln Met Ile Gly Glu Lys His	
345 350 355 360	
tat gaa gtc gct acc ggt atc cag cag gtt tta caa aaa tac aag gat	1157
Tyr Glu Val Ala Thr Gly Ile Gln Gln Val Leu Gln Lys Tyr Lys Asp	
365 370 375	
ttg caa gac att att gcg att ttg gga tta gac gaa ttg agc gaa gag	1205
Leu Gln Asp Ile Ile Ala Ile Leu Gly Leu Asp Glu Leu Ser Glu Glu	
380 385 390	
gat aaa aaa acg gtt gaa agg gcc aga aaa att gag aag ttt tta tcc	1253
Asp Lys Lys Thr Val Glu Arg Ala Arg Lys Ile Glu Lys Phe Leu Ser	
395 400 405	
cag ccg ttc ttt gtg gct gaa gtg ttt aca gga agt cct ggt aaa tat	1301
Gln Pro Phe Phe Val Ala Glu Val Phe Thr Gly Ser Pro Gly Lys Tyr	
410 415 420	
gta acc ctt caa gag act tta gag ggc ttt gga ggg att tta gag ggc	1349
Val Thr Leu Gln Glu Thr Leu Glu Gly Phe Gly Gly Ile Leu Glu Gly	
425 430 435 440	
aaa tac gat cat att ccc gag aac gcg ttt tat atg gtg ggt agc att	1397
Lys Tyr Asp His Ile Pro Glu Asn Ala Phe Tyr Met Val Gly Ser Ile	
445 450 455	
caa gag gtt tta gaa aaa gct aaa aac atg aaa aat tcc taagggtttt	1446
Gln Glu Val Leu Glu Lys Ala Lys Asn Met Lys Asn Ser	
460 465	
gtgatggcctt tggtgaaaat ta	1468
<210> 260	
<211> 469	
<212> PRT	
<213> Helicobacter pylori	
<400> 260	
Met Lys Ala Met Glu Gly Lys Ile Ile Gln Val Leu Gly Pro Val Val	
1 5 10 15	

Asp	Val	Glu	Phe	Glu	Ser	Tyr	Leu	Pro	Ala	Ile	Phe	Glu	Ala	Leu	Asp
			20					25					30		
Ile	Asn	Phe	Glu	Val	Asn	Gly	Val	Gln	Lys	Ser	Leu	Val	Leu	Glu	Val
		35				40					45				
Ala	Ala	His	Leu	Gly	Gly	Asn	Arg	Val	Arg	Ala	Ile	Ala	Met	Asp	Met
	50				55					60					
Thr	Glu	Gly	Leu	Val	Arg	Asn	Gln	Val	Ile	Lys	Ala	Arg	Gly	Lys	Met
65					70				75					80	
Ile	Glu	Val	Pro	Val	Gly	Glu	Glu	Val	Leu	Gly	Arg	Ile	Phe	Asn	Val
			85					90					95		
Val	Gly	Glu	Ser	Ile	Asp	Asn	Leu	Glu	Pro	Leu	Lys	Pro	Ser	Leu	Thr
			100				105					110			
Trp	Pro	Ile	His	Arg	Lys	Ala	Pro	Ser	Phe	Glu	Gln	Gln	Ser	Thr	Lys
	115					120					125				
Thr	Glu	Met	Phe	Glu	Thr	Gly	Ile	Lys	Val	Ile	Asp	Leu	Leu	Ala	Pro
	130					135					140				
Tyr	Ser	Lys	Gly	Gly	Lys	Val	Gly	Leu	Phe	Gly	Gly	Ala	Gly	Val	Gly
145					150				155					160	
Lys	Thr	Val	Ile	Ile	Met	Glu	Leu	Ile	His	Asn	Val	Ala	Tyr	Lys	His
			165					170					175		
Asn	Gly	Tyr	Ser	Val	Phe	Ala	Gly	Val	Gly	Glu	Arg	Thr	Arg	Glu	Gly
		180					185					190			
Asn	Asp	Leu	Tyr	Phe	Glu	Met	Lys	Glu	Gly	Gly	Val	Leu	Asp	Lys	Val
	195					200					205				
Ala	Leu	Cys	Tyr	Gly	Gln	Met	Asn	Glu	Pro	Pro	Gly	Ala	Arg	Asn	Arg
	210				215					220					
Ile	Ala	Phe	Thr	Gly	Leu	Thr	Met	Ala	Glu	Tyr	Phe	Arg	Asp	Glu	Lys
225					230				235					240	
Gly	Leu	Asp	Val	Leu	Met	Phe	Ile	Asp	Asn	Ile	Phe	Arg	Tyr	Ala	Gln
			245					250					255		
Ser	Gly	Ala	Glu	Met	Ser	Ala	Leu	Leu	Gly	Arg	Ile	Pro	Ser	Ala	Val
		260					265					270			
Gly	Tyr	Gln	Pro	Thr	Leu	Ala	Gly	Glu	Met	Gly	Lys	Leu	Gln	Glu	Arg
	275					280					285				
Ile	Ala	Ser	Thr	Lys	Asn	Gly	Ser	Ile	Thr	Ser	Val	Gln	Ala	Val	Tyr
	290				295					300					
Val	Pro	Ala	Asp	Asp	Leu	Thr	Asp	Pro	Ala	Pro	Ala	Ser	Val	Phe	Ala
305					310				315					320	
His	Leu	Asp	Ala	Thr	Thr	Val	Leu	Asn	Arg	Lys	Ile	Ala	Glu	Lys	Gly
			325					330					335		
Ile	Tyr	Pro	Ala	Val	Asp	Pro	Leu	Asp	Ser	Thr	Ser	Arg	Ile	Leu	Ser
		340					345					350			
Pro	Gln	Met	Ile	Gly	Glu	Lys	His	Tyr	Glu	Val	Ala	Thr	Gly	Ile	Gln
	355					360					365				
Gln	Val	Leu	Gln	Lys	Tyr	Lys	Asp	Leu	Gln	Asp	Ile	Ile	Ala	Ile	Leu
	370				375					380					
Gly	Leu	Asp	Glu	Leu	Ser	Glu	Glu	Asp	Lys	Lys	Thr	Val	Glu	Arg	Ala
385					390				395					400	
Arg	Lys	Ile	Glu	Lys	Phe	Leu	Ser	Gln	Pro	Phe	Phe	Val	Ala	Glu	Val
			405					410					415		
Phe	Thr	Gly	Ser	Pro	Gly	Lys	Tyr	Val	Thr	Leu	Gln	Glu	Thr	Leu	Glu
		420					425					430			
Gly	Phe	Gly	Gly	Ile	Leu	Glu	Gly	Lys	Tyr	Asp	His	Ile	Pro	Glu	Asn
	435					440					445				
Ala	Phe	Tyr	Met	Val	Gly	Ser	Ile	Gln	Glu	Val	Leu	Glu	Lys	Ala	Lys
	450				455						460				
Asn	Met	Lys	Asn	Ser											
465															

```
<210> 261
<211> 2716
<212> DNA
<213> Helicobacter pylori
```

tac	caa	cca	gaa	gag	ata	gaa	aaa	aag	att	tat	gaa	att	tgc	tct	cat	102
Tyr	Gln	Pro	Glu	Glu	Ile	Glu	Lys	Lys	Ile	Tyr	Glu	Ile	Cys	Ser	His	
10					15					20					25	

cac ata ggg cat gcc ctg act tta agc ttg caa gat att tta gcg cgt 246
His Ile Gly His Ala Leu Thr Leu Ser Leu Gln Asp Ile Leu Ala Arg
 60 65 70

caa ggg att aaa aaa gaa gat tta ggg cgt gaa gag ttc att aaa aaa 390
Gln Gly Ile Lys Lys Glu Asp Leu Gly Arg Glu Glu Phe Ile Lys Lys
110 115 120

gat aag ggc ttg caa aga gcg gtc aaa ttg gcg ttt ttg aaa tgg tat 534
Asp Lys Gly Leu Gln Arg Ala Val Lys Leu Ala Phe Leu Lys Trp Tyr
155 160 165

Lys	Asp	Gly	Ala	Leu	Ser	Asp	Ile	Glu	Val	Glu	Tyr	Glu	Glu	Arg	Lys		
				190					195					200			
ggg	gcg	ttg	tat	tat	att	aga	tat	tat	tta	gaa	aat	caa	aaa	gat	tat	678	
Gly	Ala	Leu	Tyr	Tyr	Ile	Arg	Tyr	Tyr	Leu	Glu	Asn	Gln	Lys	Asp	Tyr		
			205					210					215				
tta	gtg	gtg	gct	acc	aca	cgc	cct	gaa	acc	ttg	ttt	ggc	gat	agc	gcg	726	
Leu	Val	Val	Ala	Thr	Thr	Arg	Pro	Glu	Thr	Leu	Phe	Gly	Asp	Ser	Ala		
			220				225					230					
ctt	atg	gtc	aat	cct	aac	gat	gag	aga	tac	aag	cat	ttg	gtg	ggg	caa	774	
Leu	Met	Val	Asn	Pro	Asn	Asp	Glu	Arg	Tyr	Lys	His	Leu	Val	Gly	Gln		
	235					240					245						
aaa	gcg	atc	ttg	cct	tta	atc	cat	cgc	aca	atc	cct	att	atc	gct	gat	822	
Lys	Ala	Ile	Leu	Pro	Leu	Ile	His	Arg	Thr	Ile	Pro	Ile	Ile	Ala	Asp		
	250				255					260					265		
gaa	cat	gtt	gaa	atg	gag	ttt	ggc	aca	ggg	tgt	gtg	aaa	gta	acc	cct	870	
Glu	His	Val	Glu	Met	Glu	Phe	Gly	Thr	Gly	Cys	Val	Lys	Val	Thr	Pro		
				270					275					280			
ggg	cat	gat	ttt	aac	gat	tat	gaa	gtg	ggc	aaa	cgc	cac	cat	ttg	gaa	918	
Gly	His	Asp	Phe	Asn	Asp	Tyr	Glu	Val	Gly	Lys	Arg	His	His	Leu	Glu		
			285					290					295				
acg	att	aaa	atc	ttt	gat	gaa	aag	ggg	att	tta	aac	gcg	cat	tgc	ggg	966	
Thr	Ile	Lys	Ile	Phe	Asp	Glu	Lys	Gly	Ile	Leu	Asn	Ala	His	Cys	Gly		
		300					305					310					
gag	ttt	gaa	aat	tta	gaa	cga	tta	gaa	gct	aga	gat	aag	gtc	gta	gaa	1014	
Glu	Phe	Glu	Asn	Leu	Glu	Arg	Leu	Glu	Ala	Arg	Asp	Lys	Val	Val	Glu		
	315					320					325						
aga	tta	aaa	gaa	aac	gcc	cta	ttg	gaa	aaa	ata	gaa	gaa	cac	acg	cat	1062	
Arg	Leu	Lys	Glu	Asn	Ala	Leu	Leu	Glu	Lys	Ile	Glu	Glu	His	Thr	His		
	330				335					340					345		
caa	gtg	ggg	cat	tgc	tat	cgt	tgt	cat	aat	gtg	gta	gaa	cct	tat	gtg	1110	
Gln	Val	Gly	His	Cys	Tyr	Arg	Cys	His	Asn	Val	Val	Glu	Pro	Tyr	Val		
				350					355					360			
tct	aag	caa	tgg	ttt	gtc	aag	cct	gaa	atc	gct	caa	agt	tct	att	gaa	1158	
Ser	Lys	Gln	Trp	Phe	Val	Lys	Pro	Glu	Ile	Ala	Gln	Ser	Ser	Ile	Glu		
			365					370					375				
aaa	atc	caa	caa	ggt	ttg	gcg	cga	ttc	tac	cct	tct	aat	tgg	atc	aat	1206	
Lys	Ile	Gln	Gln	Gly	Leu	Ala	Arg	Phe	Tyr	Pro	Ser	Asn	Trp	Ile	Asn		
		380					385					390					
aat	tac	aac	gct	tgg	atg	agg	gaa	tta	cgc	cct	tgg	tgt	atc	agc	agg	1254	
Asn	Tyr	Asn	Ala	Trp	Met	Arg	Glu	Leu	Arg	Pro	Trp	Cys	Ile	Ser	Arg		
	395					400					405						
caa	ttg	ttt	tgg	ggg	cat	caa	ata	ccg	gta	ttc	act	tgc	gag	aat	aac	1302	
Gln	Leu	Phe	Trp	Gly	His	Gln	Ile	Pro	Val	Phe	Thr	Cys	Glu	Asn	Asn		
	410				415					420					425		

cac	cag	ttc	gta	agc	tta	gac	acc	ccc	tta	agt	tgc	cct	act	tgt	aag	1350
His	Gln	Phe	Val	Ser	Leu	Asp	Thr	Pro	Leu	Ser	Cys	Pro	Thr	Cys	Lys	
				430					435					440		
agc	gaa	aca	cta	gag	caa	gat	aag	gat	gtg	cta	gac	aca	tgg	ttt	agt	1398
Ser	Glu	Thr	Leu	Glu	Gln	Asp	Lys	Asp	Val	Leu	Asp	Thr	Trp	Phe	Ser	
			445					450					455			
tca	ggg	cta	tgg	gcg	ttt	tcc	act	cta	ggg	tgg	ggg	caa	gaa	aaa	agc	1446
Ser	Gly	Leu	Trp	Ala	Phe	Ser	Thr	Leu	Gly	Trp	Gly	Gln	Glu	Lys	Ser	
		460					465					470				
ggt	ttg	ttt	aat	gaa	agc	gat	ttg	aaa	gat	ttc	tac	cct	aac	aca	acg	1494
Gly	Leu	Phe	Asn	Glu	Ser	Asp	Leu	Lys	Asp	Phe	Tyr	Pro	Asn	Thr	Thr	
	475					480					485					
ctc	att	act	ggg	ttt	gac	atc	ctc	ttt	ttt	tgg	gtg	gct	agg	atg	ctt	1542
Leu	Ile	Thr	Gly	Phe	Asp	Ile	Leu	Phe	Phe	Trp	Val	Ala	Arg	Met	Leu	
490					495					500					505	
ttt	tgc	agc	gaa	tcg	ctt	tta	ggc	gaa	ttg	ccc	ttt	aaa	gat	att	tac	1590
Phe	Cys	Ser	Glu	Ser	Leu	Leu	Gly	Glu	Leu	Pro	Phe	Lys	Asp	Ile	Tyr	
				510					515					520		
ttg	cac	gcc	tta	gtg	aga	gat	gaa	aag	ggt	gaa	aaa	atg	agc	aaa	tct	1638
Leu	His	Ala	Leu	Val	Arg	Asp	Glu	Lys	Gly	Glu	Lys	Met	Ser	Lys	Ser	
			525					530					535			
aag	ggt	aat	gtg	atc	gat	cct	tta	gag	atg	ata	gaa	aaa	tac	ggc	gcg	1686
Lys	Gly	Asn	Val	Ile	Asp	Pro	Leu	Glu	Met	Ile	Glu	Lys	Tyr	Gly	Ala	
		540					545					550				
gat	agc	ttg	cgt	ttc	act	tta	gcc	aat	ttg	tgc	gct	acg	ggt	agg	gac	1734
Asp	Ser	Leu	Arg	Phe	Thr	Leu	Ala	Asn	Leu	Cys	Ala	Thr	Gly	Arg	Asp	
	555					560					565					
att	aag	ctt	tcc	act	acg	cat	tta	gaa	aat	aac	aag	aat	ttc	gcc	aac	1782
Ile	Lys	Leu	Ser	Thr	Thr	His	Leu	Glu	Asn	Asn	Lys	Asn	Phe	Ala	Asn	
570					575					580					585	
aag	ctt	ttt	aat	gcg	gcg	agt	tac	ttg	aag	ctc	aaa	caa	gaa	tct	ttc	1830
Lys	Leu	Phe	Asn	Ala	Ala	Ser	Tyr	Leu	Lys	Leu	Lys	Gln	Glu	Ser	Phe	
				590					595					600		
aaa	gat	aaa	gag	cgt	ttg	aat	gaa	tac	caa	acg	cct	ttg	ggg	cgt	tat	1878
Lys	Asp	Lys	Glu	Arg	Leu	Asn	Glu	Tyr	Gln	Thr	Pro	Leu	Gly	Arg	Tyr	
			605					610					615			
gcg	aaa	tcg	cgc	ttg	aat	tca	gcg	act	aaa	gag	gcg	cgt	aac	gct	tta	1926
Ala	Lys	Ser	Arg	Leu	Asn	Ser	Ala	Thr	Lys	Glu	Ala	Arg	Asn	Ala	Leu	
		620					625					630				
gat	aat	tat	cgt	ttt	aat	gac	gcc	acg	act	ttg	tta	tac	cgc	ttt	ttg	1974
Asp	Asn	Tyr	Arg	Phe	Asn	Asp	Ala	Thr	Thr	Leu	Leu	Tyr	Arg	Phe	Leu	
	635					640					645					
tgg	ggg	gaa	ttt	tgc	gac	tgg	ttc	att	gaa	ttt	tct	aaa	gtg	gaa	aat	2022
Trp	Gly	Glu	Phe	Cys	Asp	Trp	Phe	Ile	Glu	Phe	Ser	Lys	Val	Glu	Asn	
650					655					660					665	

gaa gcg ata gac gaa tta ggg agc gtg tta aaa gag gct tta aaa ctc	2070
Glu Ala Ile Asp Glu Leu Gly Ser Val Leu Lys Glu Ala Leu Lys Leu	
670 675 680	
ttg cac cct ttc atg ccc ttt atc agc gag tct tta tac cac aag ctc	2118
Leu His Pro Phe Met Pro Phe Ile Ser Glu Ser Leu Tyr His Lys Leu	
685 690 695	
agc aat acg gaa cta gaa aac act gaa tct atc atg gtc atg cct tac	2166
Ser Asn Thr Glu Leu Glu Asn Thr Glu Ser Ile Met Val Met Pro Tyr	
700 705 710	
cct aaa gat ttg gcg caa gat gaa aaa tta gag cat gaa ttt gaa gtg	2214
Pro Lys Asp Leu Ala Gln Asp Glu Lys Leu Glu His Glu Phe Glu Val	
715 720 725	
att aaa gat tgc att gtg tct tta agg cgt tta aaa atc atg cta gaa	2262
Ile Lys Asp Cys Ile Val Ser Leu Arg Arg Leu Lys Ile Met Leu Glu	
730 735 740 745	
acc cca ccg att gtt cta aaa gaa gcg agc gtg gga tta aga gaa gcc	2310
Thr Pro Pro Ile Val Leu Lys Glu Ala Ser Val Gly Leu Arg Glu Ala	
750 755 760	
ata gaa aac aca gag cgt ttg caa act tac gcc caa aaa tta gcg agg	2358
Ile Glu Asn Thr Glu Arg Leu Gln Thr Tyr Ala Gln Lys Leu Ala Arg	
765 770 775	
ttg gaa aaa gtc agc gtg att agt tct aag cct tta aaa agc gtg agc	2406
Leu Glu Lys Val Ser Val Ile Ser Ser Lys Pro Leu Lys Ser Val Ser	
780 785 790	
gat gtg ggg gaa ttt tgc cag act tat gcg aat tta gaa aat ctt gat	2454
Asp Val Gly Glu Phe Cys Gln Thr Tyr Ala Asn Leu Glu Asn Leu Asp	
795 800 805	
tta agc ccg ctt gtt gcg cgt ttg aaa aag cag ttg gaa aaa ttg gaa	2502
Leu Ser Pro Leu Val Ala Arg Leu Lys Lys Gln Leu Glu Lys Leu Glu	
810 815 820 825	
aaa gaa aaa tta aaa ctc aat ttg cac aat gaa aat ttt gtc aaa aac	2550
Lys Glu Lys Leu Lys Leu Asn Leu His Asn Glu Asn Phe Val Lys Asn	
830 835 840	
gcg cct aaa agc gtg cta gaa aaa gct aaa gag agt tta aaa acg ctt	2598
Ala Pro Lys Ser Val Leu Glu Lys Ala Lys Glu Ser Leu Lys Thr Leu	
845 850 855	
tta gaa aaa gaa agt aaa att aag caa gaa ttg gac ttg tta gaa caa	2646
Leu Glu Lys Glu Ser Lys Ile Lys Gln Glu Leu Asp Leu Leu Glu Gln	
860 865 870	
cca taataaaagg atagaaaatg tttcaagcgt taagcgatgg gtttaaaaac	2699
Pro	
gcgctcaata aaatccg	2716

<210> 262
 <211> 874
 <212> PRT
 <213> Helicobacter pylori

<400> 262
 Met Ile Met Lys Gln Glu Pro Thr Thr Tyr Gln Pro Glu Glu Ile Glu
 1 5 10 15
 Lys Lys Ile Tyr Glu Ile Cys Ser His Arg Gly Tyr Phe Glu Ile Asp
 20 25 30
 Gly Asn Glu Ala Ile Gln Glu Lys Asn Lys Arg Phe Cys Leu Met Met
 35 40 45
 Pro Pro Pro Asn Val Thr Gly Val Leu His Ile Gly His Ala Leu Thr
 50 55 60
 Leu Ser Leu Gln Asp Ile Leu Ala Arg Tyr Lys Arg Met Asp Gly Tyr
 65 70 75 80
 Lys Thr Leu Tyr Gln Pro Gly Leu Asp His Ala Gly Ile Ala Thr Gln
 85 90 95
 Asn Val Val Glu Lys Gln Leu Leu Ser Gln Gly Ile Lys Lys Glu Asp
 100 105 110
 Leu Gly Arg Glu Glu Phe Ile Lys Lys Val Trp Glu Trp Lys Glu Lys
 115 120 125
 Ser Gly Gly Ala Ile Leu Glu Gln Met Lys Arg Leu Gly Val Ser Ala
 130 135 140
 Ala Phe Ser Arg Thr Arg Phe Thr Met Asp Lys Gly Leu Gln Arg Ala
 145 150 155 160
 Val Lys Leu Ala Phe Leu Lys Trp Tyr Glu Lys Gly Leu Ile Ile Gln
 165 170 175
 Asp Asn Tyr Met Val Asn Trp Cys Thr Lys Asp Gly Ala Leu Ser Asp
 180 185 190
 Ile Glu Val Glu Tyr Glu Glu Arg Lys Gly Ala Leu Tyr Tyr Ile Arg
 195 200 205
 Tyr Tyr Leu Glu Asn Gln Lys Asp Tyr Leu Val Val Ala Thr Thr Arg
 210 215 220
 Pro Glu Thr Leu Phe Gly Asp Ser Ala Leu Met Val Asn Pro Asn Asp
 225 230 235 240
 Glu Arg Tyr Lys His Leu Val Gly Gln Lys Ala Ile Leu Pro Leu Ile
 245 250 255
 His Arg Thr Ile Pro Ile Ile Ala Asp Glu His Val Glu Met Glu Phe
 260 265 270
 Gly Thr Gly Cys Val Lys Val Thr Pro Gly His Asp Phe Asn Asp Tyr
 275 280 285
 Glu Val Gly Lys Arg His His Leu Glu Thr Ile Lys Ile Phe Asp Glu
 290 295 300
 Lys Gly Ile Leu Asn Ala His Cys Gly Glu Phe Glu Asn Leu Glu Arg
 305 310 315 320
 Leu Glu Ala Arg Asp Lys Val Val Glu Arg Leu Lys Glu Asn Ala Leu
 325 330 335
 Leu Glu Lys Ile Glu Glu His Thr His Gln Val Gly His Cys Tyr Arg
 340 345 350
 Cys His Asn Val Val Glu Pro Tyr Val Ser Lys Gln Trp Phe Val Lys
 355 360 365
 Pro Glu Ile Ala Gln Ser Ser Ile Glu Lys Ile Gln Gln Gly Leu Ala
 370 375 380
 Arg Phe Tyr Pro Ser Asn Trp Ile Asn Asn Tyr Asn Ala Trp Met Arg
 385 390 395 400
 Glu Leu Arg Pro Trp Cys Ile Ser Arg Gln Leu Phe Trp Gly His Gln
 405 410 415
 Ile Pro Val Phe Thr Cys Glu Asn Asn His Gln Phe Val Ser Leu Asp


```
<210> 263
<211> 509
<212> DNA
<213> Helicobacter pylori
```

<400> 263																
gggctttttt aaactttcttc ttatatcttt a atg cta gaa ata gac aac caa																52
Met Leu Glu Ile Asp Asn Gln																
1 5																
acc ccg cta gaa tca gac ttt tta tta tta gaa aaa atc gca aat gtt																100
Thr Pro Leu Glu Ser Asp Phe Leu Leu Leu Glu Lys Ile Ala Asn Val																
10 15 20																
tta gcc ccc act caa atc att gag ctt gtt ttg gtg agc gat gaa acc																148
Leu Ala Pro Thr Gln Ile Ile Glu Leu Val Leu Val Ser Asp Glu Thr																
25 30 35																
att cga gaa atc aac aag gat tta agg ggt tgc gat tac gct acc gat																196
Ile Arg Glu Ile Asn Lys Asp Leu Arg Gly Cys Asp Tyr Ala Thr Asp																
40 45 50 55																
gtt ttg agc ttc cct tta gaa gcc att cct cac acc cct tta ggg agc																244
Val Leu Ser Phe Pro Leu Glu Ala Ile Pro His Thr Pro Leu Gly Ser																
60 65 70																
gtg gtg att aat gcg cca tta gct caa act aac gct ctg aaa tta gga																292
Val Val Ile Asn Ala Pro Leu Ala Gln Thr Asn Ala Leu Lys Leu Gly																
75 80 85																
cat agc tta gaa aat gag atc gct ctt tta ttc att cat ggg gtg ttg																340
His Ser Leu Glu Asn Glu Ile Ala Leu Leu Phe Ile His Gly Val Leu																
90 95 100																
cat ttg ttg ggc tat gac cat gaa aaa gat aag ggc gaa caa cgc caa																388
His Leu Leu Gly Tyr Asp His Glu Lys Asp Lys Gly Glu Gln Arg Gln																
105 110 115																
aaa gag agc gaa ctc att aaa gcg ttt aac ttg cct ttg agt ttg att																436
Lys Glu Ser Glu Leu Ile Lys Ala Phe Asn Leu Pro Leu Ser Leu Ile																
120 125 130 135																
gaa cgc aca cag gat taggtttaga tactctacta atgctgacaa ataaagcttt																491
Glu Arg Thr Gln Asp																
140																
taattttttaa gaatggaa																509

<400> 264
Met Leu Glu Ile Asp Asn Gln Thr Pro Leu Glu Ser Asp Phe Leu Leu

110										115					120					
cat	gct	aaa	ttc	gtg	gtg	gtt	gcg	atc	ggg	aaa	atg	ggc	cag	cca	aac	435				
His	Ala	Lys	Phe	Val	Val	Val	Ala	Ile	Gly	Lys	Met	Gly	Gln	Pro	Asn					
			125					130					135							
cgc	cct	act	gct	tat	aaa	atc	cct	gtt	gcg	ctc	tct	aaa	caa	gtg	gtt	483				
Arg	Pro	Thr	Ala	Tyr	Lys	Ile	Pro	Val	Ala	Leu	Ser	Lys	Gln	Val	Val					
		140					145					150								
ttt	agc	atc	aat	gat	tgt	aag	gaa	aat	gaa	aaa	acc	ctt	gtg	atc	ggc	531				
Phe	Ser	Ile	Asn	Asp	Cys	Lys	Glu	Asn	Glu	Lys	Thr	Leu	Val	Ile	Gly					
	155					160					165									
gga	ggc	aac	tca	gcg	gtg	gaa	tac	gcc	att	gct	ttg	tgc	aaa	acc	acc	579				
Gly	Gly	Asn	Ser	Ala	Val	Glu	Tyr	Ala	Ile	Ala	Leu	Cys	Lys	Thr	Thr					
170					175				180						185					
cct	acc	acc	ctc	aat	tac	cg	aaa	aaa	gaa	ttc	agc	cg	atc	aat	gaa	627				
Pro	Thr	Thr	Leu	Asn	Tyr	Arg	Lys	Lys	Glu	Phe	Ser	Arg	Ile	Asn	Glu					
			190						195					200						
gac	aac	gct	aaa	aac	ttg	caa	gaa	gtc	cta	aac	aat	aac	acg	ctt	aaa	675				
Asp	Asn	Ala	Lys	Asn	Leu	Gln	Glu	Val	Leu	Asn	Asn	Asn	Thr	Leu	Lys					
			205					210					215							
agc	aag	ctt	gga	gtg	gat	att	gaa	agc	cta	gaa	gaa	gat	aac	act	cag	723				
Ser	Lys	Leu	Gly	Val	Asp	Ile	Glu	Ser	Leu	Glu	Glu	Asp	Asn	Thr	Gln					
		220					225					230								
att	aag	gtt	aac	ttc	acc	gat	aac	acg	agc	gaa	agt	ttt	gat	cgt	ttg	771				
Ile	Lys	Val	Asn	Phe	Thr	Asp	Asn	Thr	Ser	Glu	Ser	Phe	Asp	Arg	Leu					
	235					240					245									
ctg	tat	gcg	atc	ggc	ggc	tct	acc	cct	tta	gag	ttt	ttt	aaa	cg	tgt	819				
Leu	Tyr	Ala	Ile	Gly	Gly	Ser	Thr	Pro	Leu	Glu	Phe	Phe	Lys	Arg	Cys					
250					255					260					265					
tct	tta	gag	ctg	gat	cct	agc	acc	aat	atc	cct	gtg	gtg	aaa	gaa	aat	867				
Ser	Leu	Glu	Leu	Asp	Pro	Ser	Thr	Asn	Ile	Pro	Val	Val	Lys	Glu	Asn					
				270					275					280						
tta	gag	agc	aac	aat	atc	cct	aat	ttg	ttc	atc	gtg	ggc	gat	att	tta	915				
Leu	Glu	Ser	Asn	Asn	Ile	Pro	Asn	Leu	Phe	Ile	Val	Gly	Asp	Ile	Leu					
			285					290					295							
ttc	aaa	tca	ggg	gcg	agc	atc	gct	acc	gct	tta	aac	cat	ggc	tat	gat	963				
Phe	Lys	Ser	Gly	Ala	Ser	Ile	Ala	Thr	Ala	Leu	Asn	His	Gly	Tyr	Asp					
		300					305					310								
gtt	gct	ata	gaa	atc	gct	aaa	agg	ttg	cac	tct	taaagccgct	cactcatcaa	1016							
Val	Ala	Ile	Glu	Ile	Ala	Lys	Arg	Leu	His	Ser										
	315					320														
acggcttagc	cttatacaaa	aa														1038				

<210> 266

<211> 324

<212> PRT

<213> Helicobacter pylori

<400> 266

```
Met Asn Gln Glu Ile Leu Asp Val Leu Ile Val Gly Ala Gly Pro Gly
 1          5          10          15
Gly Ile Ala Thr Ala Val Glu Cys Glu Ile Ala Gly Val Lys Lys Val
 20          25          30
Leu Leu Cys Glu Lys Thr Glu Ser His Ser Gly Met Leu Glu Lys Phe
 35          40          45
Tyr Lys Ala Gly Lys Arg Ile Asp Lys Asp Tyr Lys Lys Gln Val Val
 50          55          60
Glu Leu Lys Gly His Ile Pro Phe Lys Asp Ser Phe Lys Glu Glu Thr
 65          70          75          80
Leu Glu Asn Phe Thr Asn Leu Leu Lys Glu His His Ile Thr Pro Ser
 85          90          95
Tyr Lys Thr Asp Ile Glu Ser Val Lys Lys Glu Gly Glu Tyr Phe Lys
100          105          110
Ile Thr Thr Thr Ser Asn Thr Thr Tyr His Ala Lys Phe Val Val Val
115          120          125
Ala Ile Gly Lys Met Gly Gln Pro Asn Arg Pro Thr Ala Tyr Lys Ile
130          135          140
Pro Val Ala Leu Ser Lys Gln Val Val Phe Ser Ile Asn Asp Cys Lys
145          150          155          160
Glu Asn Glu Lys Thr Leu Val Ile Gly Gly Asn Ser Ala Val Glu
165          170          175
Tyr Ala Ile Ala Leu Cys Lys Thr Thr Pro Thr Thr Leu Asn Tyr Arg
180          185          190
Lys Lys Glu Phe Ser Arg Ile Asn Glu Asp Asn Ala Lys Asn Leu Gln
195          200          205
Glu Val Leu Asn Asn Asn Thr Leu Lys Ser Lys Leu Gly Val Asp Ile
210          215          220
Glu Ser Leu Glu Glu Asp Asn Thr Gln Ile Lys Val Asn Phe Thr Asp
225          230          235          240
Asn Thr Ser Glu Ser Phe Asp Arg Leu Leu Tyr Ala Ile Gly Gly Ser
245          250          255
Thr Pro Leu Glu Phe Phe Lys Arg Cys Ser Leu Glu Leu Asp Pro Ser
260          265          270
Thr Asn Ile Pro Val Val Lys Glu Asn Leu Glu Ser Asn Asn Ile Pro
275          280          285
Asn Leu Phe Ile Val Gly Asp Ile Leu Phe Lys Ser Gly Ala Ser Ile
290          295          300
Ala Thr Ala Leu Asn His Gly Tyr Asp Val Ala Ile Glu Ile Ala Lys
305          310          315          320
Arg Leu His Ser
```

<210> 267

<211> 704

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (20)...(670)

<400> 267

```
atttttaagg tatagcggtt atg gca tta gat tgg gat ttt atg ttt cac tcc 52
                        Met Ala Leu Asp Trp Asp Phe Met Phe His Ser
```


	1	5	10	
atc cct gcg ttt ttt aag ggg tta gaa ctc acg ctt tat att tct ttc				100
Ile Pro Ala Phe Phe Lys Gly Leu Glu Leu Thr Leu Tyr Ile Ser Phe	15	20	25	
ttt ggg att ttg ctc tct ctt ttg gtg ggg ttt ttg tgc gcg atc gtt				148
Phe Gly Ile Leu Leu Ser Leu Leu Val Gly Phe Leu Cys Ala Ile Val	30	35	40	
ttg tat ttt aaa acg cgc ttt ctc tct cct gtt gtc tat atc tat ggc				196
Leu Tyr Phe Lys Thr Arg Phe Leu Ser Pro Val Val Tyr Ile Tyr Gly	45	50	55	
gaa atc gct agg aac acg ccc ctg ctc atc cag ctt ttc ttt ttg tat				244
Glu Ile Ala Arg Asn Thr Pro Leu Leu Ile Gln Leu Phe Phe Leu Tyr	60	65	70	75
tac ggg ttg aat gaa atc ggt ttg agc gct tta gag tgc gcg att tta				292
Tyr Gly Leu Asn Glu Ile Gly Leu Ser Ala Leu Glu Cys Ala Ile Leu	80	85	90	
gcg tta ggg ttt ttg ggt ggg ggg tat atg agt caa agt ttt ttg ctt				340
Ala Leu Gly Phe Leu Gly Gly Gly Tyr Met Ser Gln Ser Phe Leu Leu	95	100	105	
ggg ttt aag agc cta gct tcc att caa aga gaa agc gct ttg agt ttg				388
Gly Phe Lys Ser Leu Ala Ser Ile Gln Arg Glu Ser Ala Leu Ser Leu	110	115	120	
ggg ttt agc cct ttg aaa atg atg tat tat att att ctg cct caa agt				436
Gly Phe Ser Pro Leu Lys Met Met Tyr Tyr Ile Ile Leu Pro Gln Ser	125	130	135	
tta agc gtt tct atg cct tcc ata ggg gcg aat gtg att ttt tta ctc				484
Leu Ser Val Ser Met Pro Ser Ile Gly Ala Asn Val Ile Phe Leu Leu	140	145	150	155
aaa gaa act tcg gtg gtg ggc gcg ata gcc cta acc gat att atg ttt				532
Lys Glu Thr Ser Val Val Gly Ala Ile Ala Leu Thr Asp Ile Met Phe	160	165	170	
gtg gcg aaa gat ttt att ggc att tat tat aaa acg act gaa agc ctt				580
Val Ala Lys Asp Phe Ile Gly Ile Tyr Tyr Lys Thr Thr Glu Ser Leu	175	180	185	
ttg atg tta agc ctc act tat ttg atc gct tta ctc cct tta agc gtt				628
Leu Met Leu Ser Leu Thr Tyr Leu Ile Ala Leu Leu Pro Leu Ser Val	190	195	200	
ttg ttt gtg atc tta gag cgt ttc ttt aaa aag aaa gtg gct				670
Leu Phe Val Ile Leu Glu Arg Phe Phe Lys Lys Lys Val Ala	205	210	215	
taaaatggga gttttactag aattagacaa cttt				704

<210> 268
 <211> 217
 <212> PRT

<213> Helicobacter pylori

<400> 268

Met	Ala	Leu	Asp	Trp	Asp	Phe	Met	Phe	His	Ser	Ile	Pro	Ala	Phe	Phe	
1				5					10					15		
Lys	Gly	Leu	Glu	Leu	Thr	Leu	Tyr	Ile	Ser	Phe	Phe	Gly	Ile	Leu	Leu	
		20						25					30			
Ser	Leu	Leu	Val	Gly	Phe	Leu	Cys	Ala	Ile	Val	Leu	Tyr	Phe	Lys	Thr	
		35					40					45				
Arg	Phe	Leu	Ser	Pro	Val	Val	Tyr	Ile	Tyr	Gly	Glu	Ile	Ala	Arg	Asn	
	50					55					60					
Thr	Pro	Leu	Leu	Ile	Gln	Leu	Phe	Phe	Leu	Tyr	Tyr	Gly	Leu	Asn	Glu	
65					70					75				80		
Ile	Gly	Leu	Ser	Ala	Leu	Glu	Cys	Ala	Ile	Leu	Ala	Leu	Gly	Phe	Leu	
				85					90					95		
Gly	Gly	Gly	Tyr	Met	Ser	Gln	Ser	Phe	Leu	Leu	Gly	Phe	Lys	Ser	Leu	
			100					105					110			
Ala	Ser	Ile	Gln	Arg	Glu	Ser	Ala	Leu	Ser	Leu	Gly	Phe	Ser	Pro	Leu	
		115					120					125				
Lys	Met	Met	Tyr	Tyr	Ile	Ile	Leu	Pro	Gln	Ser	Leu	Ser	Val	Ser	Met	
	130					135					140					
Pro	Ser	Ile	Gly	Ala	Asn	Val	Ile	Phe	Leu	Leu	Lys	Glu	Thr	Ser	Val	
145					150					155					160	
Val	Gly	Ala	Ile	Ala	Leu	Thr	Asp	Ile	Met	Phe	Val	Ala	Lys	Asp	Phe	
				165					170					175		
Ile	Gly	Ile	Tyr	Tyr	Lys	Thr	Thr	Glu	Ser	Leu	Leu	Met	Leu	Ser	Leu	
		180						185					190			
Thr	Tyr	Leu	Ile	Ala	Leu	Leu	Pro	Leu	Ser	Val	Leu	Phe	Val	Ile	Leu	
		195					200					205				
Glu	Arg	Phe	Phe	Lys	Lys	Lys	Val	Ala								
	210					215										

<210> 269

<211> 737

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (31)...(699)

<400> 269

agcgttttctt	taaaaagaaa	gtggcttaaa	atg	gga	gtt	tta	cta	gaa	tta	gac	54					
			Met	Gly	Val	Leu	Leu	Glu	Leu	Asp						
			1			5										
aac	ctt	aag	cgt	ttg	tta	gaa	ggg	ttt	gaa	acc	act	ctt	ttg	atc	gct	102
Asn	Leu	Lys	Arg	Leu	Leu	Glu	Gly	Phe	Glu	Thr	Thr	Leu	Leu	Ile	Ala	
	10					15					20					
ctt	agc	tct	gca	atg	att	tca	atc	att	gtt	gga	atg	ctt	ttg	ggg	agc	150
Leu	Ser	Ser	Ala	Met	Ile	Ser	Ile	Ile	Val	Gly	Met	Leu	Leu	Gly	Ser	
	25				30					35				40		
ttg	atg	gcg	ttt	ggt	tct	caa	ata	gtg	gtt	ttg	gcg	tgt	cgt	gtg	tat	198
Leu	Met	Ala	Phe	Gly	Ser	Gln	Ile	Val	Val	Leu	Ala	Cys	Arg	Val	Tyr	
				45					50					55		

tta gaa agc att cgc atc atc ccg ctt tta gca tgg ctt ttt att gtg	246
Leu Glu Ser Ile Arg Ile Ile Pro Leu Leu Ala Trp Leu Phe Ile Val	
60 65 70	
tat ttc ggg tta gcg agc tgg ttt gat ttg cat att agc gcg gtt ttg	294
Tyr Phe Gly Leu Ala Ser Trp Phe Asp Leu His Ile Ser Ala Val Leu	
75 80 85	
gca agc gtt att gtt ttt agc ttg tgg ggt ggc gct gaa atg atg gat	342
Ala Ser Val Ile Val Phe Ser Leu Trp Gly Gly Ala Glu Met Met Asp	
90 95 100	
tta act agg ggg gtt tta act tcc gtg agc aaa cac caa ata gaa agc	390
Leu Thr Arg Gly Val Leu Thr Ser Val Ser Lys His Gln Ile Glu Ser	
105 110 115 120	
gct ctg gct tta ggc tta gat tca aaa aag gtg att ttt aat att att	438
Ala Leu Ala Leu Gly Leu Asp Ser Lys Lys Val Ile Phe Asn Ile Ile	
125 130 135	
ttc cct caa agc ttt ttg tct tta ttg ccc tca agc ctt aat ttg ttc	486
Phe Pro Gln Ser Phe Leu Ser Leu Leu Pro Ser Ser Leu Asn Leu Phe	
140 145 150	
acg cgc atg atc aaa acc acg gct tta gtt tct ctc att gga gcg att	534
Thr Arg Met Ile Lys Thr Thr Ala Leu Val Ser Leu Ile Gly Ala Ile	
155 160 165	
gat ttg cta aaa gtg ggc cag caa atc ata gag ctt aac ctc tta cgc	582
Asp Leu Leu Lys Val Gly Gln Gln Ile Ile Glu Leu Asn Leu Leu Arg	
170 175 180	
atg cct aat gcg agc ttt gtg gtt tat ggc gtt atc tta atg ttt tat	630
Met Pro Asn Ala Ser Phe Val Val Tyr Gly Val Ile Leu Met Phe Tyr	
185 190 195 200	
ttt agt tta tgc tat agt ttg agc ctg tat agt tcc tat tta gaa aaa	678
Phe Ser Leu Cys Tyr Ser Leu Ser Leu Tyr Ser Ser Tyr Leu Glu Lys	
205 210 215	
aaa ttc caa cac att aga ggg taaaatgagc gtgatttttag aaaccaaagg	729
Lys Phe Gln His Ile Arg Gly	
220	
gttaaaaa	737
<210> 270	
<211> 223	
<212> PRT	
<213> Helicobacter pylori	
<400> 270	
Met Gly Val Leu Leu Glu Leu Asp Asn Leu Lys Arg Leu Leu Glu Gly	
1 5 10 15	
Phe Glu Thr Thr Leu Leu Ile Ala Leu Ser Ser Ala Met Ile Ser Ile	
20 25 30	
Ile Val Gly Met Leu Leu Gly Ser Leu Met Ala Phe Gly Ser Gln Ile	
35 40 45	
Val Val Leu Ala Cys Arg Val Tyr Leu Glu Ser Ile Arg Ile Ile Pro	

50		55		60
Leu	Leu	Ala	Trp	Leu
65		70		75
Asp	Leu	His	Ile	Ser
		85		90
Trp	Gly	Gly	Ala	Glu
		100		105
Val	Ser	Lys	His	Gln
		115		120
Lys	Lys	Val	Ile	Phe
		130		135
Leu	Pro	Ser	Ser	Leu
145				150
Leu	Val	Ser	Leu	Ile
				165
Ile	Ile	Glu	Leu	Asn
				180
Tyr	Gly	Val	Ile	Leu
				195
Leu	Tyr	Ser	Ser	Tyr
				210
				215
				220

<210> 271
 <211> 807
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (31)...(774)

<400> 271
 aaaaaaaatt ccaacacatt agagggtaaa atg agc gtg att tta gaa acc aaa 54
 Met Ser Val Ile Leu Glu Thr Lys
 1 5

ggg tta aaa aaa acc tat caa aac cat ttg gtt tta gac ggc atc aat 102
 Gly Leu Lys Lys Thr Tyr Gln Asn His Leu Val Leu Asp Gly Ile Asn
 10 15 20

ttc act tta aat aag ggt gaa gtg gca gtg att tta ggg cct agc ggg 150
 Phe Thr Leu Asn Lys Gly Glu Val Ala Val Ile Leu Gly Pro Ser Gly
 25 30 35 40

tgc ggg aaa agc act ttt tta aaa tgc cta aac ggg ctt gaa aag att 198
 Cys Gly Lys Ser Thr Phe Leu Lys Cys Leu Asn Gly Leu Glu Lys Ile
 45 50 55

aat gaa ggt gaa atc ctt ttt gaa aac act aac ctt aac aat aag gcc 246
 Asn Glu Gly Glu Ile Leu Phe Glu Asn Thr Asn Leu Asn Asn Lys Ala
 60 65 70

act aac tgg aat caa atg cgc caa aaa ata ggc atg gtg ttt caa aat 294
 Thr Asn Trp Asn Gln Met Arg Gln Lys Ile Gly Met Val Phe Gln Asn
 75 80 85

tat gaa ttg ttc ccg cat tta aat gtg tta gat aat atc tta ctc gct 342
 Tyr Glu Leu Phe Pro His Leu Asn Val Leu Asp Asn Ile Leu Leu Ala

90	95	100	
cct atg aaa gtg caa aaa cga tcc aaa gat gag gtt att tct caa gcc			390
Pro Met Lys Val Gln Lys Arg Ser Lys Asp Glu Val Ile Ser Gln Ala			
105	110	115	120
ata gag ctt tta aag cga gtg ggt ttg gag cat aaa caa caa gct tac			438
Ile Glu Leu Leu Lys Arg Val Gly Leu Glu His Lys Gln Gln Ala Tyr			
	125	130	135
cct aaa gaa ttg agc ggc gga caa aaa caa cga gta gcg atc gtg cgc			486
Pro Lys Glu Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Ile Val Arg			
	140	145	150
tct tta tgc atg cga cca aaa atc atg ctt ttt gat gaa gta acc gcc			534
Ser Leu Cys Met Arg Pro Lys Ile Met Leu Phe Asp Glu Val Thr Ala			
	155	160	165
tct tta gac cct gaa atg gtt aaa gaa gtt tta gaa gtg att tta gaa			582
Ser Leu Asp Pro Glu Met Val Lys Glu Val Leu Glu Val Ile Leu Glu			
	170	175	180
tta gcc aca aca ggc atg agc atg gtg att gta acg cat gaa atg aaa			630
Leu Ala Thr Thr Gly Met Ser Met Val Ile Val Thr His Glu Met Lys			
	185	190	200
ttc gcg caa aaa atc gct cat aaa atc gtg ttt ttt gat agc ggt aaa			678
Phe Ala Gln Lys Ile Ala His Lys Ile Val Phe Phe Asp Ser Gly Lys			
	205	210	215
atc gct gaa gaa aac aac gct aaa gaa ttt ttt aac cac ccg aaa tct			726
Ile Ala Glu Glu Asn Asn Ala Lys Glu Phe Phe Asn His Pro Lys Ser			
	220	225	230
caa aga gcg caa aaa ttt tta gaa act ttc cat ttt tta ggg agc tgt			774
Gln Arg Ala Gln Lys Phe Leu Glu Thr Phe His Phe Leu Gly Ser Cys			
	235	240	245
taaataaagt ttgctaaaaa gatgattcta att			807

<210> 272

<211> 248

<212> PRT

<213> Helicobacter pylori

<400> 272

Met Ser Val Ile Leu Glu Thr Lys Gly Leu Lys Lys Thr Tyr Gln Asn	
1 5 10 15	
His Leu Val Leu Asp Gly Ile Asn Phe Thr Leu Asn Lys Gly Glu Val	
20 25 30	
Ala Val Ile Leu Gly Pro Ser Gly Cys Gly Lys Ser Thr Phe Leu Lys	
35 40 45	
Cys Leu Asn Gly Leu Glu Lys Ile Asn Glu Gly Glu Ile Leu Phe Glu	
50 55 60	
Asn Thr Asn Leu Asn Asn Lys Ala Thr Asn Trp Asn Gln Met Arg Gln	
65 70 75 80	
Lys Ile Gly Met Val Phe Gln Asn Tyr Glu Leu Phe Pro His Leu Asn	
85 90 95	
Val Leu Asp Asn Ile Leu Leu Ala Pro Met Lys Val Gln Lys Arg Ser	


```

acc ggc gat aat acc aca ggc ctt gat tct aaa gag ttc ccc aag caa 387
Thr Gly Asp Asn Thr Thr Gly Leu Asp Ser Lys Glu Phe Pro Lys Gln
110 115 120 125

agt cgt gag aaa aag ggc cga gtg atc act tta atc ggt aaa ggt gaa 435
Ser Arg Glu Lys Lys Gly Arg Val Ile Thr Leu Ile Gly Lys Gly Glu
130 135 140

gtg cct tat ctt att tta gaa acc gat tgc caa gtg ggt gat att gca 483
Val Pro Tyr Leu Ile Leu Glu Thr Asp Cys Gln Val Gly Asp Ile Ala
145 150 155

aag atc tct ttg gtg ggt aat ttt gat ggc act ggg ttt ctt acg gaa 531
Lys Ile Ser Leu Val Gly Asn Phe Asp Gly Thr Gly Phe Leu Thr Glu
160 165 170

tat aaa ttc aaa gac gct aaa ccc att tac tagtctttat tcttcgcttc 581
Tyr Lys Phe Lys Asp Ala Lys Pro Ile Tyr
175 180

```

```

attcttaa 589

```

```

<210> 274
<211> 183
<212> PRT
<213> Helicobacter pylori

```

```

<400> 274
Met Ser Tyr Phe Tyr Lys His Cys Leu Lys Phe Ser Leu Val Gly Leu
1 5 10 15
Leu Gly Leu Leu Ser Val Gln Leu Asp Ala Arg Ser Phe Val Asp Gly
20 25 30
Asp Leu Asp Ile Gln Lys Phe Ser Tyr Glu Asp Ser Leu Leu Lys Lys
35 40 45
Gly Asp Pro Asn Gly Val His Lys Val Gln Val Arg Asp Tyr Lys Gly
50 55 60
Lys Met Gln Glu Ala Glu Ile His Ser Glu Ile Arg Ile Ala Leu Lys
65 70 75 80
Pro Gly Val Lys Lys Glu Val Lys Lys Gly Lys Ile Tyr Ser Ala Gln
85 90 95
Ile Asn Asp Gly Met Cys Tyr Ala Phe Arg Met Leu Gln Thr Gly Asp
100 105 110
Asn Thr Thr Gly Leu Asp Ser Lys Glu Phe Pro Lys Gln Ser Arg Glu
115 120 125
Lys Lys Gly Arg Val Ile Thr Leu Ile Gly Lys Gly Glu Val Pro Tyr
130 135 140
Leu Ile Leu Glu Thr Asp Cys Gln Val Gly Asp Ile Ala Lys Ile Ser
145 150 155 160
Leu Val Gly Asn Phe Asp Gly Thr Gly Phe Leu Thr Glu Tyr Lys Phe
165 170 175
Lys Asp Ala Lys Pro Ile Tyr
180

```

```

<210> 275
<211> 925
<212> DNA
<213> Helicobacter pylori

```

<220>
 <221> CDS
 <222> (30)...(875)

<400> 275

ggaatttttg ggtgctactc ctttctcgt	atg ggt atc gct ttt gcc cac tct	53
	Met Gly Ile Ala Phe Ala His Ser	
	1 5	
att ttt tgg tcc atc acg gct tct tta gtc att cgt gtc gcg cca aga	101	
Ile Phe Trp Ser Ile Thr Ala Ser Leu Val Ile Arg Val Ala Pro Arg		
10 15 20		
aat aaa aaa caa cag gcc tta ggg ctg tta gcg tta ggg agt tcg tta	149	
Asn Lys Lys Gln Gln Ala Leu Gly Leu Leu Ala Leu Gly Ser Ser Leu		
25 30 35 40		
gcg atg att tta ggg ttg ccg ctt ggg agg atc att ggg caa att cta	197	
Ala Met Ile Leu Gly Leu Pro Leu Gly Arg Ile Ile Gly Gln Ile Leu		
45 50 55		
gat tgg cgt tcc act ttt ggc gtg atc ggg ggc gtt gcg acc ctt ata	245	
Asp Trp Arg Ser Thr Phe Gly Val Ile Gly Gly Val Ala Thr Leu Ile		
60 65 70		
gcg ttg ctt atg tgg aaa ttg ctc ccg cat cta ccc agt aga aac gca	293	
Ala Leu Leu Met Trp Lys Leu Leu Pro His Leu Pro Ser Arg Asn Ala		
75 80 85		
ggc acg ctc gca agt gtc cct gta tta atg aaa cgg ccg ctt tta atg	341	
Gly Thr Leu Ala Ser Val Pro Val Leu Met Lys Arg Pro Leu Leu Met		
90 95 100		
ggg att tat ttg ctt gtg atc atg gtc atc tct ggg cat ttc acc act	389	
Gly Ile Tyr Leu Leu Val Ile Met Val Ile Ser Gly His Phe Thr Thr		
105 110 115 120		
tat agt tat att gag cct ttt atc att caa atc agc caa ttt tct cct	437	
Tyr Ser Tyr Ile Glu Pro Phe Ile Ile Gln Ile Ser Gln Phe Ser Pro		
125 130 135		
gac att aca acg cta atg ttg ttt gtg ttt ggg tta gcg ggc gtg gtg	485	
Asp Ile Thr Thr Leu Met Leu Phe Val Phe Gly Leu Ala Gly Val Val		
140 145 150		
ggg agt ttt ttg ttc ggc cgt ttg tat gca aaa aat tca aga aaa ttt	533	
Gly Ser Phe Leu Phe Gly Arg Leu Tyr Ala Lys Asn Ser Arg Lys Phe		
155 160 165		
atc gct ttt gcg atg gtt tta gtc att tgc ccg caa ctc ttg ctt ttt	581	
Ile Ala Phe Ala Met Val Leu Val Ile Cys Pro Gln Leu Leu Leu Phe		
170 175 180		
gtg ttt aaa aac tta gag tgg gtg gtt ttc ttg caa att ttc tta tgg	629	
Val Phe Lys Asn Leu Glu Trp Val Val Phe Leu Gln Ile Phe Leu Trp		
185 190 195 200		
ggg att ggg atc act tcg ctt ggg att tcc ttg caa atg agg gtg ttg	677	
Gly Ile Gly Ile Thr Ser Leu Gly Ile Ser Leu Gln Met Arg Val Leu		

205										210					215					
cag	ctt	gcg	ccg	gat	gcc	acg	gat	gtt	gcg	agt	gcg	att	tac	tca	ggg	725				
Gln	Leu	Ala	Pro	Asp	Ala	Thr	Asp	Val	Ala	Ser	Ala	Ile	Tyr	Ser	Gly					
			220					225					230							
agc	tat	aat	gtg	ggg	att	gga	tca	gga	gcg	ctg	ttt	ggc	agt	att	gtg	773				
Ser	Tyr	Asn	Val	Gly	Ile	Gly	Ser	Gly	Ala	Leu	Phe	Gly	Ser	Ile	Val					
		235					240					245								
atc	cac	caa	cta	ggg	cta	gga	tat	att	ggc	ttt	gtg	ggt	ggg	gct	tta	821				
Ile	His	Gln	Leu	Gly	Leu	Gly	Tyr	Ile	Gly	Phe	Val	Gly	Gly	Ala	Leu					
		250				255					260									
ggt	ttg	ttg	gcg	ctc	ttt	tgg	ctt	aga	ttc	att	acg	ata	aag	ttt	aaa	869				
Gly	Leu	Leu	Ala	Leu	Phe	Trp	Leu	Arg	Phe	Ile	Thr	Ile	Lys	Phe	Lys					
265					270				275						280					
aaa	aca	taa	agagcgt	taaa	aggatt	agcccaataa	aggagaatcc	ctttcgcact								925				
Lys	Thr																			

<210> 276
 <211> 282
 <212> PRT
 <213> Helicobacter pylori

<400> 276

Met	Gly	Ile	Ala	Phe	Ala	His	Ser	Ile	Phe	Trp	Ser	Ile	Thr	Ala	Ser
1				5					10					15	
Leu	Val	Ile	Arg	Val	Ala	Pro	Arg	Asn	Lys	Lys	Gln	Gln	Ala	Leu	Gly
			20					25					30		
Leu	Leu	Ala	Leu	Gly	Ser	Ser	Leu	Ala	Met	Ile	Leu	Gly	Leu	Pro	Leu
		35					40					45			
Gly	Arg	Ile	Ile	Gly	Gln	Ile	Leu	Asp	Trp	Arg	Ser	Thr	Phe	Gly	Val
	50				55					60					
Ile	Gly	Gly	Val	Ala	Thr	Leu	Ile	Ala	Leu	Leu	Met	Trp	Lys	Leu	Leu
65					70				75					80	
Pro	His	Leu	Pro	Ser	Arg	Asn	Ala	Gly	Thr	Leu	Ala	Ser	Val	Pro	Val
				85					90					95	
Leu	Met	Lys	Arg	Pro	Leu	Leu	Met	Gly	Ile	Tyr	Leu	Leu	Val	Ile	Met
			100					105					110		
Val	Ile	Ser	Gly	His	Phe	Thr	Thr	Tyr	Ser	Tyr	Ile	Glu	Pro	Phe	Ile
		115					120					125			
Ile	Gln	Ile	Ser	Gln	Phe	Ser	Pro	Asp	Ile	Thr	Thr	Leu	Met	Leu	Phe
	130				135					140					
Val	Phe	Gly	Leu	Ala	Gly	Val	Val	Gly	Ser	Phe	Leu	Phe	Gly	Arg	Leu
145					150				155					160	
Tyr	Ala	Lys	Asn	Ser	Arg	Lys	Phe	Ile	Ala	Phe	Ala	Met	Val	Leu	Val
			165					170						175	
Ile	Cys	Pro	Gln	Leu	Leu	Leu	Phe	Val	Phe	Lys	Asn	Leu	Glu	Trp	Val
			180					185					190		
Val	Phe	Leu	Gln	Ile	Phe	Leu	Trp	Gly	Ile	Gly	Ile	Thr	Ser	Leu	Gly
	195						200					205			
Ile	Ser	Leu	Gln	Met	Arg	Val	Leu	Gln	Leu	Ala	Pro	Asp	Ala	Thr	Asp
	210					215					220				
Val	Ala	Ser	Ala	Ile	Tyr	Ser	Gly	Ser	Tyr	Asn	Val	Gly	Ile	Gly	Ser

gtt agc acc tat caa gcc gtg agt ggg gca ggg aac aag ggc ata gag	534
Val Ser Thr Tyr Gln Ala Val Ser Gly Ala Gly Asn Lys Gly Ile Glu	
155 160 165	
agt tta aaa aat gag tta aaa acc gct tta gag tgt ttg gaa aaa gac	582
Ser Leu Lys Asn Glu Leu Lys Thr Ala Leu Glu Cys Leu Glu Lys Asp	
170 175 180 185	
ccc act att gat tta aac caa gtc ttg caa gct ggg gct ttc gct tat	630
Pro Thr Ile Asp Leu Asn Gln Val Leu Gln Ala Gly Ala Phe Ala Tyr	
190 195 200	
ccg atc gct ttc aat gcg atc gct cat att gat act ttt aag gag aat	678
Pro Ile Ala Phe Asn Ala Ile Ala His Ile Asp Thr Phe Lys Glu Asn	
205 210 215	
ggg tac acg aaa gaa gag cta aaa atg ctg cat gaa acc cat aaa atc	726
Gly Tyr Thr Lys Glu Glu Leu Lys Met Leu His Glu Thr His Lys Ile	
220 225 230	
atg ggc gtg gat ttc cct atc agc gcg act tgc gtg cgc gtg ccg gta	774
Met Gly Val Asp Phe Pro Ile Ser Ala Thr Cys Val Arg Val Pro Val	
235 240 245	
ttg agg agc cat agc gag agt ttg agt atc gct ttt gaa aaa gaa ttc	822
Leu Arg Ser His Ser Glu Ser Leu Ser Ile Ala Phe Glu Lys Glu Phe	
250 255 260 265	
gat ctc aaa gaa gtc tat gaa gtt tta aaa aac gcc cct agc gtg gct	870
Asp Leu Lys Glu Val Tyr Glu Val Leu Lys Asn Ala Pro Ser Val Ala	
270 275 280	
gtt tgc gat gat ccc agt cat aat ctt tac ccc acg ccc cta aaa gcg	918
Val Cys Asp Asp Pro Ser His Asn Leu Tyr Pro Thr Pro Leu Lys Ala	
285 290 295	
agc cac acg gat agc gtc ttt ata ggg cgc ttg agg aag gat ttg ttt	966
Ser His Thr Asp Ser Val Phe Ile Gly Arg Leu Arg Lys Asp Leu Phe	
300 305 310	
gat aag aaa act ttg cat ggc ttt tgt gtg gcg gat caa ttg aga gtg	1014
Asp Lys Lys Thr Leu His Gly Phe Cys Val Ala Asp Gln Leu Arg Val	
315 320 325	
ggg gca gcc acc aac gca ctc aaa atc gct ctg cat tac att aag aac	1062
Gly Ala Ala Thr Asn Ala Leu Lys Ile Ala Leu His Tyr Ile Lys Asn	
330 335 340 345	
gct tgagttttatt caaagataac aaagatgaat gt	1097
Ala	

<210> 278

<211> 346

<212> PRT

<213> Helicobacter pylori

<220>

<221> VARIANT
 <222> 81
 <223> Xaa = Any Amino Acid

<400> 278

Met	Lys	Thr	Tyr	Asn	Val	Ala	Ile	Val	Gly	Ala	Ser	Gly	Ala	Val	Gly
1				5					10					15	
Gln	Glu	Leu	Ile	Lys	Gly	Leu	Glu	Asn	Ser	Phe	Phe	Pro	Ile	Lys	Lys
			20					25					30		
Phe	Val	Pro	Leu	Ala	Ser	Thr	Arg	Ser	Ala	Gly	Lys	Lys	Ile	Lys	Ala
		35				40						45			
Phe	Asn	Lys	Asp	Tyr	Glu	Ile	Leu	Glu	Thr	Thr	His	Glu	Val	Phe	Glu
	50				55						60				
Arg	Glu	Lys	Ile	Asp	Ile	Ala	Phe	Phe	Ser	Ala	Gly	Gly	Ser	Val	Ser
65				70					75						80
Xaa	Glu	Phe	Ala	Thr	Ser	Ala	Ser	Lys	Thr	Ala	Leu	Val	Val	Asp	Asn
				85					90					95	
Thr	Ser	Phe	Phe	Arg	Leu	Asn	Lys	Asp	Val	Pro	Leu	Val	Val	Pro	Glu
			100					105					110		
Ile	Asn	Ala	Lys	Glu	Ile	Phe	Asn	Ala	Pro	Leu	Asn	Ile	Ile	Ala	Asn
		115					120					125			
Pro	Asn	Cys	Ser	Thr	Ile	Gln	Met	Thr	Gln	Ile	Leu	Asn	Pro	Leu	His
	130				135						140				
Leu	His	Phe	Lys	Ile	Lys	Ser	Val	Ile	Val	Ser	Thr	Tyr	Gln	Ala	Val
145					150					155					160
Ser	Gly	Ala	Gly	Asn	Lys	Gly	Ile	Glu	Ser	Leu	Lys	Asn	Glu	Leu	Lys
			165					170						175	
Thr	Ala	Leu	Glu	Cys	Leu	Glu	Lys	Asp	Pro	Thr	Ile	Asp	Leu	Asn	Gln
			180					185					190		
Val	Leu	Gln	Ala	Gly	Ala	Phe	Ala	Tyr	Pro	Ile	Ala	Phe	Asn	Ala	Ile
		195					200					205			
Ala	His	Ile	Asp	Thr	Phe	Lys	Glu	Asn	Gly	Tyr	Thr	Lys	Glu	Glu	Leu
	210				215						220				
Lys	Met	Leu	His	Glu	Thr	His	Lys	Ile	Met	Gly	Val	Asp	Phe	Pro	Ile
225					230					235					240
Ser	Ala	Thr	Cys	Val	Arg	Val	Pro	Val	Leu	Arg	Ser	His	Ser	Glu	Ser
				245					250					255	
Leu	Ser	Ile	Ala	Phe	Glu	Lys	Glu	Phe	Asp	Leu	Lys	Glu	Val	Tyr	Glu
			260					265					270		
Val	Leu	Lys	Asn	Ala	Pro	Ser	Val	Ala	Val	Cys	Asp	Asp	Pro	Ser	His
		275					280					285			
Asn	Leu	Tyr	Pro	Thr	Pro	Leu	Lys	Ala	Ser	His	Thr	Asp	Ser	Val	Phe
	290					295					300				
Ile	Gly	Arg	Leu	Arg	Lys	Asp	Leu	Phe	Asp	Lys	Lys	Thr	Leu	His	Gly
305					310					315					320
Phe	Cys	Val	Ala	Asp	Gln	Leu	Arg	Val	Gly	Ala	Ala	Thr	Asn	Ala	Leu
				325					330					335	
Lys	Ile	Ala	Leu	His	Tyr	Ile	Lys	Asn	Ala						
			340					345							

<210> 279
 <211> 1395
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (34)...(1359)

<400> 279

taaaatttta	gcatacaa	at	acaagg	aaat	gga	atg	att	acc	cct	aaa	gtg	ttg		54		
						Met	Ile	Thr	Pro	Lys	Val	Leu				
						1					5					
agc	ggg	ttt	aaa	gac	cgc	ttg	cct	aaa	gat	gcg	ata	caa	aaa	gcc	cag	102
Ser	Gly	Phe	Lys	Asp	Arg	Leu	Pro	Lys	Asp	Ala	Ile	Gln	Lys	Ala	Gln	
		10					15					20				
ttg	ctt	gcg	aaa	gtt	tca	gtc	gtg	ttt	caa	agt	ttt	ggt	ttt	gtg	ccg	150
Leu	Leu	Ala	Lys	Val	Ser	Val	Val	Phe	Gln	Ser	Phe	Gly	Phe	Val	Pro	
		25				30					35					
att	gaa	acc	cct	cat	ttg	gaa	tac	gct	caa	acg	tta	ttg	cct	gat	gcg	198
Ile	Glu	Thr	Pro	His	Leu	Glu	Tyr	Ala	Gln	Thr	Leu	Leu	Pro	Asp	Ala	
	40				45				50					55		
agc	agt	gat	att	caa	aaa	gaa	att	tat	cgt	ttt	aaa	gac	cat	ggg	gat	246
Ser	Ser	Asp	Ile	Gln	Lys	Glu	Ile	Tyr	Arg	Phe	Lys	Asp	His	Gly	Asp	
				60					65					70		
aga	gat	gtg	gct	tta	agg	ttt	gat	ttg	act	gtg	cca	tta	gcc	cgc	ttt	294
Arg	Asp	Val	Ala	Leu	Arg	Phe	Asp	Leu	Thr	Val	Pro	Leu	Ala	Arg	Phe	
			75				80						85			
gtc	tct	ttg	cac	cac	caa	acg	cta	ggc	atg	ccc	ttt	aaa	cgc	tac	gct	342
Val	Ser	Leu	His	His	Gln	Thr	Leu	Gly	Met	Pro	Phe	Lys	Arg	Tyr	Ala	
		90				95						100				
ata	ggc	aat	gtc	ttt	agg	ggc	gaa	agg	gcg	caa	aaa	ggg	cgt	tat	agg	390
Ile	Gly	Asn	Val	Phe	Arg	Gly	Glu	Arg	Ala	Gln	Lys	Gly	Arg	Tyr	Arg	
	105					110					115					
gaa	ttt	acg	caa	tgc	gat	ttt	gat	ttt	ata	ggg	agc	gag	agt	ttg	gtg	438
Glu	Phe	Thr	Gln	Cys	Asp	Phe	Asp	Phe	Ile	Gly	Ser	Glu	Ser	Leu	Val	
	120				125				130					135		
tgc	gat	gct	gag	atc	att	caa	gtg	att	gtc	gct	tct	tta	aaa	gcc	cta	486
Cys	Asp	Ala	Glu	Ile	Ile	Gln	Val	Ile	Val	Ala	Ser	Leu	Lys	Ala	Leu	
				140					145					150		
gat	tta	gaa	gat	ttt	tgc	gtc	tct	atc	aac	cac	aga	aaa	att	ttg	aac	534
Asp	Leu	Glu	Asp	Phe	Cys	Val	Ser	Ile	Asn	His	Arg	Lys	Ile	Leu	Asn	
			155				160						165			
ggg	ata	tgc	gaa	tat	ttt	ggg	atc	tct	caa	gtg	aat	gaa	gcg	ttg	cgc	582
Gly	Ile	Cys	Glu	Tyr	Phe	Gly	Ile	Ser	Gln	Val	Asn	Glu	Ala	Leu	Arg	
		170				175						180				
att	gtg	gat	aaa	ttg	gaa	aaa	att	ggc	ttg	aat	ggg	gtt	gaa	gaa	gaa	630
Ile	Val	Asp	Lys	Leu	Glu	Lys	Ile	Gly	Leu	Asn	Gly	Val	Glu	Glu	Glu	
	185					190					195					
tta	aaa	aaa	gag	tgc	ggt	tta	aat	tca	aac	acc	att	aaa	gag	ctt	tta	678
Leu	Lys	Lys	Glu	Cys	Gly	Leu	Asn	Ser	Asn	Thr	Ile	Lys	Glu	Leu	Leu	
	200				205					210					215	
gaa	tta	att	caa	atc	aaa	caa	aac	gat	tta	agc	cat	gcg	gaa	ttt	ttt	726
Glu	Leu	Ile	Gln	Ile	Lys	Gln	Asn	Asp	Leu	Ser	His	Ala	Glu	Phe	Phe	

220	225	230	
gaa aaa att gct tat ttg aaa gac tat aat gaa aat cta aaa aaa ggc Glu Lys Ile Ala Tyr Leu Lys Asp Tyr Asn Glu Asn Leu Lys Lys Gly 235 240 245			774
ata cag gat tta gaa agg cta tac cag ttg cta ggg gat ttg caa att Ile Gln Asp Leu Glu Arg Leu Tyr Gln Leu Leu Gly Asp Leu Gln Ile 250 255 260			822
tct caa aac ctg tat aaa att gat ttt tct atc gct agg gga tta ggg Ser Gln Asn Leu Tyr Lys Ile Asp Phe Ser Ile Ala Arg Gly Leu Gly 265 270 275			870
tat tat aca ggg att gtg tat gaa acc acg ctt aat gaa atg aag tct Tyr Tyr Thr Gly Ile Val Tyr Glu Thr Thr Leu Asn Glu Met Lys Ser 280 285 290 295			918
tta ggg agc gtg tgt tca ggg ggg cgt tat gat cat ttg act aaa aat Leu Gly Ser Val Cys Ser Gly Gly Arg Tyr Asp His Leu Thr Lys Asn 300 305 310			966
ttt tct aaa gag aat tta caa ggg gta ggg gct tct att ggg att gat Phe Ser Lys Glu Asn Leu Gln Gly Val Gly Ala Ser Ile Gly Ile Asp 315 320 325			1014
cga ttg att gtg gct ttg agt gaa atg caa tta tta gac gag cgc tcc Arg Leu Ile Val Ala Leu Ser Glu Met Gln Leu Leu Asp Glu Arg Ser 330 335 340			1062
acc caa gcc aaa gtt tta atc gct tgc atg cat gaa gag tat ttt tct Thr Gln Ala Lys Val Leu Ile Ala Cys Met His Glu Glu Tyr Phe Ser 345 350 355			1110
tac gcc aac cgc tta gcg gag tct tta agg caa agc ggg att ttt agt Tyr Ala Asn Arg Leu Ala Glu Ser Leu Arg Gln Ser Gly Ile Phe Ser 360 365 370 375			1158
gaa gtc tat cca gaa gct caa aaa atc aaa aaa ccc ttt tct tat gcc Glu Val Tyr Pro Glu Ala Gln Lys Ile Lys Lys Pro Phe Ser Tyr Ala 380 385 390			1206
aac cat aaa ggg cat gag ttt gtg gct gtc att ggc gaa gaa gaa ttt Asn His Lys Gly His Glu Phe Val Ala Val Ile Gly Glu Glu Glu Phe 395 400 405			1254
aaa agc gaa act tta agc ttg aaa aac atg cat tca ggc atg cag ttg Lys Ser Glu Thr Leu Ser Leu Lys Asn Met His Ser Gly Met Gln Leu 410 415 420			1302
aat tgc ttg agt ttt tta aaa gcc ctt gaa atc att gga gaa aac gat Asn Cys Leu Ser Phe Leu Lys Ala Leu Glu Ile Ile Gly Glu Asn Asp 425 430 435			1350
gaa gac tta taatgtcgct attgttgggg ccagtggggc ggtagg Glu Asp Leu 440			1395

<210> 280
 <211> 442
 <212> PRT
 <213> Helicobacter pylori

<400> 280
 Met Ile Thr Pro Lys Val Leu Ser Gly Phe Lys Asp Arg Leu Pro Lys
 1 5 10 15
 Asp Ala Ile Gln Lys Ala Gln Leu Leu Ala Lys Val Ser Val Val Phe
 20 25 30
 Gln Ser Phe Gly Phe Val Pro Ile Glu Thr Pro His Leu Glu Tyr Ala
 35 40 45
 Gln Thr Leu Leu Pro Asp Ala Ser Ser Asp Ile Gln Lys Glu Ile Tyr
 50 55 60
 Arg Phe Lys Asp His Gly Asp Arg Asp Val Ala Leu Arg Phe Asp Leu
 65 70 75 80
 Thr Val Pro Leu Ala Arg Phe Val Ser Leu His His Gln Thr Leu Gly
 85 90 95
 Met Pro Phe Lys Arg Tyr Ala Ile Gly Asn Val Phe Arg Gly Glu Arg
 100 105 110
 Ala Gln Lys Gly Arg Tyr Arg Glu Phe Thr Gln Cys Asp Phe Asp Phe
 115 120 125
 Ile Gly Ser Glu Ser Leu Val Cys Asp Ala Glu Ile Ile Gln Val Ile
 130 135 140
 Val Ala Ser Leu Lys Ala Leu Asp Leu Glu Asp Phe Cys Val Ser Ile
 145 150 155 160
 Asn His Arg Lys Ile Leu Asn Gly Ile Cys Glu Tyr Phe Gly Ile Ser
 165 170 175
 Gln Val Asn Glu Ala Leu Arg Ile Val Asp Lys Leu Glu Lys Ile Gly
 180 185 190
 Leu Asn Gly Val Glu Glu Glu Leu Lys Lys Glu Cys Gly Leu Asn Ser
 195 200 205
 Asn Thr Ile Lys Glu Leu Leu Glu Leu Ile Gln Ile Lys Gln Asn Asp
 210 215 220
 Leu Ser His Ala Glu Phe Phe Glu Lys Ile Ala Tyr Leu Lys Asp Tyr
 225 230 235 240
 Asn Glu Asn Leu Lys Lys Gly Ile Gln Asp Leu Glu Arg Leu Tyr Gln
 245 250 255
 Leu Leu Gly Asp Leu Gln Ile Ser Gln Asn Leu Tyr Lys Ile Asp Phe
 260 265 270
 Ser Ile Ala Arg Gly Leu Gly Tyr Tyr Thr Gly Ile Val Tyr Glu Thr
 275 280 285
 Thr Leu Asn Glu Met Lys Ser Leu Gly Ser Val Cys Ser Gly Gly Arg
 290 295 300
 Tyr Asp His Leu Thr Lys Asn Phe Ser Lys Glu Asn Leu Gln Gly Val
 305 310 315 320
 Gly Ala Ser Ile Gly Ile Asp Arg Leu Ile Val Ala Leu Ser Glu Met
 325 330 335
 Gln Leu Leu Asp Glu Arg Ser Thr Gln Ala Lys Val Leu Ile Ala Cys
 340 345 350
 Met His Glu Glu Tyr Phe Ser Tyr Ala Asn Arg Leu Ala Glu Ser Leu
 355 360 365
 Arg Gln Ser Gly Ile Phe Ser Glu Val Tyr Pro Glu Ala Gln Lys Ile
 370 375 380
 Lys Lys Pro Phe Ser Tyr Ala Asn His Lys Gly His Glu Phe Val Ala
 385 390 395 400
 Val Ile Gly Glu Glu Glu Phe Lys Ser Glu Thr Leu Ser Leu Lys Asn
 405 410 415
 Met His Ser Gly Met Gln Leu Asn Cys Leu Ser Phe Leu Lys Ala Leu

420 425 430
 Glu Ile Ile Gly Glu Asn Asp Glu Asp Leu
 435 440

<210> 281
 <211> 639
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (70)...(597)

<400> 281
 cacgcccata ggagaagtgg cagaagttat gcagctctta ttaaagaagg aaaaattaaa 60
 gcttggggg atg agt gag gca ggg tta tct agc atc caa aaa gcc cat caa 111
 Met Ser Glu Ala Gly Leu Ser Ser Ile Gln Lys Ala His Gln
 1 5 10

 att tgc cct tta agc gcg ttg cag agc gaa tat tcc ttg tgg tgg cgc 159
 Ile Cys Pro Leu Ser Ala Leu Gln Ser Glu Tyr Ser Leu Trp Trp Arg
 15 20 25 30

 gaa cct gaa aaa gag att tta ggt ttt tta gaa aaa gaa aaa att gga 207
 Glu Pro Glu Lys Glu Ile Leu Gly Phe Leu Glu Lys Glu Lys Ile Gly
 35 40 45

 ttt gtc gct ttt tcg cct ttg ggt aag ggg ttt tta ggc gcg aaa ttt 255
 Phe Val Ala Phe Ser Pro Leu Gly Lys Gly Phe Leu Gly Ala Lys Phe
 50 55 60

 gaa aaa aat gcc act ttc gct agt gag gat ttt aga agc gtt tct cct 303
 Glu Lys Asn Ala Thr Phe Ala Ser Glu Asp Phe Arg Ser Val Ser Pro
 65 70 75

 agg ttt aat caa gaa aat cta gcc aaa aat tac gcc ttg gtg gaa tta 351
 Arg Phe Asn Gln Glu Asn Leu Ala Lys Asn Tyr Ala Leu Val Glu Leu
 80 85 90

 atc caa gat cat gca cac gct aaa ggc gtt aca cca gcc caa ctg gct 399
 Ile Gln Asp His Ala His Ala Lys Gly Val Thr Pro Ala Gln Leu Ala
 95 100 105 110

 ctc tca tgg att ttg cac acg caa aaa atc att gtc cct ctc ttt ggc 447
 Leu Ser Trp Ile Leu His Thr Gln Lys Ile Ile Val Pro Leu Phe Gly
 115 120 125

 acc acc aaa gaa tct agg ctc ata gaa aat ata ggg gct ttg cag gtt 495
 Thr Thr Lys Glu Ser Arg Leu Ile Glu Asn Ile Gly Ala Leu Gln Val
 130 135 140

 tct tgg agt caa aaa gaa ttg gag att ttc caa aaa gaa ttg act gca 543
 Ser Trp Ser Gln Lys Glu Leu Glu Ile Phe Gln Lys Glu Leu Thr Ala
 145 150 155

 atc aaa ata gaa ggg gcc cgc tac cct gaa aga atc aat gaa atg gtg 591
 Ile Lys Ile Glu Gly Ala Arg Tyr Pro Glu Arg Ile Asn Glu Met Val
 160 165 170

aat caa taaaagtatt gggatattat aattgcattg gctcttttaa aa
 Asn Gln
 175

639

<210> 282
 <211> 176
 <212> PRT
 <213> Helicobacter pylori

<400> 282
 Met Ser Glu Ala Gly Leu Ser Ser Ile Gln Lys Ala His Gln Ile Cys
 1 5 10 15
 Pro Leu Ser Ala Leu Gln Ser Glu Tyr Ser Leu Trp Trp Arg Glu Pro
 20 25 30
 Glu Lys Glu Ile Leu Gly Phe Leu Glu Lys Glu Lys Ile Gly Phe Val
 35 40 45
 Ala Phe Ser Pro Leu Gly Lys Gly Phe Leu Gly Ala Lys Phe Glu Lys
 50 55 60
 Asn Ala Thr Phe Ala Ser Glu Asp Phe Arg Ser Val Ser Pro Arg Phe
 65 70 75 80
 Asn Gln Glu Asn Leu Ala Lys Asn Tyr Ala Leu Val Glu Leu Ile Gln
 85 90 95
 Asp His Ala His Ala Lys Gly Val Thr Pro Ala Gln Leu Ala Leu Ser
 100 105 110
 Trp Ile Leu His Thr Gln Lys Ile Ile Val Pro Leu Phe Gly Thr Thr
 115 120 125
 Lys Glu Ser Arg Leu Ile Glu Asn Ile Gly Ala Leu Gln Val Ser Trp
 130 135 140
 Ser Gln Lys Glu Leu Glu Ile Phe Gln Lys Glu Leu Thr Ala Ile Lys
 145 150 155 160
 Ile Glu Gly Ala Arg Tyr Pro Glu Arg Ile Asn Glu Met Val Asn Gln
 165 170 175

<210> 283
 <211> 2133
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (25)...(2088)

<400> 283
 taattttaaaa aaggaacatt aaat atg gat ttt atc acc atc aat tct agt 51
 Met Asp Phe Ile Thr Ile Asn Ser Ser
 1 5
 aac aaa acc gaa gag ttc gct ctc aaa caa gtg gcc aaa caa gcc acc 99
 Asn Lys Thr Glu Glu Phe Ala Leu Lys Gln Val Ala Lys Gln Ala Thr
 10 15 20 25
 agc tct ctt tta tac cga tta gga aaa acc att att tta gcg agc gtg 147
 Ser Ser Leu Leu Tyr Arg Leu Gly Lys Thr Ile Ile Leu Ala Ser Val
 30 35 40
 tgc gtg gaa aga gag cct gtg agt gaa gat ttt ctg cct tta gtg gtg 195

Cys	Val	Glu	Arg	Glu	Pro	Val	Ser	Glu	Asp	Phe	Leu	Pro	Leu	Val	Val		
			45					50					55				
cag	ttt	tta	gaa	aaa	tct	tat	gca	gcc	gga	aag	atc	ccg	ggc	ggg	ttt	243	
Gln	Phe	Leu	Glu	Lys	Ser	Tyr	Ala	Ala	Gly	Lys	Ile	Pro	Gly	Gly	Phe		
		60					65					70					
gtt	aaa	aga	gaa	ggc	agg	gcg	caa	gat	ttt	gaa	atc	tta	acc	tct	agg	291	
Val	Lys	Arg	Glu	Gly	Arg	Ala	Gln	Asp	Phe	Glu	Ile	Leu	Thr	Ser	Arg		
	75					80					85						
ctc	ata	gac	agg	act	tta	cgc	cct	tta	ttc	cct	aaa	gac	tac	cgc	tac	339	
Leu	Ile	Asp	Arg	Thr	Leu	Arg	Pro	Leu	Phe	Pro	Lys	Asp	Tyr	Arg	Tyr		
	90				95				100						105		
cct	aca	cag	atc	act	tta	atg	gtt	tta	agc	cat	gat	att	gaa	aat	gac	387	
Pro	Thr	Gln	Ile	Thr	Leu	Met	Val	Leu	Ser	His	Asp	Ile	Glu	Asn	Asp		
				110					115					120			
ttg	cag	gtt	tct	gct	tta	aac	gcc	gct	tca	gcc	gct	ctc	ttt	ttg	gcc	435	
Leu	Gln	Val	Ser	Ala	Leu	Asn	Ala	Ala	Ser	Ala	Ala	Leu	Phe	Leu	Ala		
			125					130					135				
cat	atc	gct	cct	att	aaa	agc	gtg	agc	gct	tgc	agg	atc	gct	agg	atg	483	
His	Ile	Ala	Pro	Ile	Lys	Ser	Val	Ser	Ala	Cys	Arg	Ile	Ala	Arg	Met		
	140						145					150					
gat	aac	gaa	ttt	atc	att	aac	cct	agc	gca	agc	ctt	ttg	aat	caa	tcc	531	
Asp	Asn	Glu	Phe	Ile	Ile	Asn	Pro	Ser	Ala	Ser	Leu	Leu	Asn	Gln	Ser		
	155					160					165						
agt	ttg	gat	ttg	ttc	gtg	tct	gga	acg	aaa	gag	agt	ttg	aac	atg	ata	579	
Ser	Leu	Asp	Leu	Phe	Val	Ser	Gly	Thr	Lys	Glu	Ser	Leu	Asn	Met	Ile		
	170				175					180					185		
gaa	atg	cgc	tct	ttg	ggg	caa	aaa	ttg	aac	gct	tta	gaa	gag	cct	tta	627	
Glu	Met	Arg	Ser	Leu	Gly	Gln	Lys	Leu	Asn	Ala	Leu	Glu	Glu	Pro	Leu		
				190				195						200			
atg	tta	gaa	gct	tta	gaa	ttg	gct	caa	aaa	agt	ttg	gaa	gaa	act	tgc	675	
Met	Leu	Glu	Ala	Leu	Glu	Leu	Ala	Gln	Lys	Ser	Leu	Glu	Glu	Thr	Cys		
			205				210						215				
acg	ctt	tat	gaa	gag	att	ttc	acg	ccc	cac	caa	aac	gag	ctg	ttt	ttc	723	
Thr	Leu	Tyr	Glu	Glu	Ile	Phe	Thr	Pro	His	Gln	Asn	Glu	Leu	Phe	Phe		
		220					225					230					
aaa	gag	agc	caa	gga	ata	gtc	ttt	aat	gaa	agg	ctg	tta	gat	tta	ttg	771	
Lys	Glu	Ser	Gln	Gly	Ile	Val	Phe	Asn	Glu	Arg	Leu	Leu	Asp	Leu	Leu		
	235					240					245						
aaa	aat	cag	tat	ttt	gat	gaa	atc	atc	aaa	ggc	att	gaa	agt	tct	gct	819	
Lys	Asn	Gln	Tyr	Phe	Asp	Glu	Ile	Ile	Lys	Gly	Ile	Glu	Ser	Ser	Ala		
	250				255				260						265		
ttg	agc	gag	cga	gaa	aat	gtt	ttc	aat	gaa	att	gcc	aga	aaa	atc	agt	867	
Leu	Ser	Glu	Arg	Glu	Asn	Val	Phe	Asn	Glu	Ile	Ala	Arg	Lys	Ile	Ser		
				270					275					280			

gaa gcc cac tca gaa ttc agt tta gaa gaa att gaa ttg tct tta gaa	915
Glu Ala His Ser Glu Phe Ser Leu Glu Glu Ile Glu Leu Ser Leu Glu	
285 290 295	
aaa gtg aaa aag act gag ata aga cgc atg atc att aag gat aaa atc	963
Lys Val Lys Lys Thr Glu Ile Arg Arg Met Ile Ile Lys Asp Lys Ile	
300 305 310	
cgc ccg gat aag cgc gcg tta gaa gaa gtg cgc ccc att ttg ata gag	1011
Arg Pro Asp Lys Arg Ala Leu Glu Glu Val Arg Pro Ile Leu Ile Glu	
315 320 325	
agc gat ttg ctc cct atg gcg cat agc tcc att tta ttc act agg ggg	1059
Ser Asp Leu Leu Pro Met Ala His Ser Ser Ile Leu Phe Thr Arg Gly	
330 335 340 345	
caa act caa agc tta gtg gta ggg gtt tta ggc acg gat aat gac gct	1107
Gln Thr Gln Ser Leu Val Val Gly Val Leu Gly Thr Asp Asn Asp Ala	
350 355 360	
caa acc cat gag agt ttg gag cat aaa gct ccc att aaa gag cgc ttc	1155
Gln Thr His Glu Ser Leu Glu His Lys Ala Pro Ile Lys Glu Arg Phe	
365 370 375	
atg ttt cat tat aat ttc cct cct ttc tgc gtg ggc gaa gcg agt tct	1203
Met Phe His Tyr Asn Phe Pro Pro Phe Cys Val Gly Glu Ala Ser Ser	
380 385 390	
att ggc gcg gct tca agg cgt gaa tta ggg cat ggc aat ttg gct aaa	1251
Ile Gly Ala Ala Ser Arg Arg Glu Leu Gly His Gly Asn Leu Ala Lys	
395 400 405	
aga gcc tta gaa acg agc att aaa aat aaa gag cag gtg ata cga ttg	1299
Arg Ala Leu Glu Thr Ser Ile Lys Asn Lys Glu Gln Val Ile Arg Leu	
410 415 420 425	
gtt tct gag att tta gaa agc aat ggt tca agc tca atg gcg agc gtg	1347
Val Ser Glu Ile Leu Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val	
430 435 440	
tgc gca ggc tct tta gcc ctt tat gca agc ggt gtg gaa att tac gat	1395
Cys Ala Gly Ser Leu Ala Leu Tyr Ala Ser Gly Val Glu Ile Tyr Asp	
445 450 455	
tta gtc gct ggg gtg gct atg ggc atg gtg agc gaa ggg caa gat cac	1443
Leu Val Ala Gly Val Ala Met Gly Met Val Ser Glu Gly Gln Asp His	
460 465 470	
gct att tta agc gat att agc ggc tta gaa gac gca gaa ggc gat atg	1491
Ala Ile Leu Ser Asp Ile Ser Gly Leu Glu Asp Ala Glu Gly Asp Met	
475 480 485	
gat ttt aag att gct ggg aat tta gaa ggc att acg gcc atg caa atg	1539
Asp Phe Lys Ile Ala Gly Asn Leu Glu Gly Ile Thr Ala Met Gln Met	
490 495 500 505	
gat acc aaa atg agc ggt atc aag cta gaa att tta tac caa gcc tta	1587
Asp Thr Lys Met Ser Gly Ile Lys Leu Glu Ile Leu Tyr Gln Ala Leu	
510 515 520	

Ser	Glu	Asp	Phe	Leu	Pro	Leu	Val	Val	Gln	Phe	Leu	Glu	Lys	Ser	Tyr
50						55					60				
Ala	Ala	Gly	Lys	Ile	Pro	Gly	Gly	Phe	Val	Lys	Arg	Glu	Gly	Arg	Ala
65					70					75					80
Gln	Asp	Phe	Glu	Ile	Leu	Thr	Ser	Arg	Leu	Ile	Asp	Arg	Thr	Leu	Arg
				85					90					95	
Pro	Leu	Phe	Pro	Lys	Asp	Tyr	Arg	Tyr	Pro	Thr	Gln	Ile	Thr	Leu	Met
			100					105					110		
Val	Leu	Ser	His	Asp	Ile	Glu	Asn	Asp	Leu	Gln	Val	Ser	Ala	Leu	Asn
		115					120					125			
Ala	Ala	Ser	Ala	Ala	Leu	Phe	Leu	Ala	His	Ile	Ala	Pro	Ile	Lys	Ser
						135					140				
Val	Ser	Ala	Cys	Arg	Ile	Ala	Arg	Met	Asp	Asn	Glu	Phe	Ile	Ile	Asn
145					150					155					160
Pro	Ser	Ala	Ser	Leu	Leu	Asn	Gln	Ser	Ser	Leu	Asp	Leu	Phe	Val	Ser
				165					170					175	
Gly	Thr	Lys	Glu	Ser	Leu	Asn	Met	Ile	Glu	Met	Arg	Ser	Leu	Gly	Gln
			180					185					190		
Lys	Leu	Asn	Ala	Leu	Glu	Glu	Pro	Leu	Met	Leu	Glu	Ala	Leu	Glu	Leu
		195					200					205			
Ala	Gln	Lys	Ser	Leu	Glu	Glu	Thr	Cys	Thr	Leu	Tyr	Glu	Glu	Ile	Phe
	210					215					220				
Thr	Pro	His	Gln	Asn	Glu	Leu	Phe	Phe	Lys	Glu	Ser	Gln	Gly	Ile	Val
225					230					235					240
Phe	Asn	Glu	Arg	Leu	Leu	Asp	Leu	Leu	Lys	Asn	Gln	Tyr	Phe	Asp	Glu
				245					250					255	
Ile	Ile	Lys	Gly	Ile	Glu	Ser	Ser	Ala	Leu	Ser	Glu	Arg	Glu	Asn	Val
			260					265					270		
Phe	Asn	Glu	Ile	Ala	Arg	Lys	Ile	Ser	Glu	Ala	His	Ser	Glu	Phe	Ser
		275					280					285			
Leu	Glu	Glu	Ile	Glu	Leu	Ser	Leu	Glu	Lys	Val	Lys	Lys	Thr	Glu	Ile
	290					295					300				
Arg	Arg	Met	Ile	Ile	Lys	Asp	Lys	Ile	Arg	Pro	Asp	Lys	Arg	Ala	Leu
305					310					315					320
Glu	Glu	Val	Arg	Pro	Ile	Leu	Ile	Glu	Ser	Asp	Leu	Leu	Pro	Met	Ala
				325					330					335	
His	Ser	Ser	Ile	Leu	Phe	Thr	Arg	Gly	Gln	Thr	Gln	Ser	Leu	Val	Val
			340					345					350		
Gly	Val	Leu	Gly	Thr	Asp	Asn	Asp	Ala	Gln	Thr	His	Glu	Ser	Leu	Glu
		355					360					365			
His	Lys	Ala	Pro	Ile	Lys	Glu	Arg	Phe	Met	Phe	His	Tyr	Asn	Phe	Pro
	370					375				380					
Pro	Phe	Cys	Val	Gly	Glu	Ala	Ser	Ser	Ile	Gly	Ala	Ala	Ser	Arg	Arg
385					390					395					400
Glu	Leu	Gly	His	Gly	Asn	Leu	Ala	Lys	Arg	Ala	Leu	Glu	Thr	Ser	Ile
				405					410					415	
Lys	Asn	Lys	Glu	Gln	Val	Ile	Arg	Leu	Val	Ser	Glu	Ile	Leu	Glu	Ser
			420					425					430		
Asn	Gly	Ser	Ser	Ser	Met	Ala	Ser	Val	Cys	Ala	Gly	Ser	Leu	Ala	Leu
		435					440					445			
Tyr	Ala	Ser	Gly	Val	Glu	Ile	Tyr	Asp	Leu	Val	Ala	Gly	Val	Ala	Met
	450					455					460				
Gly	Met	Val	Ser	Glu	Gly	Gln	Asp	His	Ala	Ile	Leu	Ser	Asp	Ile	Ser
465					470					475					480
Gly	Leu	Glu	Asp	Ala	Glu	Gly	Asp	Met	Asp	Phe	Lys	Ile	Ala	Gly	Asn
				485					490					495	
Leu	Glu	Gly	Ile	Thr	Ala	Met	Gln	Met	Asp	Thr	Lys	Met	Ser	Gly	Ile
			500					505					510		
Lys	Leu	Glu	Ile	Leu	Tyr	Gln	Ala	Leu	Gln	Ala	Lys	Glu	Ala	Arg	

90	95	100	105	
tct aaa agc tat atg aaa gct ttt gtt aaa gag tgt ggc atc aaa agt	Ser Lys Ser Tyr Met Lys Ala Phe Val Lys Glu Cys Gly Ile Lys Ser	387		
	110	115	120	
gcg tct tac ttt gaa aca aac gac tta aaa gaa gct ttg agt tac att	Ala Ser Tyr Phe Glu Thr Asn Asp Leu Lys Glu Ala Leu Ser Tyr Ile	435		
	125	130	135	
caa aac gct tct ttc ccc tta gtc att aaa gcg ttg aat aaa aac aca	Gln Asn Ala Ser Phe Pro Leu Val Ile Lys Ala Leu Asn Lys Asn Thr	483		
	140	145	150	
agc att gtc tat caa gaa gaa gaa gcg ata aaa atc ctt gaa gac gct	Ser Ile Val Tyr Gln Glu Glu Glu Ala Ile Lys Ile Leu Glu Asp Ala	531		
	155	160	165	
ttc aaa caa agc aat gag cct gtg att ata gag cct ttt tta gag gga	Phe Lys Gln Ser Asn Glu Pro Val Ile Ile Glu Pro Phe Leu Glu Gly	579		
	170	175	180	185
ttt gag ctt tca gtt aca gcg ctc ata gcc aat gat gat ttt atc ttg	Phe Glu Leu Ser Val Thr Ala Leu Ile Ala Asn Asp Asp Phe Ile Leu	627		
	190	195	200	
ttg ccc ttt tgc caa aac tac aaa cgc tta tta gag ggg gat aat ggg	Leu Pro Phe Cys Gln Asn Tyr Lys Arg Leu Leu Glu Gly Asp Asn Gly	675		
	205	210	215	
gtc aat acg ggg ggt atg ggg gcc atc gct cct gca aac ttt ttc tct	Val Asn Thr Gly Gly Met Gly Ala Ile Ala Pro Ala Asn Phe Phe Ser	723		
	220	225	230	
aat gaa tta gaa gag aaa ata aaa aat cat atc ttt aaa ccc act tta	Asn Glu Leu Glu Glu Lys Ile Lys Asn His Ile Phe Lys Pro Thr Leu	771		
	235	240	245	
gag aaa ctt cag gct gac aac acg cct ttt aaa ggg gtt tta ctc gct	Glu Lys Leu Gln Ala Asp Asn Thr Pro Phe Lys Gly Val Leu Leu Ala	819		
	250	255	260	265
gaa att gta atc ata gaa gaa aaa ggc gtt tta gag ccg tat tta ttg	Glu Ile Val Ile Ile Glu Glu Lys Gly Val Leu Glu Pro Tyr Leu Leu	867		
	270	275	280	
gat ttt agc gtg cgt ttt aaa gac att gaa tgc cag acg att tta ccc	Asp Phe Ser Val Arg Phe Lys Asp Ile Glu Cys Gln Thr Ile Leu Pro	915		
	285	290	295	
ctt tta gaa agc tcg ctt tta gat ttg tgt ttg gcc aca gcc aaa ggg	Leu Leu Glu Ser Ser Leu Leu Asp Leu Cys Leu Ala Thr Ala Lys Gly	963		
	300	305	310	
gaa tta cat tct ctt gaa ttg gtg ttt tct aaa gaa ttt gtg atg agt	Glu Leu His Ser Leu Glu Leu Val Phe Ser Lys Glu Phe Val Met Ser	1011		
	315	320	325	
gtg gcg ctt gtt tct agg aat tac ccc act agc tct tcg ccc aaa caa		1059		

Val	Ala	Leu	Val	Ser	Arg	Asn	Tyr	Pro	Thr	Ser	Ser	Ser	Pro	Lys	Gln		
330					335					340					345		
acc	ctt	tat	att	gat	ccg	gtt	gat	gaa	aaa	aag	ggt	cat	ttg	att	tta		1107
Thr	Leu	Tyr	Ile	Asp	Pro	Val	Asp	Glu	Lys	Lys	Gly	His	Leu	Ile	Leu		
				350					355					360			
ggg	gag	gtg	gag	cag	gat	aat	ggc	gtg	ttt	gaa	agc	agt	ggg	ggg	agg		1155
Gly	Glu	Val	Glu	Gln	Asp	Asn	Gly	Val	Phe	Glu	Ser	Ser	Gly	Gly	Arg		
			365					370					375				
gtg	atc	ttt	gcc	att	ggg	agg	gga	aaa	tcc	tta	tta	gaa	gcc	aga	aac		1203
Val	Ile	Phe	Ala	Ile	Gly	Arg	Gly	Lys	Ser	Leu	Leu	Glu	Ala	Arg	Asn		
		380					385					390					
cat	gct	tat	gaa	atc	gct	caa	aag	gtg	cat	ttt	gaa	ggc	atg	ttt	tat		1251
His	Ala	Tyr	Glu	Ile	Ala	Gln	Lys	Val	His	Phe	Glu	Gly	Met	Phe	Tyr		
	395					400					405						
cgc	aag	gat	att	ggg	ttt	aag	gtg	tta	gat	ttg	aaa	gaa	tat	tct			1296
Arg	Lys	Asp	Ile	Gly	Phe	Lys	Val	Leu	Asp	Leu	Lys	Glu	Tyr	Ser			
410				415				420									
taaaggttaa	agtttaagac	aaaccaaaga	gtttgtcttg	tttg													1340

<210> 286

<211> 424

<212> PRT

<213> Helicobacter pylori

<400> 286

Met	Lys	Asp	Asn	Asn	Asn	Tyr	Asn	Val	Leu	Ile	Val	Gly	Asn	Lys	Gly	
1			5					10					15			
Arg	Glu	Tyr	Ala	Leu	Ala	Gln	Arg	Leu	Gln	Gln	Asp	Glu	Arg	Val	Asn	
			20					25				30				
Ala	Leu	Tyr	Phe	Cys	Leu	Gly	Asn	Gly	Gly	Thr	Gln	Asp	Leu	Gly	Glu	
		35				40					45					
Asn	Leu	Glu	Cys	Glu	His	Tyr	Glu	His	Ile	Val	Glu	Leu	Ala	Leu	Lys	
	50				55					60						
Lys	Gln	Ile	His	Leu	Ala	Ile	Ile	Ser	Glu	Glu	Phe	Leu	Val	Leu		
65				70					75					80		
Gly	Leu	Thr	Glu	Met	Leu	Glu	Lys	Ala	Gly	Ile	Leu	Val	Phe	Gly	Ala	
			85					90					95			
Ser	Lys	Glu	Ala	Ala	Lys	Leu	Glu	Ala	Ser	Lys	Ser	Tyr	Met	Lys	Ala	
			100					105					110			
Phe	Val	Lys	Glu	Cys	Gly	Ile	Lys	Ser	Ala	Ser	Tyr	Phe	Glu	Thr	Asn	
		115				120						125				
Asp	Leu	Lys	Glu	Ala	Leu	Ser	Tyr	Ile	Gln	Asn	Ala	Ser	Phe	Pro	Leu	
	130				135						140					
Val	Ile	Lys	Ala	Leu	Asn	Lys	Asn	Thr	Ser	Ile	Val	Tyr	Gln	Glu	Glu	
145				150					155						160	
Glu	Ala	Ile	Lys	Ile	Leu	Glu	Asp	Ala	Phe	Lys	Gln	Ser	Asn	Glu	Pro	
			165					170						175		
Val	Ile	Ile	Glu	Pro	Phe	Leu	Glu	Gly	Phe	Glu	Leu	Ser	Val	Thr	Ala	
		180					185						190			
Leu	Ile	Ala	Asn	Asp	Asp	Phe	Ile	Leu	Leu	Pro	Phe	Cys	Gln	Asn	Tyr	
	195				200							205				
Lys	Arg	Leu	Leu	Glu	Gly	Asp	Asn	Gly	Val	Asn	Thr	Gly	Gly	Met	Gly	
	210				215						220					

Ala	Ile	Ala	Pro	Ala	Asn	Phe	Phe	Ser	Asn	Glu	Leu	Glu	Glu	Lys	Ile
225					230					235					240
Lys	Asn	His	Ile	Phe	Lys	Pro	Thr	Leu	Glu	Lys	Leu	Gln	Ala	Asp	Asn
				245					250					255	
Thr	Pro	Phe	Lys	Gly	Val	Leu	Leu	Ala	Glu	Ile	Val	Ile	Ile	Glu	Glu
			260					265					270		
Lys	Gly	Val	Leu	Glu	Pro	Tyr	Leu	Leu	Asp	Phe	Ser	Val	Arg	Phe	Lys
		275					280					285			
Asp	Ile	Glu	Cys	Gln	Thr	Ile	Leu	Pro	Leu	Leu	Glu	Ser	Ser	Leu	Leu
	290					295					300				
Asp	Leu	Cys	Leu	Ala	Thr	Ala	Lys	Gly	Glu	Leu	His	Ser	Leu	Glu	Leu
305					310					315					320
Val	Phe	Ser	Lys	Glu	Phe	Val	Met	Ser	Val	Ala	Leu	Val	Ser	Arg	Asn
			325						330					335	
Tyr	Pro	Thr	Ser	Ser	Ser	Pro	Lys	Gln	Thr	Leu	Tyr	Ile	Asp	Pro	Val
			340					345					350		
Asp	Glu	Lys	Lys	Gly	His	Leu	Ile	Leu	Gly	Glu	Val	Glu	Gln	Asp	Asn
		355					360					365			
Gly	Val	Phe	Glu	Ser	Ser	Gly	Gly	Arg	Val	Ile	Phe	Ala	Ile	Gly	Arg
	370					375					380				
Gly	Lys	Ser	Leu	Leu	Glu	Ala	Arg	Asn	His	Ala	Tyr	Glu	Ile	Ala	Gln
385					390					395					400
Lys	Val	His	Phe	Glu	Gly	Met	Phe	Tyr	Arg	Lys	Asp	Ile	Gly	Phe	Lys
			405						410					415	
Val	Leu	Asp	Leu	Lys	Glu	Tyr	Ser								
			420												

<210> 287
 <211> 827
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (17)...(769)

<400> 287
 ttaaaatgaa gtgaaa atg aga gaa ata aat atg att tta tac att cat atc 52
 Met Arg Glu Ile Asn Met Ile Leu Tyr Ile His Ile
 1 5 10

ccc ttt tgt gaa aat aaa tgc ggc tat tgc gct ttc aat tcc tat gaa 100
 Pro Phe Cys Glu Asn Lys Cys Gly Tyr Cys Ala Phe Asn Ser Tyr Glu
 15 20 25

aac aag cat ggg tta aaa gaa gaa tac act caa gcg tta tgc ctg gat 148
 Asn Lys His Gly Leu Lys Glu Glu Tyr Thr Gln Ala Leu Cys Leu Asp
 30 35 40

tta aag cat gcg tta agt caa act gac gaa cca att gaa agc gtt ttt 196
 Leu Lys His Ala Leu Ser Gln Thr Asp Glu Pro Ile Glu Ser Val Phe
 45 50 55 60

att ggt ggc ggc acg cct aac act tta agc gtg aag gct ttt gaa agg 244
 Ile Gly Gly Gly Thr Pro Asn Thr Leu Ser Val Lys Ala Phe Glu Arg
 65 70 75

att ttt gaa agc att tat caa cat gcg agc ttg agc ttg gat tgt gag 292

Ile	Phe	Glu	Ser	Ile	Tyr	Gln	His	Ala	Ser	Leu	Ser	Leu	Asp	Cys	Glu	
			80					85					90			
atc	acc	act	gaa	gct	aac	ccc	gaa	ttg	att	act	aaa	gct	tgg	tgt	caa	340
Ile	Thr	Thr	Glu	Ala	Asn	Pro	Glu	Leu	Ile	Thr	Lys	Ala	Trp	Cys	Gln	
		95					100					105				
ggc	tta	aaa	ggt	tta	ggg	atc	aac	cgc	ttg	agt	tta	ggg	gtg	caa	agt	388
Gly	Leu	Lys	Gly	Leu	Gly	Ile	Asn	Arg	Leu	Ser	Leu	Gly	Val	Gln	Ser	
	110					115					120					
ttt	agg	gaa	gat	aaa	tta	ttg	ttt	tta	gag	cgc	caa	cat	tcc	aaa	aat	436
Phe	Arg	Glu	Asp	Lys	Leu	Leu	Phe	Leu	Glu	Arg	Gln	His	Ser	Lys	Asn	
125					130					135					140	
atc	gct	cct	gcg	ata	gaa	act	att	tta	aaa	agc	ggg	att	gaa	aat	atc	484
Ile	Ala	Pro	Ala	Ile	Glu	Thr	Ile	Leu	Lys	Ser	Gly	Ile	Glu	Asn	Ile	
				145					150					155		
agc	att	gat	ttg	att	tat	aac	acc	cca	tta	gac	aat	gaa	aac	tct	cta	532
Ser	Ile	Asp	Leu	Ile	Tyr	Asn	Thr	Pro	Leu	Asp	Asn	Glu	Asn	Ser	Leu	
			160					165					170			
aaa	gaa	gaa	tta	aaa	ctc	gct	aaa	gaa	ctc	cct	atc	aac	cac	ttg	agc	580
Lys	Glu	Glu	Leu	Lys	Leu	Ala	Lys	Glu	Leu	Pro	Ile	Asn	His	Leu	Ser	
		175					180					185				
gct	tac	gct	ttg	agc	gtt	gaa	aaa	aac	acg	aat	tta	gaa	aaa	aac	gcc	628
Ala	Tyr	Ala	Leu	Ser	Val	Glu	Lys	Asn	Thr	Asn	Leu	Glu	Lys	Asn	Ala	
	190					195					200					
aaa	aaa	ccc	tca	tgc	gct	cat	ttt	gac	aat	gtg	gtg	aga	gag	att	tta	676
Lys	Lys	Pro	Ser	Cys	Ala	His	Phe	Asp	Asn	Val	Val	Arg	Glu	Ile	Leu	
205					210					215					220	
gag	ggc	ttt	tct	ttc	aag	caa	tac	gag	tgt	cta	att	acg	cta	gaa	att	724
Glu	Gly	Phe	Ser	Phe	Lys	Gln	Tyr	Glu	Cys	Leu	Ile	Thr	Leu	Glu	Ile	
				225					230					235		
atc	aag	tca	aac	aca	act	tgg	ctt	act	ggg	ggg	cta	aag	att	att		769
Ile	Lys	Ser	Asn	Thr	Thr	Trp	Leu	Thr	Gly	Gly	Leu	Lys	Ile	Ile		
			240					245					250			
taggggtgcgg	ggctgggggct	gtgggctgcg	tggcgaatga	gcgctttttt	gcaaaaaa											827

<210> 288
 <211> 251
 <212> PRT
 <213> Helicobacter pylori

<400> 288
 Met Arg Glu Ile Asn Met Ile Leu Tyr Ile His Ile Pro Phe Cys Glu
 1 5 10 15
 Asn Lys Cys Gly Tyr Cys Ala Phe Asn Ser Tyr Glu Asn Lys His Gly
 20 25 30
 Leu Lys Glu Tyr Thr Gln Ala Leu Cys Leu Asp Leu Lys His Ala
 35 40 45
 Leu Ser Gln Thr Asp Glu Pro Ile Glu Ser Val Phe Ile Gly Gly Gly
 50 55 60

Thr	Pro	Asn	Thr	Leu	Ser	Val	Lys	Ala	Phe	Glu	Arg	Ile	Phe	Glu	Ser
65					70					75				80	
Ile	Tyr	Gln	His	Ala	Ser	Leu	Ser	Leu	Asp	Cys	Glu	Ile	Thr	Thr	Glu
			85						90					95	
Ala	Asn	Pro	Glu	Leu	Ile	Thr	Lys	Ala	Trp	Cys	Gln	Gly	Leu	Lys	Gly
		100						105					110		
Leu	Gly	Ile	Asn	Arg	Leu	Ser	Leu	Gly	Val	Gln	Ser	Phe	Arg	Glu	Asp
		115					120					125			
Lys	Leu	Leu	Phe	Leu	Glu	Arg	Gln	His	Ser	Lys	Asn	Ile	Ala	Pro	Ala
	130					135					140				
Ile	Glu	Thr	Ile	Leu	Lys	Ser	Gly	Ile	Glu	Asn	Ile	Ser	Ile	Asp	Leu
145					150					155				160	
Ile	Tyr	Asn	Thr	Pro	Leu	Asp	Asn	Glu	Asn	Ser	Leu	Lys	Glu	Glu	Leu
			165					170						175	
Lys	Leu	Ala	Lys	Glu	Leu	Pro	Ile	Asn	His	Leu	Ser	Ala	Tyr	Ala	Leu
		180						185					190		
Ser	Val	Glu	Lys	Asn	Thr	Asn	Leu	Glu	Lys	Asn	Ala	Lys	Lys	Pro	Ser
	195					200					205				
Cys	Ala	His	Phe	Asp	Asn	Val	Val	Arg	Glu	Ile	Leu	Glu	Gly	Phe	Ser
	210				215						220				
Phe	Lys	Gln	Tyr	Glu	Cys	Leu	Ile	Thr	Leu	Glu	Ile	Ile	Lys	Ser	Asn
225					230					235					240
Thr	Thr	Trp	Leu	Thr	Gly	Gly	Leu	Lys	Ile	Ile					
			245						250						

<210> 289
 <211> 1291
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (76)...(1257)

<400> 289
 gccaaagtcac tgcttatttc aaaagagagg ggtatttata ggggtgtaac cggtcaaaaa 60
 tacggcggca cgagc atg ggc agc ata gaa agg atc cac aat gtc gct caa 111
 Met Gly Ser Ile Glu Arg Ile His Asn Val Ala Gln
 1 5 10

agg gtt tta gaa agc gtt aca tta ggg cat caa gtc gtg gtg gtg gtt 159
 Arg Val Leu Glu Ser Val Thr Leu Gly His Gln Val Val Val Val Val
 15 20 25

tca gcg atg agc ggc gaa acc gac agg ctt tta gaa ttt ggc aag aat 207
 Ser Ala Met Ser Gly Glu Thr Asp Arg Leu Leu Glu Phe Gly Lys Asn
 30 35 40

ttt agc cat aac cct aac aag cga gag atg gac agg att gta agc gtg 255
 Phe Ser His Asn Pro Asn Lys Arg Glu Met Asp Arg Ile Val Ser Val
 45 50 55 60

ggg gaa ttg gtt tca agt gcg gct ttg agc atg gcg tta gaa agg tat 303
 Gly Glu Leu Val Ser Ser Ala Ala Leu Ser Met Ala Leu Glu Arg Tyr
 65 70 75

ggg cat aga gcc att tcc ttg agc ggg aaa gaa gcg ggc att tta acc 351
 Gly His Arg Ala Ile Ser Leu Ser Gly Lys Glu Ala Gly Ile Leu Thr

80					85					90						
agc	tcg	cat	ttt	caa	aac	gcc	gtg	atc	caa	tcc	att	gac	acc	aaa	cgc	399
Ser	Ser	His	Phe	Gln	Asn	Ala	Val	Ile	Gln	Ser	Ile	Asp	Thr	Lys	Arg	
		95					100					105				
atc	aca	gag	ctt	tta	gaa	aaa	aac	tac	att	gtg	gtg	atc	gct	ggg	ttt	447
Ile	Thr	Glu	Leu	Leu	Glu	Lys	Asn	Tyr	Ile	Val	Val	Ile	Ala	Gly	Phe	
	110					115					120					
caa	ggc	gct	gat	att	caa	ggt	gaa	aca	acg	act	tta	ggg	cgt	ggg	ggg	495
Gln	Gly	Ala	Asp	Ile	Gln	Gly	Glu	Thr	Thr	Thr	Leu	Gly	Arg	Gly	Gly	
125					130				135						140	
agc	gat	ttg	agc	gcg	gtt	gct	ttg	gcc	ggg	gct	tta	aaa	gcg	cat	ttg	543
Ser	Asp	Leu	Ser	Ala	Val	Ala	Leu	Ala	Gly	Ala	Leu	Lys	Ala	His	Leu	
				145					150					155		
tgc	gaa	atc	tat	acg	gat	gtg	gat	ggc	gtt	tat	acc	acc	gat	ccg	cgc	591
Cys	Glu	Ile	Tyr	Thr	Asp	Val	Asp	Gly	Val	Tyr	Thr	Thr	Asp	Pro	Arg	
			160					165					170			
att	gaa	gaa	aag	gct	caa	aaa	atc	gcg	caa	atc	agc	tat	gat	gaa	atg	639
Ile	Glu	Glu	Lys	Ala	Gln	Lys	Ile	Ala	Gln	Ile	Ser	Tyr	Asp	Glu	Met	
		175					180					185				
ctt	gaa	ctg	gct	tct	atg	ggg	gct	aaa	gtt	tta	tta	aac	cgc	tcg	gtg	687
Leu	Glu	Leu	Ala	Ser	Met	Gly	Ala	Lys	Val	Leu	Leu	Asn	Arg	Ser	Val	
	190					195					200					
gaa	tta	gcc	aaa	aag	ctc	agc	gtg	aag	tta	gtg	act	cgc	aat	tcg	ttt	735
Glu	Leu	Ala	Lys	Lys	Leu	Ser	Val	Lys	Leu	Val	Thr	Arg	Asn	Ser	Phe	
205					210					215					220	
aac	cat	agc	gaa	ggc	acg	ctc	att	gtg	gct	gaa	aaa	gac	ttt	aaa	gga	783
Asn	His	Ser	Glu	Gly	Thr	Leu	Ile	Val	Ala	Glu	Lys	Asp	Phe	Lys	Gly	
				225					230					235		
gaa	cgc	atg	gaa	acc	cct	ata	gtg	agt	ggg	atc	gca	ttg	gat	aaa	aat	831
Glu	Arg	Met	Glu	Thr	Pro	Ile	Val	Ser	Gly	Ile	Ala	Leu	Asp	Lys	Asn	
			240					245					250			
cag	gct	cgt	gtg	agc	atg	gag	ggc	gtg	gaa	gat	cgg	cca	ggc	att	gcc	879
Gln	Ala	Arg	Val	Ser	Met	Glu	Gly	Val	Glu	Asp	Arg	Pro	Gly	Ile	Ala	
		255					260					265				
gct	gaa	atc	ttt	ggc	gct	tta	gcg	gag	tat	cgc	att	aac	gtg	gat	atg	927
Ala	Glu	Ile	Phe	Gly	Ala	Leu	Ala	Glu	Tyr	Arg	Ile	Asn	Val	Asp	Met	
	270					275					280					
atc	gtc	caa	acg	atc	ggc	aga	gac	ggc	aaa	acc	gat	ttg	gat	ttt	acg	975
Ile	Val	Gln	Thr	Ile	Gly	Arg	Asp	Gly	Lys	Thr	Asp	Leu	Asp	Phe	Thr	
285					290					295					300	
atc	gtt	aaa	acc	caa	ata	gaa	gaa	acc	aag	caa	gcc	tta	aag	cct	ttt	1023
Ile	Val	Lys	Thr	Gln	Ile	Glu	Glu	Thr	Lys	Gln	Ala	Leu	Lys	Pro	Phe	
				305					310					315		
tta	gcg	caa	atg	gat	tcc	att	gat	tat	gat	gaa	aat	atc	gct	aaa	gtc	1071

Leu	Ala	Gln	Met	Asp	Ser	Ile	Asp	Tyr	Asp	Glu	Asn	Ile	Ala	Lys	Val	
			320					325					330			
tcc	ata	gtg	ggc	gtg	ggc	atg	aag	tcg	cat	tct	ggg	gtg	gcg	agt	atc	1119
Ser	Ile	Val	Gly	Val	Gly	Met	Lys	Ser	His	Ser	Gly	Val	Ala	Ser	Ile	
		335					340					345				
gct	ttt	aaa	gcc	cta	gcc	aaa	gac	aat	atc	aat	atc	atg	atg	att	tct	1167
Ala	Phe	Lys	Ala	Leu	Ala	Lys	Asp	Asn	Ile	Asn	Ile	Met	Met	Ile	Ser	
	350					355					360					
aca	agc	gag	att	aaa	att	tcg	gtt	ttg	att	gac	att	aaa	tac	gct	gaa	1215
Thr	Ser	Glu	Ile	Lys	Ile	Ser	Val	Leu	Ile	Asp	Ile	Lys	Tyr	Ala	Glu	
365					370					375					380	
tta	gct	gtt	aga	act	ttg	cat	gcg	gtg	tat	caa	tta	gat	caa			1257
Leu	Ala	Val	Arg	Thr	Leu	His	Ala	Val	Tyr	Gln	Leu	Asp	Gln			
			385						390							
tgaaaaattt	ctacgattgg	atcaaggaat	ttgt													1291
<210> 290																
<211> 394																
<212> PRT																
<213> Helicobacter pylori																
<400> 290																
Met	Gly	Ser	Ile	Glu	Arg	Ile	His	Asn	Val	Ala	Gln	Arg	Val	Leu	Glu	
1				5					10					15		
Ser	Val	Thr	Leu	Gly	His	Gln	Val	Val	Val	Val	Val	Ser	Ala	Met	Ser	
			20					25					30			
Gly	Glu	Thr	Asp	Arg	Leu	Leu	Glu	Phe	Gly	Lys	Asn	Phe	Ser	His	Asn	
		35					40					45				
Pro	Asn	Lys	Arg	Glu	Met	Asp	Arg	Ile	Val	Ser	Val	Gly	Glu	Leu	Val	
	50					55					60					
Ser	Ser	Ala	Ala	Leu	Ser	Met	Ala	Leu	Glu	Arg	Tyr	Gly	His	Arg	Ala	
65				70						75					80	
Ile	Ser	Leu	Ser	Gly	Lys	Glu	Ala	Gly	Ile	Leu	Thr	Ser	Ser	His	Phe	
			85					90						95		
Gln	Asn	Ala	Val	Ile	Gln	Ser	Ile	Asp	Thr	Lys	Arg	Ile	Thr	Glu	Leu	
		100						105					110			
Leu	Glu	Lys	Asn	Tyr	Ile	Val	Val	Ile	Ala	Gly	Phe	Gln	Gly	Ala	Asp	
		115					120					125				
Ile	Gln	Gly	Glu	Thr	Thr	Thr	Leu	Gly	Arg	Gly	Gly	Ser	Asp	Leu	Ser	
	130					135					140					
Ala	Val	Ala	Leu	Ala	Gly	Ala	Leu	Lys	Ala	His	Leu	Cys	Glu	Ile	Tyr	
145				150					155						160	
Thr	Asp	Val	Asp	Gly	Val	Tyr	Thr	Thr	Asp	Pro	Arg	Ile	Glu	Glu	Lys	
			165						170					175		
Ala	Gln	Lys	Ile	Ala	Gln	Ile	Ser	Tyr	Asp	Glu	Met	Leu	Glu	Leu	Ala	
		180						185					190			
Ser	Met	Gly	Ala	Lys	Val	Leu	Leu	Asn	Arg	Ser	Val	Glu	Leu	Ala	Lys	
		195					200					205				
Lys	Leu	Ser	Val	Lys	Leu	Val	Thr	Arg	Asn	Ser	Phe	Asn	His	Ser	Glu	
	210					215					220					
Gly	Thr	Leu	Ile	Val	Ala	Glu	Lys	Asp	Phe	Lys	Gly	Glu	Arg	Met	Glu	
225				230					235						240	
Thr	Pro	Ile	Val	Ser	Gly	Ile	Ala	Leu	Asp	Lys	Asn	Gln	Ala	Arg	Val	
				245					250					255		

Ser Met Glu Gly Val Glu Asp Arg Pro Gly Ile Ala Ala Glu Ile Phe
 260 265 270
 Gly Ala Leu Ala Glu Tyr Arg Ile Asn Val Asp Met Ile Val Gln Thr
 275 280 285
 Ile Gly Arg Asp Gly Lys Thr Asp Leu Asp Phe Thr Ile Val Lys Thr
 290 295 300
 Gln Ile Glu Glu Thr Lys Gln Ala Leu Lys Pro Phe Leu Ala Gln Met
 305 310 315 320
 Asp Ser Ile Asp Tyr Asp Glu Asn Ile Ala Lys Val Ser Ile Val Gly
 325 330 335
 Val Gly Met Lys Ser His Ser Gly Val Ala Ser Ile Ala Phe Lys Ala
 340 345 350
 Leu Ala Lys Asp Asn Ile Asn Ile Met Met Ile Ser Thr Ser Glu Ile
 355 360 365
 Lys Ile Ser Val Leu Ile Asp Ile Lys Tyr Ala Glu Leu Ala Val Arg
 370 375 380
 Thr Leu His Ala Val Tyr Gln Leu Asp Gln
 385 390

<210> 291
 <211> 706
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (1)...(663)

<400> 291
 ggt tac tct gtg aaa aac tcc aac cgc ctt att tat acg gac aat ctt 48
 Gly Tyr Ser Val Lys Asn Ser Asn Arg Leu Ile Tyr Thr Asp Asn Leu
 1 5 10 15

 gaa gag agc cta gaa gag act gca agc ctt ttt gaa cac cac att aaa 96
 Glu Glu Ser Leu Glu Glu Thr Ala Ser Leu Phe Glu His His Ile Lys
 20 25 30

 ttc tac acg gag att att gaa aaa gac aaa aag gtg atc aaa act ttc 144
 Phe Tyr Thr Glu Ile Ile Glu Lys Asp Lys Lys Val Ile Lys Thr Phe
 35 40 45

 aac aag gat ttt aaa ata gag cat gcc aaa gaa gtc att tcc aaa gct 192
 Asn Lys Asp Phe Lys Ile Glu His Ala Lys Glu Val Ile Ser Lys Ala
 50 55 60

 cac cta aaa cac agc gaa tta aac gct ttt tta atc gcc gct cct agt 240
 His Leu Lys His Ser Glu Leu Asn Ala Phe Leu Ile Ala Ala Pro Ser
 65 70 75 80

 tat ggt ata gaa gcc caa aac gcg ctt tta aaa atc tta gaa gaa ccc 288
 Tyr Gly Ile Glu Ala Gln Asn Ala Leu Leu Lys Ile Leu Glu Glu Pro
 85 90 95

 ccg aat aac gtt tgt ttt atc atg ttc gct aaa agc caa aac cat gtg 336
 Pro Asn Asn Val Cys Phe Ile Met Phe Ala Lys Ser Gln Asn His Val
 100 105 110

 tta gcc acc att aaa tcc cgc cta att aaa gaa gac aaa cgc caa aaa 384

Leu	Ala	Thr	Ile	Lys	Ser	Arg	Leu	Ile	Lys	Glu	Asp	Lys	Arg	Gln	Lys		
		115					120					125					
atc	ccc	cta	aaa	cct	tta	gat	ttg	gat	tta	tcc	aag	ctg	gat	ttg	aaa	432	
Ile	Pro	Leu	Lys	Pro	Leu	Asp	Leu	Asp	Leu	Ser	Lys	Leu	Asp	Leu	Lys		
		130				135					140						
gac	att	tat	gcg	ttt	tta	aaa	aat	tta	gac	aaa	gaa	aat	ttt	gat	tcc	480	
Asp	Ile	Tyr	Ala	Phe	Leu	Lys	Asn	Leu	Asp	Lys	Glu	Asn	Phe	Asp	Ser		
					150					155					160		
aga	gaa	aat	cag	agg	gaa	agg	att	gaa	agc	ctg	tta	gag	agc	gtt	aac	528	
Arg	Glu	Asn	Gln	Arg	Glu	Arg	Ile	Glu	Ser	Leu	Leu	Glu	Ser	Val	Asn		
				165					170					175			
agg	cat	aag	atc	ccc	tta	aac	gag	caa	gaa	ttg	caa	gcc	ttt	gat	tta	576	
Arg	His	Lys	Ile	Pro	Leu	Asn	Glu	Gln	Glu	Leu	Gln	Ala	Phe	Asp	Leu		
				180				185						190			
gcg	atc	aag	gct	aac	agc	tct	tat	tac	aag	ctc	agc	tat	aat	ctt	tta	624	
Ala	Ile	Lys	Ala	Asn	Ser	Ser	Tyr	Tyr	Lys	Leu	Ser	Tyr	Asn	Leu	Leu		
		195					200					205					
ccc	ctg	ctt	tta	agc	ctt	tta	tcc	aaa	aag	aaa	acg	cca	tgattgtaaa			673	
Pro	Leu	Leu	Leu	Ser	Leu	Leu	Ser	Lys	Lys	Lys	Thr	Pro					
		210				215					220						
acgccttaac	cctgatgcgc	tcaaaaaacgc	tct													706	

<210> 292

<211> 221

<212> PRT

<213> Helicobacter pylori

<400> 292

Gly	Tyr	Ser	Val	Lys	Asn	Ser	Asn	Arg	Leu	Ile	Tyr	Thr	Asp	Asn	Leu		
1				5					10					15			
Glu	Glu	Ser	Leu	Glu	Glu	Thr	Ala	Ser	Leu	Phe	Glu	His	His	Ile	Lys		
			20					25					30				
Phe	Tyr	Thr	Glu	Ile	Ile	Glu	Lys	Asp	Lys	Lys	Val	Ile	Lys	Thr	Phe		
		35					40					45					
Asn	Lys	Asp	Phe	Lys	Ile	Glu	His	Ala	Lys	Glu	Val	Ile	Ser	Lys	Ala		
		50				55					60						
His	Leu	Lys	His	Ser	Glu	Leu	Asn	Ala	Phe	Leu	Ile	Ala	Ala	Pro	Ser		
		65			70					75				80			
Tyr	Gly	Ile	Glu	Ala	Gln	Asn	Ala	Leu	Leu	Lys	Ile	Leu	Glu	Glu	Pro		
			85					90						95			
Pro	Asn	Asn	Val	Cys	Phe	Ile	Met	Phe	Ala	Lys	Ser	Gln	Asn	His	Val		
			100					105					110				
Leu	Ala	Thr	Ile	Lys	Ser	Arg	Leu	Ile	Lys	Glu	Asp	Lys	Arg	Gln	Lys		
		115					120					125					
Ile	Pro	Leu	Lys	Pro	Leu	Asp	Leu	Asp	Leu	Ser	Lys	Leu	Asp	Leu	Lys		
		130				135					140						
Asp	Ile	Tyr	Ala	Phe	Leu	Lys	Asn	Leu	Asp	Lys	Glu	Asn	Phe	Asp	Ser		
					150					155					160		
Arg	Glu	Asn	Gln	Arg	Glu	Arg	Ile	Glu	Ser	Leu	Leu	Glu	Ser	Val	Asn		
				165					170					175			
Arg	His	Lys	Ile	Pro	Leu	Asn	Glu	Gln	Glu	Leu	Gln	Ala	Phe	Asp	Leu		
			180					185						190			

Ala	Ile	Lys	Ala	Asn	Ser	Ser	Tyr	Tyr	Lys	Leu	Ser	Tyr	Asn	Leu	Leu
		195					200					205			
Pro	Leu	Leu	Leu	Ser	Leu	Leu	Ser	Lys	Lys	Lys	Thr	Pro			
	210					215					220				

<210> 293
 <211> 1102
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (58)...(1059)

<400> 293
 tattctctcg caataattgt tattgttatt gcgacaaaac ttttagaagg agttatt atg 60
 Met
 1

gga	agt	atc	ggt	agt	atg	ggc	aaa	cct	att	gaa	ggg	ttt	tta	gtg	gca	108
Gly	Ser	Ile	Gly	Ser	Met	Gly	Lys	Pro	Ile	Glu	Gly	Phe	Leu	Val	Ala	
			5					10					15			

gcc	att	cag	ttt	cct	gtg	cca	att	gtc	aat	agc	cgt	aag	gat	att	gat	156
Ala	Ile	Gln	Phe	Pro	Val	Pro	Ile	Val	Asn	Ser	Arg	Lys	Asp	Ile	Asp	
		20					25					30				

cac	aat	att	gaa	agc	att	att	aga	acc	ttg	cat	gcg	act	aaa	gcg	ggg	204
His	Asn	Ile	Glu	Ser	Ile	Ile	Arg	Thr	Leu	His	Ala	Thr	Lys	Ala	Gly	
	35					40					45					

tat	ccg	gga	gtg	gag	ctt	atc	att	ttc	cct	gag	tat	agc	acg	caa	ggt	252
Tyr	Pro	Gly	Val	Glu	Leu	Ile	Ile	Phe	Pro	Glu	Tyr	Ser	Thr	Gln	Gly	
	50				55					60					65	

ttg	aat	acc	gct	aag	tgg	ctt	agc	gaa	gag	ttt	tta	tta	gat	gtc	ccg	300
Leu	Asn	Thr	Ala	Lys	Trp	Leu	Ser	Glu	Glu	Phe	Leu	Leu	Asp	Val	Pro	
				70					75					80		

ggt	aaa	gag	aca	gag	cta	tac	gct	aag	gcg	tgt	aaa	gag	gcg	aaa	gtt	348
Gly	Lys	Glu	Thr	Glu	Leu	Tyr	Ala	Lys	Ala	Cys	Lys	Glu	Ala	Lys	Val	
			85					90					95			

tat	ggt	gtt	ttt	tca	atc	atg	gaa	cgc	aat	cct	gat	tct	aac	aaa	aac	396
Tyr	Gly	Val	Phe	Ser	Ile	Met	Glu	Arg	Asn	Pro	Asp	Ser	Asn	Lys	Asn	
		100					105					110				

ccc	tac	aac	acc	gcc	att	atc	att	gat	ccg	caa	ggt	gaa	atc	att	tta	444
Pro	Tyr	Asn	Thr	Ala	Ile	Ile	Ile	Asp	Pro	Gln	Gly	Glu	Ile	Ile	Leu	
		115				120					125					

aaa	tac	cgc	aag	cta	ttc	cca	tgg	aat	ccc	att	gag	cca	tgg	tat	cct	492
Lys	Tyr	Arg	Lys	Leu	Phe	Pro	Trp	Asn	Pro	Ile	Glu	Pro	Trp	Tyr	Pro	
	130				135					140					145	

ggg	gat	tta	gga	atg	cct	gtg	tgc	gag	ggt	ccg	ggc	gga	tca	aaa	tta	540
Gly	Asp	Leu	Gly	Met	Pro	Val	Cys	Glu	Gly	Pro	Gly	Gly	Ser	Lys	Leu	
				150					155					160		


```

gcc gtg tgc att tgc cat gac ggc atg att cca gag ctc gcc aga gaa 588
Ala Val Cys Ile Cys His Asp Gly Met Ile Pro Glu Leu Ala Arg Glu
165 170 175

gcg gcc tat aaa ggg tgc aat gtg tat atc cgc att tca ggc tat agc 636
Ala Ala Tyr Lys Gly Cys Asn Val Tyr Ile Arg Ile Ser Gly Tyr Ser
180 185 190

act caa gtc aat gat caa tgg att ttg acc aac cgc tcc aac gca tgg 684
Thr Gln Val Asn Asp Gln Trp Ile Leu Thr Asn Arg Ser Asn Ala Trp
195 200 205

cac aat ttg atg tat acc gtg agc gtg aat tta gcc ggc tat gat aat 732
His Asn Leu Met Tyr Thr Val Ser Val Asn Leu Ala Gly Tyr Asp Asn
210 215 220 225

gtc ttt tac tac ttt ggt gag ggg caa atc tgt aac ttt gat ggc acg 780
Val Phe Tyr Tyr Phe Gly Glu Gly Gln Ile Cys Asn Phe Asp Gly Thr
230 235 240

act ctt gtt caa ggg cac cgc aac cct tgg gag att gta acc ggg gaa 828
Thr Leu Val Gln Gly His Arg Asn Pro Trp Glu Ile Val Thr Gly Glu
245 250 255

atc tat ccc aaa atg gca gac aac gct cgc tta agc tgg gga tta gaa 876
Ile Tyr Pro Lys Met Ala Asp Asn Ala Arg Leu Ser Trp Gly Leu Glu
260 265 270

aac aac att tac aac cta ggc cat aga ggg tat gtg gct aaa ccg ggc 924
Asn Asn Ile Tyr Asn Leu Gly His Arg Gly Tyr Val Ala Lys Pro Gly
275 280 285

gga gaa cat gac gca ggc tta acc tat atc aaa gac tta gcg gcc ggt 972
Gly Glu His Asp Ala Gly Leu Thr Tyr Ile Lys Asp Leu Ala Ala Gly
290 295 300 305

aaa tac aaa ttg cct tgg gaa gat cac atg aaa atc aaa gac ggc tct 1020
Lys Tyr Lys Leu Pro Trp Glu Asp His Met Lys Ile Lys Asp Gly Ser
310 315 320

att tat ggc tac cct acc acc ggt ggg cgt ttt ggg aaa taatccctaa 1069
Ile Tyr Gly Tyr Pro Thr Thr Gly Gly Arg Phe Gly Lys
325 330

ccttgcat ttt ttgctagaac ccgtttttaa ggg 1102

<210> 294
<211> 334
<212> PRT
<213> Helicobacter pylori

<400> 294
Met Gly Ser Ile Gly Ser Met Gly Lys Pro Ile Glu Gly Phe Leu Val
1 5 10 15
Ala Ala Ile Gln Phe Pro Val Pro Ile Val Asn Ser Arg Lys Asp Ile
20 25 30
Asp His Asn Ile Glu Ser Ile Ile Arg Thr Leu His Ala Thr Lys Ala
35 40 45

```

Gly	Tyr	Pro	Gly	Val	Glu	Leu	Ile	Ile	Phe	Pro	Glu	Tyr	Ser	Thr	Gln
50						55					60				
Gly	Leu	Asn	Thr	Ala	Lys	Trp	Leu	Ser	Glu	Glu	Phe	Leu	Leu	Asp	Val
65					70				75						80
Pro	Gly	Lys	Glu	Thr	Glu	Leu	Tyr	Ala	Lys	Ala	Cys	Lys	Glu	Ala	Lys
			85					90					95		
Val	Tyr	Gly	Val	Phe	Ser	Ile	Met	Glu	Arg	Asn	Pro	Asp	Ser	Asn	Lys
			100					105					110		
Asn	Pro	Tyr	Asn	Thr	Ala	Ile	Ile	Ile	Asp	Pro	Gln	Gly	Glu	Ile	Ile
		115				120						125			
Leu	Lys	Tyr	Arg	Lys	Leu	Phe	Pro	Trp	Asn	Pro	Ile	Glu	Pro	Trp	Tyr
130					135						140				
Pro	Gly	Asp	Leu	Gly	Met	Pro	Val	Cys	Glu	Gly	Pro	Gly	Gly	Ser	Lys
145					150					155					160
Leu	Ala	Val	Cys	Ile	Cys	His	Asp	Gly	Met	Ile	Pro	Glu	Leu	Ala	Arg
			165						170						175
Glu	Ala	Ala	Tyr	Lys	Gly	Cys	Asn	Val	Tyr	Ile	Arg	Ile	Ser	Gly	Tyr
			180					185					190		
Ser	Thr	Gln	Val	Asn	Asp	Gln	Trp	Ile	Leu	Thr	Asn	Arg	Ser	Asn	Ala
		195				200						205			
Trp	His	Asn	Leu	Met	Tyr	Thr	Val	Ser	Val	Asn	Leu	Ala	Gly	Tyr	Asp
210					215						220				
Asn	Val	Phe	Tyr	Tyr	Phe	Gly	Glu	Gly	Gln	Ile	Cys	Asn	Phe	Asp	Gly
225					230					235					240
Thr	Thr	Leu	Val	Gln	Gly	His	Arg	Asn	Pro	Trp	Glu	Ile	Val	Thr	Gly
			245					250						255	
Glu	Ile	Tyr	Pro	Lys	Met	Ala	Asp	Asn	Ala	Arg	Leu	Ser	Trp	Gly	Leu
			260					265					270		
Glu	Asn	Asn	Ile	Tyr	Asn	Leu	Gly	His	Arg	Gly	Tyr	Val	Ala	Lys	Pro
		275					280					285			
Gly	Gly	Glu	His	Asp	Ala	Gly	Leu	Thr	Tyr	Ile	Lys	Asp	Leu	Ala	Ala
290						295					300				
Gly	Lys	Tyr	Lys	Leu	Pro	Trp	Glu	Asp	His	Met	Lys	Ile	Lys	Asp	Gly
305				310						315					320
Ser	Ile	Tyr	Gly	Tyr	Pro	Thr	Thr	Gly	Gly	Arg	Phe	Gly	Lys		
			325						330						

<210> 295

<211> 1152

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (52)...(1095)

<400> 295

tagctatgga	ttttcgccgt	atttgtggtg	gataaaagaa	aaggatcttc	a	atg	att	57
						Met	Ile	
						1		

gct	tac	att	ctc	aaa	cgc	ttg	ctt	ttg	att	atc	cct	act	tta	tta	gct	105
Ala	Tyr	Ile	Leu	Lys	Arg	Leu	Leu	Leu	Ile	Ile	Pro	Thr	Leu	Leu	Ala	
		5						10					15			

atc	atg	acc	att	aat	ttc	ttt	ttg	atc	caa	tcg	gct	cct	gga	ggc	cct	153
Ile	Met	Thr	Ile	Asn	Phe	Phe	Leu	Ile	Gln	Ser	Ala	Pro	Gly	Gly	Pro	
	20					25					30					

ata gag cag atg atg gct aaa atc aat aac acg cag tcc aaa gag att	201
Ile Glu Gln Met Met Ala Lys Ile Asn Asn Thr Gln Ser Lys Glu Ile	
35 40 45 50	
caa ggc gtt gtt aaa gag cgt tcg tat agg gcg tct caa ggg ttg gag	249
Gln Gly Val Val Lys Glu Arg Ser Tyr Arg Ala Ser Gln Gly Leu Glu	
55 60 65	
agc gat ttg tta gaa aat tta aaa aaa ctc tat ggt ttt gac aag ccc	297
Ser Asp Leu Leu Glu Asn Leu Lys Lys Leu Tyr Gly Phe Asp Lys Pro	
70 75 80	
ata ggg gag cgc tac ctt ctc atg ctc aaa aaa tat ctg caa ttt gat	345
Ile Gly Glu Arg Tyr Leu Leu Met Leu Lys Lys Tyr Leu Gln Phe Asp	
85 90 95	
ttt ggg gag agc ttt tat cgc cag att aaa gtg ata gat ttg att aag	393
Phe Gly Glu Ser Phe Tyr Arg Gln Ile Lys Val Ile Asp Leu Ile Lys	
100 105 110	
gaa aaa ttg ccc gta tcc att tcg tta ggg ctt ttt agc acg ctt ttg	441
Glu Lys Leu Pro Val Ser Ile Ser Leu Gly Leu Phe Ser Thr Leu Leu	
115 120 125 130	
att tat ctt att tct atc cct tta ggg att ttc aag gcc aaa cgc aat	489
Ile Tyr Leu Ile Ser Ile Pro Leu Gly Ile Phe Lys Ala Lys Arg Asn	
135 140 145	
aac gag cct tta gac gtg tta agc agc gtg gtg atc att gtc gct aac	537
Asn Glu Pro Leu Asp Val Leu Ser Ser Val Val Ile Ile Val Ala Asn	
150 155 160	
gct atc ccg gcc ttt ttg ttt gcg gtg gtg ttg atc gtg ttt ttt gct	585
Ala Ile Pro Ala Phe Leu Phe Ala Val Val Leu Ile Val Phe Phe Ala	
165 170 175	
gga ggg aat tat tgg cat tgg ttc cct tta aag ggg cta gtg agc gat	633
Gly Gly Asn Tyr Trp His Trp Phe Pro Leu Lys Gly Leu Val Ser Asp	
180 185 190	
aat ttt gaa agt ttg agc gcg tta ggt aaa atc aag gat tat tta tgg	681
Asn Phe Glu Ser Leu Ser Ala Leu Gly Lys Ile Lys Asp Tyr Leu Trp	
195 200 205 210	
cat atc act ttg ccc gtt ctt tgc att tct tta ggg ggt ttt gca agc	729
His Ile Thr Leu Pro Val Leu Cys Ile Ser Leu Gly Gly Phe Ala Ser	
215 220 225	
ctt acg ctt tta gtg aaa aac tct ttt tta gat gaa atg ggc aag ctc	777
Leu Thr Leu Leu Val Lys Asn Ser Phe Leu Asp Glu Met Gly Lys Leu	
230 235 240	
tat gta ctg agc gct aag gct aag ggt tgt tca gtg ggg cgt att ttt	825
Tyr Val Leu Ser Ala Lys Ala Lys Gly Cys Ser Val Gly Arg Ile Phe	
245 250 255	
tat gcg cat gtg ttc cgt aat gcg att tta tta gtg gtg gcg ggt ttc	873
Tyr Ala His Val Phe Arg Asn Ala Ile Leu Leu Val Val Ala Gly Phe	

260	265	270	
ccg caa gct ttt ttg ggc atg ttc ttt agc tca agt ttg ttg ata gag			921
Pro Gln Ala Phe Leu Gly Met Phe Phe Ser Ser Ser Leu Leu Ile Glu			
275	280	285	290
att gtt ttt agc cta gac ggg tta ggg ctt tta ggg tat gaa agc att			969
Ile Val Phe Ser Leu Asp Gly Leu Gly Leu Leu Gly Tyr Glu Ser Ile			
	295	300	305
gtg agt agg gat tat ccc gtt gtg ttt ggt tcg ctt tat att ttc acg			1017
Val Ser Arg Asp Tyr Pro Val Val Phe Gly Ser Leu Tyr Ile Phe Thr			
	310	315	320
ctt tta ggt ttg gta gcg agt ttg ata agc gat ttg ctc tgt gtg gtg			1065
Leu Leu Gly Leu Val Ala Ser Leu Ile Ser Asp Leu Leu Cys Val Val			
	325	330	335
att gac cct agg att gat ttt gaa aag cgt tgagggtagg aatgaaaact			1115
Ile Asp Pro Arg Ile Asp Phe Glu Lys Arg			
340	345		
gagatgaaat cttctttaaa actttttatg cggcctt			1152
<210> 296			
<211> 348			
<212> PRT			
<213> Helicobacter pylori			
<400> 296			
Met Ile Ala Tyr Ile Leu Lys Arg Leu Leu Leu Ile Ile Pro Thr Leu			
1 5 10 15			
Leu Ala Ile Met Thr Ile Asn Phe Phe Leu Ile Gln Ser Ala Pro Gly			
20 25 30			
Gly Pro Ile Glu Gln Met Met Ala Lys Ile Asn Asn Thr Gln Ser Lys			
35 40 45			
Glu Ile Gln Gly Val Val Lys Glu Arg Ser Tyr Arg Ala Ser Gln Gly			
50 55 60			
Leu Glu Ser Asp Leu Leu Glu Asn Leu Lys Lys Leu Tyr Gly Phe Asp			
65 70 75 80			
Lys Pro Ile Gly Glu Arg Tyr Leu Leu Met Leu Lys Lys Tyr Leu Gln			
85 90 95			
Phe Asp Phe Gly Glu Ser Phe Tyr Arg Gln Ile Lys Val Ile Asp Leu			
100 105 110			
Ile Lys Glu Lys Leu Pro Val Ser Ile Ser Leu Gly Leu Phe Ser Thr			
115 120 125			
Leu Leu Ile Tyr Leu Ile Ser Ile Pro Leu Gly Ile Phe Lys Ala Lys			
130 135 140			
Arg Asn Asn Glu Pro Leu Asp Val Leu Ser Ser Val Val Ile Ile Val			
145 150 155 160			
Ala Asn Ala Ile Pro Ala Phe Leu Phe Ala Val Val Leu Ile Val Phe			
165 170 175			
Phe Ala Gly Gly Asn Tyr Trp His Trp Phe Pro Leu Lys Gly Leu Val			
180 185 190			
Ser Asp Asn Phe Glu Ser Leu Ser Ala Leu Gly Lys Ile Lys Asp Tyr			
195 200 205			
Leu Trp His Ile Thr Leu Pro Val Leu Cys Ile Ser Leu Gly Gly Phe			
210 215 220			
Ala Ser Leu Thr Leu Leu Val Lys Asn Ser Phe Leu Asp Glu Met Gly			

tgc gct aaa gtt tta gaa gaa aag ggt gct caa atc gtg gct ttt ggt	435
Cys Ala Lys Val Leu Glu Glu Lys Gly Ala Gln Ile Val Ala Phe Gly	
125 130 135 140	

gct tta gct aat cgg ggc att tgc aag cgt gct cat tct cat tta aaa	483
Ala Leu Ala Asn Arg Gly Ile Cys Lys Arg Ala His Ser His Leu Lys	
145 150 155	

gcc caa gag gga gcg tgt ttg cct agc cat ttg ccc ctt ttt gct tta	531
Ala Gln Glu Gly Ala Cys Leu Pro Ser His Leu Pro Leu Phe Ala Leu	
160 165 170	

gaa gat ttt gtt ttt gac atg cac aag cct agt tct tgc cct tta tgc	579
Glu Asp Phe Val Phe Asp Met His Lys Pro Ser Ser Cys Pro Leu Cys	
175 180 185	

gct act agc gtt gct ata aag cca gga agt cgt ggc aac taaaaaaca	628
Ala Thr Ser Val Ala Ile Lys Pro Gly Ser Arg Gly Asn	
190 195 200	

aaaaaaaata aaaccccaaa aaaaaagcaa gcgt	662
---------------------------------------	-----

<210> 298

<211> 201

<212> PRT

<213> *Helicobacter pylori*

<400> 298

Met Asp Ile Lys Ala Cys Tyr Gln Asn Ala Lys Ala Leu Leu Glu Gly	
1 5 10 15	
His Phe Leu Leu Ser Ser Gly Phe His Ser Asn Tyr Tyr Leu Gln Ser	
20 25 30	
Ala Lys Val Leu Glu Asp Pro Lys Leu Ala Glu Gln Leu Ala Leu Glu	
35 40 45	
Leu Ala Lys Gln Ile Gln Glu Ala His Leu Asn Ile Glu Cys Val Cys	
50 55 60	
Ser Pro Ala Ile Gly Gly Ile Leu Ala Gly Tyr Glu Leu Ala Arg Ala	
65 70 75 80	
Leu Gly Val Arg Phe Ile Phe Thr Glu Arg Val Asp Asn Thr Met Ala	
85 90 95	
Leu Arg Arg Gly Phe Glu Val Lys Lys Asn Glu Lys Ile Leu Val Cys	
100 105 110	
Glu Asp Ile Ile Thr Thr Gly Lys Ser Ala Met Glu Cys Ala Lys Val	
115 120 125	
Leu Glu Glu Lys Gly Ala Gln Ile Val Ala Phe Gly Ala Leu Ala Asn	
130 135 140	
Arg Gly Ile Cys Lys Arg Ala His Ser His Leu Lys Ala Gln Glu Gly	
145 150 155 160	
Ala Cys Leu Pro Ser His Leu Pro Leu Phe Ala Leu Glu Asp Phe Val	
165 170 175	
Phe Asp Met His Lys Pro Ser Ser Cys Pro Leu Cys Ala Thr Ser Val	
180 185 190	
Ala Ile Lys Pro Gly Ser Arg Gly Asn	
195 200	

<210> 299

<211> 401

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (40)...(384)

<400> 299

```
ctctctttgc gcctaaaggc ctttatcacc gatattttt atg att tat acc ccc 54
                               Met Ile Tyr Thr Pro
                               1 5

atg ctt tat ata atg act tat gcg att tta ggg agc gcg aag gat ttt 102
Met Leu Tyr Ile Met Thr Tyr Ala Ile Leu Gly Ser Ala Lys Asp Phe
                        10 15 20

agg gaa aac cag agc gcg att ttt tta tgc ctg ctt ttt tac gcc cta 150
Arg Glu Asn Gln Ser Ala Ile Phe Leu Cys Leu Leu Phe Tyr Ala Leu
                        25 30 35

aca cac agc ttt ttt atc gct ttt aaa tcc caa agc cct ggc atg cgt 198
Thr His Ser Phe Phe Ile Ala Phe Lys Ser Gln Ser Pro Gly Met Arg
                        40 45 50

tac gct cgg ttt aaa tta atc aaa aat aat ggc gaa aaa gtg ggc ttt 246
Tyr Ala Arg Phe Lys Leu Ile Lys Asn Asn Gly Glu Lys Val Gly Phe
                        55 60 65

ttt tta gct ttg tgg cgc ttt gtt ttg tgg gtg ttg agc atg ggg tta 294
Phe Leu Ala Leu Trp Arg Phe Val Leu Trp Val Leu Ser Met Gly Leu
                        70 75 80 85

ctc ata ggg ttt gtt acg cct ttt att ttt aag ttt ttt ttg cat gac 342
Leu Ile Gly Phe Val Thr Pro Phe Ile Phe Lys Phe Phe Leu His Asp
                        90 95 100

aaa ctc agc ggc act cat att gaa acc atc aag gag gca aca 384
Lys Leu Ser Gly Thr His Ile Glu Thr Ile Lys Glu Ala Thr
                        105 110 115

tgaaaaattt agtaatc 401
```

<210> 300

<211> 115

<212> PRT

<213> Helicobacter pylori

<400> 300

```
Met Ile Tyr Thr Pro Met Leu Tyr Ile Met Thr Tyr Ala Ile Leu Gly
1 5 10 15
Ser Ala Lys Asp Phe Arg Glu Asn Gln Ser Ala Ile Phe Leu Cys Leu
20 25 30
Leu Phe Tyr Ala Leu Thr His Ser Phe Phe Ile Ala Phe Lys Ser Gln
35 40 45
Ser Pro Gly Met Arg Tyr Ala Arg Phe Lys Leu Ile Lys Asn Asn Gly
50 55 60
Glu Lys Val Gly Phe Phe Leu Ala Leu Trp Arg Phe Val Leu Trp Val
65 70 75 80
Leu Ser Met Gly Leu Leu Ile Gly Phe Val Thr Pro Phe Ile Phe Lys
85 90 95
```

Phe Phe Leu His Asp Lys Leu Ser Gly Thr His Ile Glu Thr Ile Lys
 100 105 110
 Glu Ala Thr
 115

<210> 301
 <211> 717
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (53)...(667)

<400> 301
 agcggggctg gtatttcagc agaaagcggg attaaaacct ttagagacgc tg atg gct 58
 Met Ala
 1

tgt ggg aaa ggg cat gac atc atg gaa gtt gcc tcg cct tat ggc tgg 106
 Cys Gly Lys Gly His Asp Ile Met Glu Val Ala Ser Pro Tyr Gly Trp
 5 10 15

aaa aag aac ccg caa aag gtg ttg gat ttt tac aac caa agg cgc cga 154
 Lys Lys Asn Pro Gln Lys Val Leu Asp Phe Tyr Asn Gln Arg Arg Arg
 20 25 30

cag ctt ttt gaa gtt tat cct aac aaa gcc cat aag gct tta gcg gaa 202
 Gln Leu Phe Glu Val Tyr Pro Asn Lys Ala His Lys Ala Leu Ala Glu
 35 40 45 50

ttg gaa aaa cac tat caa gtc aat atc atc acc caa aat gta gat gat 250
 Leu Glu Lys His Tyr Gln Val Asn Ile Ile Thr Gln Asn Val Asp Asp
 55 60 65

ttg cat gaa aga gcg ggt tct tct cgc att ttg cac ttg cat ggg gaa 298
 Leu His Glu Arg Ala Gly Ser Ser Arg Ile Leu His Leu His Gly Glu
 70 75 80

tta ttg agc gtt cgc agc gag aaa gat cct aat tta gtt tat agg tgg 346
 Leu Leu Ser Val Arg Ser Glu Lys Asp Pro Asn Leu Val Tyr Arg Trp
 85 90 95

gaa aag gac ttg aat tta ggc gac ttg gcc aaa gac aaa tcg caa tta 394
 Glu Lys Asp Leu Asn Leu Gly Asp Leu Ala Lys Asp Lys Ser Gln Leu
 100 105 110

cgc cct gat att gtg tgg ttt ggc gaa gcg gtg cct ttg ctt aaa gaa 442
 Arg Pro Asp Ile Val Trp Phe Gly Glu Ala Val Pro Leu Leu Lys Glu
 115 120 125 130

gcg att tct tta gtc aaa caa gcg cat ctt tta atc atc att ggc act 490
 Ala Ile Ser Leu Val Lys Gln Ala His Leu Leu Ile Ile Ile Gly Thr
 135 140 145

tct ttg caa gtc tat ccc gcc gct agc ctc tac acg cat gcg cat aaa 538
 Ser Leu Gln Val Tyr Pro Ala Ala Ser Leu Tyr Thr His Ala His Lys
 150 155 160

gac gct ctc att tat tac att gac cct aag gct aaa aac gcc cat tta 586
 Asp Ala Leu Ile Tyr Tyr Ile Asp Pro Lys Ala Lys Asn Ala His Leu
 165 170 175

ccc cag aat gtc caa tgc att aat gaa agc gcg gtg cat gcc atg caa 634
 Pro Gln Asn Val Gln Cys Ile Asn Glu Ser Ala Val His Ala Met Gln
 180 185 190

gat tta atg ccc aaa ctc ata gaa atg gct tct taagaaatgt taaaataatt 687
 Asp Leu Met Pro Lys Leu Ile Glu Met Ala Ser
 195 200 205

tttatttttt cagctaacga ttagcaaaaa 717

<210> 302
 <211> 205
 <212> PRT
 <213> Helicobacter pylori

<400> 302
 Met Ala Cys Gly Lys Gly His Asp Ile Met Glu Val Ala Ser Pro Tyr
 1 5 10 15
 Gly Trp Lys Lys Asn Pro Gln Lys Val Leu Asp Phe Tyr Asn Gln Arg
 20 25 30
 Arg Arg Gln Leu Phe Glu Val Tyr Pro Asn Lys Ala His Lys Ala Leu
 35 40 45
 Ala Glu Leu Glu Lys His Tyr Gln Val Asn Ile Ile Thr Gln Asn Val
 50 55 60
 Asp Asp Leu His Glu Arg Ala Gly Ser Ser Arg Ile Leu His Leu His
 65 70 75 80
 Gly Glu Leu Leu Ser Val Arg Ser Glu Lys Asp Pro Asn Leu Val Tyr
 85 90 95
 Arg Trp Glu Lys Asp Leu Asn Leu Gly Asp Leu Ala Lys Asp Lys Ser
 100 105 110
 Gln Leu Arg Pro Asp Ile Val Trp Phe Gly Glu Ala Val Pro Leu Leu
 115 120 125
 Lys Glu Ala Ile Ser Leu Val Lys Gln Ala His Leu Leu Ile Ile Ile
 130 135 140
 Gly Thr Ser Leu Gln Val Tyr Pro Ala Ala Ser Leu Tyr Thr His Ala
 145 150 155 160
 His Lys Asp Ala Leu Ile Tyr Tyr Ile Asp Pro Lys Ala Lys Asn Ala
 165 170 175
 His Leu Pro Gln Asn Val Gln Cys Ile Asn Glu Ser Ala Val His Ala
 180 185 190
 Met Gln Asp Leu Met Pro Lys Leu Ile Glu Met Ala Ser
 195 200 205

<210> 303
 <211> 468
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (23)...(421)

<400> 303

atttaaaggag	tttgagagtc	tg	atg	caa	caa	gcc	aca	gaa	gca	ttg	aat	cac					52
			Met	Gln	Gln	Ala	Thr	Glu	Ala	Leu	Asn	His					
			1				5					10					
ccc	tat	ttt	ggc	gtt	ttt	gtt	tta	ttg	gta	ttc	acc	ttt	tgg	gtg	ttt		100
Pro	Tyr	Phe	Gly	Val	Phe	Val	Leu	Leu	Val	Phe	Thr	Phe	Trp	Val	Phe		
				15					20					25			
aac	tta	acc	tta	agg	atc	caa	agg	ttt	tta	agc	cgt	aaa	atg	gct	caa		148
Asn	Leu	Thr	Leu	Arg	Ile	Gln	Arg	Phe	Leu	Ser	Arg	Lys	Met	Ala	Gln		
			30					35					40				
aaa	aag	ggc	gaa	aag	ctc	aag	ctc	gct	ccc	tat	gaa	tgc	ggg	cct	gtg		196
Lys	Lys	Gly	Glu	Lys	Leu	Lys	Leu	Ala	Pro	Tyr	Glu	Cys	Gly	Pro	Val		
		45					50					55					
gct	ctc	aaa	cag	cct	aat	agg	gtg	tcg	cac	cat	ttc	tat	atc	atg	gcc		244
Ala	Leu	Lys	Gln	Pro	Asn	Arg	Val	Ser	His	His	Phe	Tyr	Ile	Met	Ala		
	60					65					70						
atg	ctt	ttt	att	tta	ttt	gat	gta	gaa	atc	gtt	ttc	atg	ttc	cct	tgg		292
Met	Leu	Phe	Ile	Leu	Phe	Asp	Val	Glu	Ile	Val	Phe	Met	Phe	Pro	Trp		
	75				80					85					90		
gcg	att	ggt	ttt	aaa	aaa	tta	ggc	ttg	ttt	gga	ctc	gtt	gaa	atg	cta		340
Ala	Ile	Gly	Phe	Lys	Lys	Leu	Gly	Leu	Phe	Gly	Leu	Val	Glu	Met	Leu		
				95				100						105			
ggc	ttt	gtc	ttc	ttt	tta	acc	att	ggt	ttt	att	tac	gct	tta	aag	cga		388
Gly	Phe	Val	Phe	Phe	Leu	Thr	Ile	Gly	Phe	Ile	Tyr	Ala	Leu	Lys	Arg		
			110					115					120				
aac	gct	ttg	agc	tgg	caa	aaa	tta	gag	gtg	aaa	taatgcaaca	agcaccgggtt					441
Asn	Ala	Leu	Ser	Trp	Gln	Lys	Leu	Glu	Val	Lys							
		125				130											
gttctaagca	ctttggataa	attattg															468
<210>	304																
<211>	133																
<212>	PRT																
<213>	Helicobacter pylori																
<400>	304																
Met	Gln	Gln	Ala	Thr	Glu	Ala	Leu	Asn	His	Pro	Tyr	Phe	Gly	Val	Phe		
1				5				10						15			
Val	Leu	Leu	Val	Phe	Thr	Phe	Trp	Val	Phe	Asn	Leu	Thr	Leu	Arg	Ile		
			20					25					30				
Gln	Arg	Phe	Leu	Ser	Arg	Lys	Met	Ala	Gln	Lys	Lys	Gly	Glu	Lys	Leu		
		35					40					45</					

115
Lys Leu Glu Val Lys
130

120

125

<210> 305
<211> 864
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (37)...(831)

<221> misc_feature
<222> 388
<223> n = A,T,C or G

<400> 305
agcgatcaaa caagacgctc ccaaaagggtt agtgtg atg gta aga aaa caa tcc 54
Met Val Arg Lys Gln Ser
1 5

ccc tat gaa gat gtg caa aaa caa tcg cgc cag cat gac ccc tat aaa 102
Pro Tyr Glu Asp Val Gln Lys Gln Ser Arg Gln His Asp Pro Tyr Lys
10 15 20

atc ata gaa ccc acc cct aaa aaa tat tta gag ggc agc gct tat gag 150
Ile Ile Glu Pro Thr Pro Lys Lys Tyr Leu Glu Gly Ser Ala Tyr Glu
25 30 35

gtc att tac aac cac ctt tct tac aaa cat gag att tta gac aaa tac 198
Val Ile Tyr Asn His Leu Ser Tyr Lys His Glu Ile Leu Asp Lys Tyr
40 45 50

ata gag act aac acg gct gtg ttt tgg atc aaa aaa gac gat att ttt 246
Ile Glu Thr Asn Thr Ala Val Phe Trp Ile Lys Lys Asp Asp Ile Phe
55 60 65 70

tct gtc gct acg att tta agg cat ttg ggt tat gag tgt ttg agc gaa 294
Ser Val Ala Thr Ile Leu Arg His Leu Gly Tyr Glu Cys Leu Ser Glu
75 80 85

atg agc gcg ata gat ttg tgc gct aaa aaa ggg cat ttt gaa ttg ttt 342
Met Ser Ala Ile Asp Leu Cys Ala Lys Lys Gly His Phe Glu Leu Phe
90 95 100

tat cag ttc gtg ggc ttt agc gat agc tgc aag aac cgc cgt agg ntg 390
Tyr Gln Phe Val Gly Phe Ser Asp Ser Cys Lys Asn Arg Arg Arg Xaa
105 110 115

cgc gtg aag tgc gtt ttg ttg cct aat gag agc gtg gat tct ttg agt 438
Arg Val Lys Cys Val Leu Leu Pro Asn Glu Ser Val Asp Ser Leu Ser
120 125 130

ttt tta tac cga tcg gct aat tgg agc gaa agg gaa gcg tat gac atg 486
Phe Leu Tyr Arg Ser Ala Asn Trp Ser Glu Arg Glu Ala Tyr Asp Met
135 140 145 150

ctt ggt att gtg ttt gac aaa cac ccc tat ttg aaa cgc ctt att atg 534
 Leu Gly Ile Val Phe Asp Lys His Pro Tyr Leu Lys Arg Leu Ile Met
 155 160 165

 ccg cat gat tgg gta ggc cac cca tta ttg cgc tct tac ccg ctc aaa 582
 Pro His Asp Trp Val Gly His Pro Leu Leu Arg Ser Tyr Pro Leu Lys
 170 175 180

 ggc gat gaa ttc gcc caa tgg tat gaa gtg gat aaa att ttt ggt aaa 630
 Gly Asp Glu Phe Ala Gln Trp Tyr Glu Val Asp Lys Ile Phe Gly Lys
 185 190 195

 gaa tac cga gaa gtg gtg ggt aaa gag cag aga gac agc gca aga gtg 678
 Glu Tyr Arg Glu Val Val Gly Lys Glu Gln Arg Asp Ser Ala Arg Val
 200 205 210

 gat gaa aaa gac act ttc aat ttt gca aaa att ggc tat gaa cag ggc 726
 Asp Glu Lys Asp Thr Phe Asn Phe Ala Lys Ile Gly Tyr Glu Gln Gly
 215 220 225 230

 aag ggc gaa gaa tta aaa gaa gta gaa gaa aag cat gcg ttt aag aaa 774
 Lys Gly Glu Glu Leu Lys Glu Val Glu Glu Lys His Ala Phe Lys Lys
 235 240 245

 atc cct ttt gtc aaa gat ttg cac aaa atc gcc ccc act atc tta aaa 822
 Ile Pro Phe Val Lys Asp Leu His Lys Ile Ala Pro Thr Ile Leu Lys
 250 255 260

 aag agg cta taaaatggct caaaatttca cgaaactcaa ccc 864
 Lys Arg Leu
 265

<210> 306
 <211> 265
 <212> PRT
 <213> Helicobacter pylori

<220>
 <221> VARIANT
 <222> 118
 <223> Xaa = Any Amino Acid

<400> 306
 Met Val Arg Lys Gln Ser Pro Tyr Glu Asp Val Gln Lys Gln Ser Arg
 1 5 10 15
 Gln His Asp Pro Tyr Lys Ile Ile Glu Pro Thr Pro Lys Lys Tyr Leu
 20 25 30
 Glu Gly Ser Ala Tyr Glu Val Ile Tyr Asn His Leu Ser Tyr Lys His
 35 40 45
 Glu Ile Leu Asp Lys Tyr Ile Glu Thr Asn Thr Ala Val Phe Trp Ile
 50 55 60
 Lys Lys Asp Asp Ile Phe Ser Val Ala Thr Ile Leu Arg His Leu Gly
 65 70 75 80
 Tyr Glu Cys Leu Ser Glu Met Ser Ala Ile Asp Leu Cys Ala Lys Lys
 85 90 95
 Gly His Phe Glu Leu Phe Tyr Gln Phe Val Gly Phe Ser Asp Ser Cys
 100 105 110
 Lys Asn Arg Arg Arg Xaa Arg Val Lys Cys Val Leu Leu Pro Asn Glu

gat aag agt ggg gag tgc gaa ttg caa gac atg acg cat tta acc ggc	393
Asp Lys Ser Gly Glu Cys Glu Leu Gln Asp Met Thr His Leu Thr Gly	
100 105 110 115	
gta gag cac caa ccc tat gcg gtg gct gat gat ttt aaa gca ctg gat	441
Val Glu His Gln Pro Tyr Ala Val Ala Asp Asp Phe Lys Ala Leu Asp	
120 125 130	
ttt tgg gca aaa gcc ttg tat gat cct aat ttg tgc atc atg tgt gaa	489
Phe Trp Ala Lys Ala Leu Tyr Asp Pro Asn Leu Cys Ile Met Cys Glu	
135 140 145	
agg tgc gta acc act tgt aag gac aat gtg ggc gaa aac aac ctt aaa	537
Arg Cys Val Thr Thr Cys Lys Asp Asn Val Gly Glu Asn Asn Leu Lys	
150 155 160	
gcc act aaa gcc gac ttg cat gct ccg gat aaa ttt aaa gac agc atg	585
Ala Thr Lys Ala Asp Leu His Ala Pro Asp Lys Phe Lys Asp Ser Met	
165 170 175	
tcc aaa gac gct ttt agc gtg tgg agt cgt aag caa aaa ggc att att	633
Ser Lys Asp Ala Phe Ser Val Trp Ser Arg Lys Gln Lys Gly Ile Ile	
180 185 190 195	
tct ttt gtg ggc agc gtg cct tgc tat gat tgc ggg gaa tgc att gca	681
Ser Phe Val Gly Ser Val Pro Cys Tyr Asp Cys Gly Glu Cys Ile Ala	
200 205 210	
gta tgc cct gtg ggc gct ttg agc tat aaa gat ttc gct tac acg gct	729
Val Cys Pro Val Gly Ala Leu Ser Tyr Lys Asp Phe Ala Tyr Thr Ala	
215 220 225	
aac gca tgg gag tta aaa aag atc cat tct act tgt tcg cat tgc tcg	777
Asn Ala Trp Glu Leu Lys Lys Ile His Ser Thr Cys Ser His Cys Ser	
230 235 240	
gcc ggg tgt ttg att tct tat gat gtg cgc cat ttt gat act cta ggc	825
Ala Gly Cys Leu Ile Ser Tyr Asp Val Arg His Phe Asp Thr Leu Gly	
245 250 255	
gaa gaa tct aaa att ttt aga gtg ctt aat gat ttt tac cat aac cct	873
Glu Glu Ser Lys Ile Phe Arg Val Leu Asn Asp Phe Tyr His Asn Pro	
260 265 270 275	
att tgt ggg gca ggc cgt ttc gct ttt gat gtg agc tct agc cct aaa	921
Ile Cys Gly Ala Gly Arg Phe Ala Phe Asp Val Ser Ser Ser Pro Lys	
280 285 290	
ggc agt gct aat ctt aaa gaa gcg caa aac gcc ctc aaa gaa tgc gaa	969
Gly Ser Ala Asn Leu Lys Glu Ala Gln Asn Ala Leu Lys Glu Cys Glu	
295 300 305	
gcg gtg cga ata ggt ggg gat att acg aat gaa gag gcg ttt tta ata	1017
Ala Val Arg Ile Gly Gly Asp Ile Thr Asn Glu Glu Ala Phe Leu Ile	
310 315 320	
gag cgt tta aga aaa gag ctt gat ttt aaa atc tac aat caa gaa gcg	1065
Glu Arg Leu Arg Lys Glu Leu Asp Phe Lys Ile Tyr Asn Gln Glu Ala	
325 330 335	

tat	cgt	ttc	cag	caa	ttc	tta	aaa	gta	ttg	ggc	gaa	att	aaa	cgc	ccc	1113
Tyr	Arg	Phe	Gln	Gln	Phe	Leu	Lys	Val	Leu	Gly	Glu	Ile	Lys	Arg	Pro	
340					345					350					355	
agc	gtt	gaa	gag	att	aaa	act	tct	cat	tta	gtc	gtt	acg	ata	gga	tct	1161
Ser	Val	Glu	Glu	Ile	Lys	Thr	Ser	His	Leu	Val	Val	Thr	Ile	Gly	Ser	
				360					365					370		
tct	atc	aaa	aca	gaa	aac	cct	ttg	gtg	cgc	tat	gcc	atc	aat	aac	gct	1209
Ser	Ile	Lys	Thr	Glu	Asn	Pro	Leu	Val	Arg	Tyr	Ala	Ile	Asn	Asn	Ala	
			375					380					385			
ctc	aaa	ctc	aat	aaa	gct	tct	tta	atc	gct	atg	cac	cct	att	aag	gat	1257
Leu	Lys	Leu	Asn	Lys	Ala	Ser	Leu	Ile	Ala	Met	His	Pro	Ile	Lys	Asp	
			390				395					400				
aac	gcg	cta	gcg	aat	ttg	tgc	cga	agc	tct	ttt	tgc	atc	acc	cat	gaa	1305
Asn	Ala	Leu	Ala	Asn	Leu	Cys	Arg	Ser	Ser	Phe	Cys	Ile	Thr	His	Glu	
	405					410					415					
gtg	ggg	gct	gaa	gaa	atc	ctt	tta	ggc	atg	ctt	tta	aaa	atg	ctt	aac	1353
Val	Gly	Ala	Glu	Glu	Ile	Leu	Leu	Gly	Met	Leu	Leu	Lys	Met	Leu	Asn	
420					425					430					435	
att	gaa	agc	gcg	gcc	cta	aaa	agc	tta	gaa	gat	tcc	aag	caa	aat	att	1401
Ile	Glu	Ser	Ala	Ala	Leu	Lys	Ser	Leu	Glu	Asp	Ser	Lys	Gln	Asn	Ile	
				440					445					450		
gta	gat	gaa	gcg	gct	ctt	aaa	gcc	tta	gaa	gaa	gag	cga	aaa	aaa	gct	1449
Val	Asp	Glu	Ala	Ala	Leu	Lys	Ala	Leu	Glu	Glu	Glu	Arg	Lys	Lys	Ala	
			455					460					465			
tta	gaa	caa	gcc	gag	caa	ggg	tgc	agt	att	gga	gaa	aat	aag	gca	gaa	1497
Leu	Glu	Gln	Ala	Glu	Gln	Gly	Cys	Ser	Ile	Gly	Glu	Asn	Lys	Ala	Glu	
		470				475						480				
aat	caa	gaa	gag	aat	aaa	aca	gaa	gcg	act	acc	cca	aaa	gaa	gaa	aat	1545
Asn	Gln	Glu	Glu	Asn	Lys	Thr	Glu	Ala	Thr	Thr	Pro	Lys	Glu	Glu	Asn	
	485					490					495					
caa	gaa	gaa	aac	aag	aca	gag	gtt	aaa	gaa	gaa	aaa	att	gaa	gtc	cct	1593
Gln	Glu	Glu	Asn	Lys	Thr	Glu	Val	Lys	Glu	Glu	Lys	Ile	Glu	Val	Pro	
500					505					510					515	
acc	aaa	acc	act	tat	ttg	ctg	ctt	gaa	gaa	gcg	ggc	atc	aat	tta	gaa	1641
Thr	Lys	Thr	Thr	Tyr	Leu	Leu	Leu	Glu	Glu	Ala	Gly	Ile	Asn	Leu	Glu	
				520					525					530		
act	tat	gaa	aaa	att	ctg	gct	ctt	ttg	caa	aaa	tca	aat	aac	acc	ctg	1689
Thr	Tyr	Glu	Lys	Ile	Leu	Ala	Leu	Leu	Gln	Lys	Ser	Asn	Asn	Thr	Leu	
			535					540					545			
cta	gtg	gtt	ggc	gaa	gaa	atc	tat	agc	cat	aag	caa	gcc	cac	aat	atc	1737
Leu	Val	Val	Gly	Glu	Glu	Ile	Tyr	Ser	His	Lys	Gln	Ala	His	Asn	Ile	
		550					555					560				
gct	aaa	atg	ttg	cgt	ttg	cta	gcc	caa	aaa	agc	gct	att	aaa	ctc	att	1785
Ala	Lys	Met	Leu	Arg	Leu	Leu	Ala	Gln	Lys	Ser	Ala	Ile	Lys	Leu	Ile	

565	570	575	
ctt atc ccc cca agc gcc aac gct tta ggc atc gct tct att tgt caa Leu Ile Pro Pro Ser Ala Asn Ala Leu Gly Ile Ala Ser Ile Cys Gln 580 585 590 595			1833
ttg agc gaa gaa att ttt gaa cat gaa aaa att gta ggc att cgc gct Leu Ser Glu Glu Ile Phe Glu His Glu Lys Ile Val Gly Ile Arg Ala 600 605 610			1881
caa ggg gat ttc act atc aat agc gat gat agg gtt ttt gga aaa gac Gln Gly Asp Phe Thr Ile Asn Ser Asp Asp Arg Val Phe Gly Lys Asp 615 620 625			1929
gct gcc agc aaa gtg gat ttt att tta ccc agt ctc aac cag cta gaa Ala Ala Ser Lys Val Asp Phe Ile Leu Pro Ser Leu Asn Gln Leu Glu 630 635 640			1977
ggc acg atc acc aat att gaa ggg cgt gtg ttg ccc tta aaa ccg gct Gly Thr Ile Thr Asn Ile Glu Gly Arg Val Leu Pro Leu Lys Pro Ala 645 650 655			2025
ttg agg ttt gag ggc tat gat ttg agc gat att atg caa ggc ttt ggc Leu Arg Phe Glu Gly Tyr Asp Leu Ser Asp Ile Met Gln Gly Phe Gly 660 665 670 675			2073
ttt gtg gaa gaa aac ctc ata gaa tgc acc cac aaa ctc cct aca gaa Phe Val Glu Glu Asn Leu Ile Glu Cys Thr His Lys Leu Pro Thr Glu 680 685 690			2121
gcg ggc ttt aaa gcc ata gaa ttt gat tat tta acc aac tat ttc gct Ala Gly Phe Lys Ala Ile Glu Phe Asp Tyr Leu Thr Asn Tyr Phe Ala 695 700 705			2169
aac gac aga gtc aac cac aga ggc tat ctg cta gga aca agc cat ttt Asn Asp Arg Val Asn His Arg Gly Tyr Leu Leu Gly Thr Ser His Phe 710 715 720			2217
gaa aag agc gct aaa gaa tgc gaa acc ata gaa tgc gag cct atc aag Glu Lys Ser Ala Lys Glu Cys Glu Thr Ile Glu Cys Glu Pro Ile Lys 725 730 735			2265
cct tta aaa gaa aaa atc gct ttc aac gcg tat tta aaa tac cca gaa Pro Leu Lys Glu Lys Ile Ala Phe Asn Ala Tyr Leu Lys Tyr Pro Glu 740 745 750 755			2313
acg caa ttc aat aac gct act aat aaa agc gag aat ttg caa tta aaa Thr Gln Phe Asn Asn Ala Thr Asn Lys Ser Glu Asn Leu Gln Leu Lys 760 765 770			2361
gcc ggt gtc tat gtg tct aaa gct ttc tta aag aaa ttg aat aaa gaa Ala Gly Val Tyr Val Ser Lys Ala Phe Leu Lys Lys Leu Asn Lys Glu 775 780 785			2409
gtg ggg caa aac atc act tta tct aaa gaa gaa gag gaa tta aca ggc Val Gly Gln Asn Ile Thr Leu Ser Lys Glu Glu Glu Glu Leu Thr Gly 790 795 800			2457
gtt ttg tat ctt gat gag agc ttg gat cag gaa gtg ttt gtt atc tcg			2505

Val	Leu	Tyr	Leu	Asp	Glu	Ser	Leu	Asp	Gln	Glu	Val	Phe	Val	Ile	Ser		
805						810					815						
cct	tct	ctt	ttg	aaa	aac	cat	tct	ggc	ttt	ttt	aga	gag	ggc	gtg	ttt	2553	
Pro	Ser	Leu	Leu	Lys	Asn	His	Ser	Gly	Phe	Phe	Arg	Glu	Gly	Val	Phe		
820					825					830					835		
gat	agc	gtg	gat	tta	aag	gag	caa	gca	tgagcgc	tta	tatcattgaa					2600	
Asp	Ser	Val	Asp	Leu	Lys	Glu	Gln	Ala									
					840												
accctgatta	aaattttgat	ttt														2623	
<210> 308																	
<211> 844																	
<212> PRT																	
<213> Helicobacter pylori																	
<400> 308																	
Met	Ile	Thr	Met	Asn	Ile	Asn	Gly	Lys	Thr	Ile	Glu	Cys	Gln	Glu	Gly		
1				5				10					15				
Gln	Ser	Val	Leu	Glu	Ala	Ala	Arg	Ser	Ala	Gly	Ile	Tyr	Ile	Pro	Thr		
		20					25						30				
Ile	Cys	Tyr	Leu	Ser	Gly	Cys	Ser	Pro	Thr	Val	Ala	Cys	Lys	Met	Cys		
		35					40						45				
Met	Val	Glu	Met	Asp	Gly	Lys	Arg	Val	Tyr	Ser	Cys	Asn	Thr	Lys	Ala		
	50					55					60						
Lys	Asn	Asn	Ala	Thr	Ile	Leu	Thr	Asn	Thr	Pro	Thr	Leu	Met	Asp	Glu		
65					70					75					80		
Arg	Lys	Ser	Ile	Met	Gln	Thr	Tyr	Asp	Val	Asn	His	Pro	Leu	Glu	Cys		
				85				90						95			
Gly	Val	Cys	Asp	Lys	Ser	Gly	Glu	Cys	Glu	Leu	Gln	Asp	Met	Thr	His		
			100					105					110				
Leu	Thr	Gly	Val	Glu	His	Gln	Pro	Tyr	Ala	Val	Ala	Asp	Asp	Phe	Lys		
		115					120					125					
Ala	Leu	Asp	Phe	Trp	Ala	Lys	Ala	Leu	Tyr	Asp	Pro	Asn	Leu	Cys	Ile		
	130					135					140						
Met	Cys	Glu	Arg	Cys	Val	Thr	Thr	Cys	Lys	Asp	Asn	Val	Gly	Glu	Asn		
145					150					155					160		
Asn	Leu	Lys	Ala	Thr	Lys	Ala	Asp	Leu	His	Ala	Pro	Asp	Lys	Phe	Lys		
				165					170						175		
Asp	Ser	Met	Ser	Lys	Asp	Ala	Phe	Ser	Val	Trp	Ser	Arg	Lys	Gln	Lys		
		180						185					190				
Gly	Ile	Ile	Ser	Phe	Val	Gly	Ser	Val	Pro	Cys	Tyr	Asp	Cys	Gly	Glu		
		195					200					205					
Cys	Ile	Ala	Val	Cys	Pro	Val	Gly	Ala	Leu	Ser	Tyr	Lys	Asp	Phe	Ala		
	210					215					220						
Tyr	Thr	Ala	Asn	Ala	Trp	Glu	Leu	Lys	Lys	Ile	His	Ser	Thr	Cys	Ser		
225					230					235					240		
His	Cys	Ser	Ala	Gly	Cys	Leu	Ile	Ser	Tyr	Asp	Val	Arg	His	Phe	Asp		
				245					250						255		
Thr	Leu	Gly	Glu	Glu	Ser	Lys	Ile	Phe	Arg	Val	Leu	Asn	Asp	Phe	Tyr		
		260						265					270				
His	Asn	Pro	Ile	Cys	Gly	Ala	Gly	Arg	Phe	Ala	Phe	Asp	Val	Ser	Ser		
		275					280					285					
Ser	Pro	Lys	Gly	Ser	Ala	Asn	Leu	Lys	Glu	Ala	Gln	Asn	Ala	Leu	Lys		
	290					295					300						
Glu	Cys	Glu	Ala	Val	Arg	Ile	Gly	Gly	Asp	Ile	Thr	Asn	Glu	Glu	Ala		
305					310					315					320		

Phe	Leu	Ile	Glu	Arg	Leu	Arg	Lys	Glu	Leu	Asp	Phe	Lys	Ile	Tyr	Asn	
				325					330					335		
Gln	Glu	Ala	Tyr	Arg	Phe	Gln	Gln	Phe	Leu	Lys	Val	Leu	Gly	Glu	Ile	
			340					345					350			
Lys	Arg	Pro	Ser	Val	Glu	Glu	Ile	Lys	Thr	Ser	His	Leu	Val	Val	Thr	
		355					360					365				
Ile	Gly	Ser	Ser	Ile	Lys	Thr	Glu	Asn	Pro	Leu	Val	Arg	Tyr	Ala	Ile	
	370					375					380					
Asn	Asn	Ala	Leu	Lys	Leu	Asn	Lys	Ala	Ser	Leu	Ile	Ala	Met	His	Pro	
385					390					395					400	
Ile	Lys	Asp	Asn	Ala	Leu	Ala	Asn	Leu	Cys	Arg	Ser	Ser	Phe	Cys	Ile	
			405						410					415		
Thr	His	Glu	Val	Gly	Ala	Glu	Glu	Ile	Leu	Leu	Gly	Met	Leu	Leu	Lys	
			420					425					430			
Met	Leu	Asn	Ile	Glu	Ser	Ala	Ala	Leu	Lys	Ser	Leu	Glu	Asp	Ser	Lys	
		435					440					445				
Gln	Asn	Ile	Val	Asp	Glu	Ala	Ala	Leu	Lys	Ala	Leu	Glu	Glu	Glu	Arg	
	450						455				460					
Lys	Lys	Ala	Leu	Glu	Gln	Ala	Glu	Gln	Gly	Cys	Ser	Ile	Gly	Glu	Asn	
465					470					475					480	
Lys	Ala	Glu	Asn	Gln	Glu	Glu	Asn	Lys	Thr	Glu	Ala	Thr	Thr	Pro	Lys	
			485						490					495		
Glu	Glu	Asn	Gln	Glu	Glu	Asn	Lys	Thr	Glu	Val	Lys	Glu	Glu	Lys	Ile	
			500					505					510			
Glu	Val	Pro	Thr	Lys	Thr	Thr	Tyr	Leu	Leu	Leu	Glu	Glu	Ala	Gly	Ile	
		515					520					525				
Asn	Leu	Glu	Thr	Tyr	Glu	Lys	Ile	Leu	Ala	Leu	Leu	Gln	Lys	Ser	Asn	
	530					535					540					
Asn	Thr	Leu	Leu	Val	Val	Gly	Glu	Glu	Ile	Tyr	Ser	His	Lys	Gln	Ala	
545					550					555					560	
His	Asn	Ile	Ala	Lys	Met	Leu	Arg	Leu	Leu	Ala	Gln	Lys	Ser	Ala	Ile	
			565						570					575		
Lys	Leu	Ile	Leu	Ile	Pro	Pro	Ser	Ala	Asn	Ala	Leu	Gly	Ile	Ala	Ser	
			580					585					590			
Ile	Cys	Gln	Leu	Ser	Glu	Glu	Ile	Phe	Glu	His	Glu	Lys	Ile	Val	Gly	
		595					600					605				
Ile	Arg	Ala	Gln	Gly	Asp	Phe	Thr	Ile	Asn	Ser	Asp	Asp	Arg	Val	Phe	
	610					615					620					
Gly	Lys	Asp	Ala	Ala	Ser	Lys	Val	Asp	Phe	Ile	Leu	Pro	Ser	Leu	Asn	
625					630					635					640	
Gln	Leu	Glu	Gly	Thr	Ile	Thr	Asn	Ile	Glu	Gly	Arg	Val	Leu	Pro	Leu	
			645						650					655		
Lys	Pro	Ala	Leu	Arg	Phe	Glu	Gly	Tyr	Asp	Leu	Ser	Asp	Ile	Met	Gln	
			660					665					670			
Gly	Phe	Gly	Phe	Val	Glu	Glu	Asn	Leu	Ile	Glu	Cys	Thr	His	Lys	Leu	
		675					680					685				
Pro	Thr	Glu	Ala	Gly	Phe	Lys	Ala	Ile	Glu	Phe	Asp	Tyr	Leu	Thr	Asn	
		690				695					700					
Tyr	Phe	Ala	Asn	Asp	Arg	Val	Asn	His	Arg	Gly	Tyr	Leu	Leu	Gly	Thr	
705					710					715					720	
Ser	His	Phe	Glu	Lys	Ser	Ala	Lys	Glu	Cys	Glu	Thr	Ile	Glu	Cys	Glu	
			725						730					735		
Pro	Ile	Lys	Pro	Leu	Lys	Glu	Lys	Ile	Ala	Phe	Asn	Ala	Tyr	Leu	Lys	
			740					745					750			
Tyr	Pro	Glu	Thr	Gln	Phe	Asn	Asn	Ala	Thr	Asn	Lys	Ser	Glu	Asn	Leu	
		755					760						765			
Gln	Leu	Lys	Ala	Gly	Val	Tyr	Val	Ser	Lys	Ala	Phe	Leu	Lys	Lys	Leu	
	770					775					780					
Asn	Lys	Glu	Val	Gly	Gln	Asn	Ile	Thr	Leu	Ser	Lys	Glu	Glu	Glu	Glu	

Phe	Ser	Thr	Glu	Ile	Met	Leu	Asn	Ala	Ile	Asn	Ile	Gly	Phe	Val	Ala
		35					40					45			
Ile	Ser	Lys	Tyr	Thr	His	Asn	Leu	Asp	Gly	Gln	Met	Phe	Ala	Leu	Phe
	50					55					60				
Ile	Ile	Ser	Ile	Ala	Ala	Ser	Glu	Val	Ala	Ile	Gly	Leu	Gly	Leu	Val
65				70						75				80	
Ile	Leu	Trp	Phe	Lys	Lys	Phe	Lys	Ser	Leu	Asp	Ile	Asp	Ser	Leu	Asn
			85						90					95	
Ala	Met	Lys	Gly												
			100												

<210> 311
 <211> 663
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (16)...(627)

<400> 311															
ccggtggaat	aagtc	atg	caa	gca	gtg	att	tta	gcg	aat	ggg	gag	ttt	cct		51
		Met	Gln	Ala	Val	Ile	Leu	Ala	Asn	Gly	Glu	Phe	Pro		
		1				5					10				
aaa	tct	caa	aaa	tgc	tta	gac	ctt	tta	aaa	aac	gct	ccc	ttt	tta	atc
Lys	Ser	Gln	Lys	Cys	Leu	Asp	Leu	Leu	Lys	Asn	Ala	Pro	Phe	Leu	Ile
		15				20					25				99
gca	tgc	gat	ggg	gct	gtt	acc	tca	tta	cat	gcg	ctt	caa	ttc	aaa	ccc
Ala	Cys	Asp	Gly	Ala	Val	Thr	Ser	Leu	His	Ala	Leu	Gln	Phe	Lys	Pro
	30					35				40					147
agc	gtt	gtt	ata	ggc	gat	cta	gat	agc	att	gat	tcg	cat	ttg	aaa	gct
Ser	Val	Val	Ile	Gly	Asp	Leu	Asp	Ser	Ile	Asp	Ser	His	Leu	Lys	Ala
	45			50					55					60	195
ttg	tat	aac	cct	ata	cgc	atg	agt	gaa	caa	aac	agc	aac	gat	ttg	tcc
Leu	Tyr	Asn	Pro	Ile	Arg	Met	Ser	Glu	Gln	Asn	Ser	Asn	Asp	Leu	Ser
			65					70						75	243
aaa	gcc	ttt	ttt	tat	gct	tta	aat	aaa	ggc	tgt	gat	gac	ttt	att	ttt
Lys	Ala	Phe	Phe	Tyr	Ala	Leu	Asn	Lys	Gly	Cys	Asp	Asp	Phe	Ile	Phe
		80						85				90			291
tta	ggg	ttg	aat	ggc	aag	cga	gaa	gat	cac	gct	tta	gcg	aac	act	ttt
Leu	Gly	Leu	Asn	Gly	Lys	Arg	Glu	Asp	His	Ala	Leu	Ala	Asn	Thr	Phe
		95				100					105				339
tta	ttg	ttg	gaa	tat	ttt	aaa	ttt	tgc	caa	aaa	atc	caa	gcc	ata	agc
Leu	Leu	Leu	Glu	Tyr	Phe	Lys	Phe	Cys	Gln	Lys	Ile	Gln	Ala	Ile	Ser
	110					115					120				387
gac	tat	ggt	ctt	ttt	agg	gtg	tta	gaa	acc	cct	ttc	act	ttg	ccc	agt
Asp	Tyr	Gly	Leu	Phe	Arg	Val	Leu	Glu	Thr	Pro	Phe	Thr	Leu	Pro	Ser
	125				130					135				140	435
ttt	aaa	ggg	gaa	caa	atc	tcg	ctt	ttt	agc	ctg	gat	ctt	aaa	gcc	caa
															483

Phe	Lys	Gly	Glu	Gln	Ile	Ser	Leu	Phe	Ser	Leu	Asp	Leu	Lys	Ala	Gln		
				145					150					155			
ttc	act	tct	aaa	aac	ctc	aaa	tac	ccc	tta	aaa	aac	ttg	cgt	tta	aaa	531	
Phe	Thr	Ser	Lys	Asn	Leu	Lys	Tyr	Pro	Leu	Lys	Asn	Leu	Arg	Leu	Lys		
			160					165					170				
acg	ctc	ttt	tct	ggc	tcg	ctc	aat	gaa	gct	aca	gat	agt	tat	ttt	agc	579	
Thr	Leu	Phe	Ser	Gly	Ser	Leu	Asn	Glu	Ala	Thr	Asp	Ser	Tyr	Phe	Ser		
			175				180					185					
ctt	agc	tct	aca	cct	aaa	tcg	gtg	gtg	ttg	gtg	tat	caa	aaa	ttc	tta	627	
Leu	Ser	Ser	Thr	Pro	Lys	Ser	Val	Val	Leu	Val	Tyr	Gln	Lys	Phe	Leu		
			190			195					200						
taagcggggtt ttgtaggca agtttttgtc tgtata																663	

<210> 312
 <211> 204
 <212> PRT
 <213> Helicobacter pylori

<400> 312																	
Met	Gln	Ala	Val	Ile	Leu	Ala	Asn	Gly	Glu	Phe	Pro	Lys	Ser	Gln	Lys		
1				5					10					15			
Cys	Leu	Asp	Leu	Leu	Lys	Asn	Ala	Pro	Phe	Leu	Ile	Ala	Cys	Asp	Gly		
			20					25					30				
Ala	Val	Thr	Ser	Leu	His	Ala	Leu	Gln	Phe	Lys	Pro	Ser	Val	Val	Ile		
			35				40					45					
Gly	Asp	Leu	Asp	Ser	Ile	Asp	Ser	His	Leu	Lys	Ala	Leu	Tyr	Asn	Pro		
			50			55					60						
Ile	Arg	Met	Ser	Glu	Gln	Asn	Ser	Asn	Asp	Leu	Ser	Lys	Ala	Phe	Phe		
65					70					75					80		
Tyr	Ala	Leu	Asn	Lys	Gly	Cys	Asp	Asp	Phe	Ile	Phe	Leu	Gly	Leu	Asn		
			85						90					95			
Gly	Lys	Arg	Glu	Asp	His	Ala	Leu	Ala	Asn	Thr	Phe	Leu	Leu	Leu	Glu		
			100					105					110				
Tyr	Phe	Lys	Phe	Cys	Gln	Lys	Ile	Gln	Ala	Ile	Ser	Asp	Tyr	Gly	Leu		
		115					120					125					
Phe	Arg	Val	Leu	Glu	Thr	Pro	Phe	Thr	Leu	Pro	Ser	Phe	Lys	Gly	Glu		
		130				135					140						
Gln	Ile	Ser	Leu	Phe	Ser	Leu	Asp	Leu	Lys	Ala	Gln	Phe	Thr	Ser	Lys		
145					150					155					160		
Asn	Leu	Lys	Tyr	Pro	Leu	Lys	Asn	Leu	Arg	Leu	Lys	Thr	Leu	Phe	Ser		
			165						170					175			
Gly	Ser	Leu	Asn	Glu	Ala	Thr	Asp	Ser	Tyr	Phe	Ser	Leu	Ser	Ser	Thr		
			180					185					190				
Pro	Lys	Ser	Val	Val	Leu	Val	Tyr	Gln	Lys	Phe	Leu						
		195					200										

<210> 313
 <211> 1106
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (17)...(1048)

<400> 313

agtaaggggt tagagc atg aaa gtt atc aaa aca gca cct ttg atc cca tca 52
Met Lys Val Ile Lys Thr Ala Pro Leu Ile Pro Ser
1 5 10

gaa att aag gtg cta gag aaa gag ggc aat cgg gtt aag att tct ctg 100
Glu Ile Lys Val Leu Glu Lys Glu Gly Asn Arg Val Lys Ile Ser Leu
15 20 25

gct cca ttt gag ttt ggt tac gct gtt acg ctc gct cat cct att aga 148
Ala Pro Phe Glu Phe Gly Tyr Ala Val Thr Leu Ala His Pro Ile Arg
30 35 40

agg ctc ttg ctt tta agc tct gtg ggg tat gct cct gta ggt tta aag 196
Arg Leu Leu Leu Leu Ser Ser Val Gly Tyr Ala Pro Val Gly Leu Lys
45 50 55 60

att gaa ggc gtc cat cat gag ttt gac tct tta agg ggg gtt act gaa 244
Ile Glu Gly Val His His Glu Phe Asp Ser Leu Arg Gly Val Thr Glu
65 70 75

gac gtg tcg ctt ttt atc atg aat tta aaa aat atc cgc ttt ata gcc 292
Asp Val Ser Leu Phe Ile Met Asn Leu Lys Asn Ile Arg Phe Ile Ala
80 85 90

aag gcg tta gtg ggg cag gat agc tct tta gaa aac caa tcg gtt gtg 340
Lys Ala Leu Val Gly Gln Asp Ser Ser Leu Glu Asn Gln Ser Val Val
95 100 105

gtg gat tat tct ttt aaa ggg cct atg gag ctt agg gct agg gat ttg 388
Val Asp Tyr Ser Phe Lys Gly Pro Met Glu Leu Arg Ala Arg Asp Leu
110 115 120

aat tct gag cag ata gaa atc gtc aat ccg gaa atg ccc cta gcg aca 436
Asn Ser Glu Gln Ile Glu Ile Val Asn Pro Glu Met Pro Leu Ala Thr
125 130 135 140

atc aat gaa gac gct caa ttg aat ttt tcg ctc att att tat aaa gga 484
Ile Asn Glu Asp Ala Gln Leu Asn Phe Ser Leu Ile Ile Tyr Lys Gly
145 150 155

atg ggg tat gtc cca agc gaa aac aca agg gaa ttg atg cct gag ggc 532
Met Gly Tyr Val Pro Ser Glu Asn Thr Arg Glu Leu Met Pro Glu Gly
160 165 170

tac atg ccg cta gac ggc tct ttc acg ccg att aaa aag gtc gtt tat 580
Tyr Met Pro Leu Asp Gly Ser Phe Thr Pro Ile Lys Lys Val Val Tyr
175 180 185

gag att gaa aac gtt ctg gtt gag ggc gat ccc aac tat gaa aaa atc 628
Glu Ile Glu Asn Val Leu Val Glu Gly Asp Pro Asn Tyr Glu Lys Ile
190 195 200

att ttt gat att gaa aca gac ggg cag att gac cct tat aaa gcg ttt 676
Ile Phe Asp Ile Glu Thr Asp Gly Gln Ile Asp Pro Tyr Lys Ala Phe
205 210 215 220

tta tca gcg gtg aaa gtg atg agc aag caa ttg ggt gtt ttt ggc gaa 724
Leu Ser Ala Val Lys Val Met Ser Lys Gln Leu Gly Val Phe Gly Glu

225										230					235									
aga	ccc	att	gct	aac	acg	gag	tat	tca	ggc	gat	tac	gct	caa	aga	gat	772								
Arg	Pro	Ile	Ala	Asn	Thr	Glu	Tyr	Ser	Gly	Asp	Tyr	Ala	Gln	Arg	Asp									
240										245					250									
gac	gct	aaa	gac	ttg	agc	gct	aag	att	gaa	agc	atg	aat	ttg	agc	gct	820								
Asp	Ala	Lys	Asp	Leu	Ser	Ala	Lys	Ile	Glu	Ser	Met	Asn	Leu	Ser	Ala									
255										260					265									
agg	tgt	ttt	aat	tgc	ttg	gat	aaa	atc	ggc	atc	aag	tat	gtg	ggc	gaa	868								
Arg	Cys	Phe	Asn	Cys	Leu	Asp	Lys	Ile	Gly	Ile	Lys	Tyr	Val	Gly	Glu									
270										275					280									
ctc	gtg	ttg	atg	agc	gaa	gaa	gag	ctt	aag	ggc	gtg	aaa	aac	atg	ggt	916								
Leu	Val	Leu	Met	Ser	Glu	Glu	Glu	Leu	Lys	Gly	Val	Lys	Asn	Met	Gly									
285										290					295					300				
aaa	aaa	tcc	tat	gat	gaa	atc	gct	gaa	aaa	ttg	aat	gat	ttg	ggc	tat	964								
Lys	Lys	Ser	Tyr	Asp	Glu	Ile	Ala	Glu	Lys	Leu	Asn	Asp	Leu	Gly	Tyr									
305										310					315									
ccg	gta	ggc	aca	gaa	tta	agc	cct	gaa	caa	aga	gag	agt	tta	aag	aaa	1012								
Pro	Val	Gly	Thr	Glu	Leu	Ser	Pro	Glu	Gln	Arg	Glu	Ser	Leu	Lys	Lys									
320										325					330									
aga	tta	gaa	aaa	tta	gaa	gat	aaa	gga	ggt	aac	gac	tgatgagaca				1058								
Arg	Leu	Glu	Lys	Leu	Glu	Asp	Lys	Gly	Gly	Asn	Asp													
335										340														
caaacacgga taccgcaagc ttgggagaac cagctcgcac agaaaggc															1106									
<210> 314																								
<211> 344																								
<212> PRT																								
<213> Helicobacter pylori																								
<400> 314																								
Met	Lys	Val	Ile	Lys	Thr	Ala	Pro	Leu	Ile	Pro	Ser	Glu	Ile	Lys	Val									
1				5					10					15										
Leu	Glu	Lys	Glu	Gly	Asn	Arg	Val	Lys	Ile	Ser	Leu	Ala	Pro	Phe	Glu									
20										25					30									
Phe	Gly	Tyr	Ala	Val	Thr	Leu	Ala	His	Pro	Ile	Arg	Arg	Leu	Leu	Leu									
35										40					45									
Leu	Ser	Ser	Val	Gly	Tyr	Ala	Pro	Val	Gly	Leu	Lys	Ile	Glu	Gly	Val									
50										55					60									
His	His	Glu	Phe	Asp	Ser	Leu	Arg	Gly	Val	Thr	Glu	Asp	Val	Ser	Leu									
65										70					75									
Phe	Ile	Met	Asn	Leu	Lys	Asn	Ile	Arg	Phe	Ile	Ala	Lys	Ala	Leu	Val									
85										90					95									
Gly	Gln	Asp	Ser	Ser	Leu	Glu	Asn	Gln	Ser	Val	Val	Val	Asp	Tyr	Ser									
100										105					110									
Phe	Lys	Gly	Pro	Met	Glu	Leu	Arg	Ala	Arg	Asp	Leu	Asn	Ser	Glu	Gln									
115										120					125									
Ile	Glu	Ile	Val	Asn	Pro	Glu	Met	Pro	Leu	Ala	Thr	Ile	Asn	Glu	Asp									
130										135					140									
Ala	Gln	Leu	Asn	Phe	Ser	Leu	Ile	Ile	Tyr	Lys	Gly	Met	Gly	Tyr	Val									
145										150					155									
Pro	Ser	Glu	Asn	Thr	Arg	Glu	Leu	Met	Pro	Glu	Gly	Tyr	Met	Pro	Leu									

				165					170					175			
Asp	Gly	Ser	Phe	Thr	Pro	Ile	Lys	Lys	Val	Val	Tyr	Glu	Ile	Glu	Asn		
			180					185					190				
Val	Leu	Val	Glu	Gly	Asp	Pro	Asn	Tyr	Glu	Lys	Ile	Ile	Phe	Asp	Ile		
		195					200					205					
Glu	Thr	Asp	Gly	Gln	Ile	Asp	Pro	Tyr	Lys	Ala	Phe	Leu	Ser	Ala	Val		
	210					215					220						
Lys	Val	Met	Ser	Lys	Gln	Leu	Gly	Val	Phe	Gly	Glu	Arg	Pro	Ile	Ala		
225				230					235						240		
Asn	Thr	Glu	Tyr	Ser	Gly	Asp	Tyr	Ala	Gln	Arg	Asp	Asp	Ala	Lys	Asp		
				245				250						255			
Leu	Ser	Ala	Lys	Ile	Glu	Ser	Met	Asn	Leu	Ser	Ala	Arg	Cys	Phe	Asn		
		260					265						270				
Cys	Leu	Asp	Lys	Ile	Gly	Ile	Lys	Tyr	Val	Gly	Glu	Leu	Val	Leu	Met		
	275						280				285						
Ser	Glu	Glu	Glu	Leu	Lys	Gly	Val	Lys	Asn	Met	Gly	Lys	Lys	Ser	Tyr		
	290				295						300						
Asp	Glu	Ile	Ala	Glu	Lys	Leu	Asn	Asp	Leu	Gly	Tyr	Pro	Val	Gly	Thr		
305				310					315						320		
Glu	Leu	Ser	Pro	Glu	Gln	Arg	Glu	Ser	Leu	Lys	Lys	Arg	Leu	Glu	Lys		
			325				330							335			
Leu	Glu	Asp	Lys	Gly	Gly	Asn	Asp										
			340														

<210> 315
 <211> 423
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (16)...(375)

<400> 315																	
agacaaggat aaagc atg gca agg att gct ggt gta gat tta cca aaa aag	51																
Met Ala Arg Ile Ala Gly Val Asp Leu Pro Lys Lys																	
1 5 10																	
aag aga gtg gag tat gcc ctt acc tat att tat ggg att ggg ctt aag	99																
Lys Arg Val Glu Tyr Ala Leu Thr Tyr Ile Tyr Gly Ile Gly Leu Lys																	
15 20 25																	
agt tcc aga gag att tta gaa gcg gta ggc att tct ttt gac aag cgc	147																
Ser Ser Arg Glu Ile Leu Glu Ala Val Gly Ile Ser Phe Asp Lys Arg																	
30 35 40																	
gtg cat gaa ttg agc gaa gat gaa gtg tct agc atc gct aaa aaa atc	195																
Val His Glu Leu Ser Glu Asp Glu Val Ser Ser Ile Ala Lys Lys Ile																	
45 50 55 60																	
caa caa agc tac cta gta gag ggc gat ttg cgt aaa aaa gtt caa atg	243																
Gln Gln Ser Tyr Leu Val Glu Gly Asp Leu Arg Lys Lys Val Gln Met																	
65 70 75																	
gat att aaa tct tta atg gac ttg ggg aat tat cgt ggg atc agg cat	291																
Asp Ile Lys Ser Leu Met Asp Leu Gly Asn Tyr Arg Gly Ile Arg His																	
80 85 90																	

cgt aag ggt ctt cct gtg aga ggt caa acc act aaa aat aac gct agg 339
 Arg Lys Gly Leu Pro Val Arg Gly Gln Thr Thr Lys Asn Asn Ala Arg
 95 100 105

act cgt aag ggt aag aaa aaa acc gtg ggt agc aag tagcgaataa 385
 Thr Arg Lys Gly Lys Lys Lys Thr Val Gly Ser Lys
 110 115 120

ggagatgatg atttaatggc taagagaaat gtaacggc 423

<210> 316
 <211> 120
 <212> PRT
 <213> Helicobacter pylori

<400> 316
 Met Ala Arg Ile Ala Gly Val Asp Leu Pro Lys Lys Lys Arg Val Glu
 1 5 10 15
 Tyr Ala Leu Thr Tyr Ile Tyr Gly Ile Gly Leu Lys Ser Ser Arg Glu
 20 25 30
 Ile Leu Glu Ala Val Gly Ile Ser Phe Asp Lys Arg Val His Glu Leu
 35 40 45
 Ser Glu Asp Glu Val Ser Ser Ile Ala Lys Lys Ile Gln Gln Ser Tyr
 50 55 60
 Leu Val Glu Gly Asp Leu Arg Lys Lys Val Gln Met Asp Ile Lys Ser
 65 70 75 80
 Leu Met Asp Leu Gly Asn Tyr Arg Gly Ile Arg His Arg Lys Gly Leu
 85 90 95
 Pro Val Arg Gly Gln Thr Thr Lys Asn Asn Ala Arg Thr Arg Lys Gly
 100 105 110
 Lys Lys Lys Thr Val Gly Ser Lys
 115 120

<210> 317
 <211> 649
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (19)...(621)

<400> 317
 aagcgtaggg tggttttta atg att ttt tat aga aag gaa gct aca atg aac 51
 Met Ile Phe Tyr Arg Lys Glu Ala Thr Met Asn
 1 5 10

 gca ttg aaa aaa tta agt ttc tgc gcc ttg tta tcc cta ggc ctc ttc 99
 Ala Leu Lys Lys Leu Ser Phe Cys Ala Leu Leu Ser Leu Gly Leu Phe
 15 20 25

 gct caa aca gcg cat gct aag cat tta aag ggc acg att aac tat cct 147
 Ala Gln Thr Ala His Ala Lys His Leu Lys Gly Thr Ile Asn Tyr Pro
 30 35 40

 gat tgg ctt gaa atc aat ttt ttt gac gaa aaa aac ccg ccc aat caa 195
 Asp Trp Leu Glu Ile Asn Phe Phe Asp Glu Lys Asn Pro Pro Asn Gln
 45 50 55

tat gtc gga tcg gct tca att tct ggt aaa agg aac gat ttt tac gcc	243
Tyr Val Gly Ser Ala Ser Ile Ser Gly Lys Arg Asn Asp Phe Tyr Ala	
60 65 70 75	

aat tac atc ccc tat gat gac caa ttg ccc cct gaa caa aac gct gaa	291
Asn Tyr Ile Pro Tyr Asp Asp Gln Leu Pro Pro Glu Gln Asn Ala Glu	
80 85 90	

aaa atc gct ctt tta agg gcc aga ata aac gct tac agc act tta gag	339
Lys Ile Ala Leu Leu Arg Ala Arg Ile Asn Ala Tyr Ser Thr Leu Glu	
95 100 105	

agc att tta ctc act aaa atg cac aat cgt att gtt aag gtg ctt caa	387
Ser Ile Leu Leu Thr Lys Met His Asn Arg Ile Val Lys Val Leu Gln	
110 115 120	

gtt aaa aat aat gtt atc agc cat tta ttc ggg ctt gtt gat ttt tta	435
Val Lys Asn Asn Val Ile Ser His Leu Phe Gly Leu Val Asp Phe Leu	
125 130 135	

acc tct aaa tcc att ttg gct aaa agg ttc gtg gat acc aca aat cat	483
Thr Ser Lys Ser Ile Leu Ala Lys Arg Phe Val Asp Thr Thr Asn His	
140 145 150 155	

cgt gtg tat gtc atg gtg caa ttc cct ttc att cag cct gaa gac ttg	531
Arg Val Tyr Val Met Val Gln Phe Pro Phe Ile Gln Pro Glu Asp Leu	
160 165 170	

atc gct tac ttt aaa gcc aaa cgc atc gac ctt tct tca gcg agc gct	579
Ile Ala Tyr Phe Lys Ala Lys Arg Ile Asp Leu Ser Ser Ala Ser Ala	
175 180 185	

acc cat ctc agc gcc ctt tta aat aag gcg ttg ttc cac ctc	621
Thr His Leu Ser Ala Leu Leu Asn Lys Ala Leu Phe His Leu	
190 195 200	

taagagtttg ggatttaaga tgcggttt	649
--------------------------------	-----

<210> 318

<211> 201

<212> PRT

<213> Helicobacter pylori

<400> 318

Met Ile Phe Tyr Arg Lys Glu Ala Thr Met Asn Ala Leu Lys Lys Leu	
1 5 10 15	
Ser Phe Cys Ala Leu Leu Ser Leu Gly Leu Phe Ala Gln Thr Ala His	
20 25 30	
Ala Lys His Leu Lys Gly Thr Ile Asn Tyr Pro Asp Trp Leu Glu Ile	
35 40 45	
Asn Phe Phe Asp Glu Lys Asn Pro Pro Asn Gln Tyr Val Gly Ser Ala	
50 55 60	
Ser Ile Ser Gly Lys Arg Asn Asp Phe Tyr Ala Asn Tyr Ile Pro Tyr	
65 70 75 80	
Asp Asp Gln Leu Pro Pro Glu Gln Asn Ala Glu Lys Ile Ala Leu Leu	
85 90 95	
Arg Ala Arg Ile Asn Ala Tyr Ser Thr Leu Glu Ser Ile Leu Leu Thr	
100 105 110	

Lys	Met	His	Asn	Arg	Ile	Val	Lys	Val	Leu	Gln	Val	Lys	Asn	Asn	Val
		115					120					125			
Ile	Ser	His	Leu	Phe	Gly	Leu	Val	Asp	Phe	Leu	Thr	Ser	Lys	Ser	Ile
	130					135					140				
Leu	Ala	Lys	Arg	Phe	Val	Asp	Thr	Thr	Asn	His	Arg	Val	Tyr	Val	Met
145					150					155					160
Val	Gln	Phe	Pro	Phe	Ile	Gln	Pro	Glu	Asp	Leu	Ile	Ala	Tyr	Phe	Lys
				165					170					175	
Ala	Lys	Arg	Ile	Asp	Leu	Ser	Ser	Ala	Ser	Ala	Thr	His	Leu	Ser	Ala
			180					185					190		
Leu	Leu	Asn	Lys	Ala	Leu	Phe	His	Leu							
		195					200								

<210> 319
 <211> 540
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (16)...(513)

<400> 319

gcatgctctt	agagt	atg	tct	gta	tcg	cat	gtt	gct	tta	atc	tta	agg	aaa	51		
		Met	Ser	Val	Ser	His	Val	Ala	Leu	Ile	Leu	Arg	Lys			
		1				5					10					
ttg	ttt	tat	cat	aga	caa	gga	gtt	ttt	atg	ggc	ggt	ttt	tca	gtg	gga	99
Leu	Phe	Tyr	His	Arg	Gln	Gly	Val	Phe	Met	Gly	Gly	Phe	Ser	Val	Gly	
		15					20					25				
atg	ttg	aaa	gat	tat	gtg	gac	ata	ttt	gtt	ttt	gcg	gtg	ctt	ggc	gtg	147
Met	Leu	Lys	Asp	Tyr	Val	Asp	Ile	Phe	Val	Phe	Ala	Val	Leu	Gly	Val	
	30					35					40					
gcc	agt	ttt	tta	gct	ttg	tgg	ttt	gcg	att	gaa	agg	gtt	att	ttt	tat	195
Ala	Ser	Phe	Leu	Ala	Leu	Trp	Phe	Ala	Ile	Glu	Arg	Val	Ile	Phe	Tyr	
	45				50					55					60	
tct	aaa	gtc	gat	ttg	aaa	gct	tat	gac	gat	ata	gat	gcc	ctg	aat	ttg	243
Ser	Lys	Val	Asp	Leu	Lys	Ala	Tyr	Asp	Asp	Ile	Asp	Ala	Leu	Asn	Leu	
				65					70					75		
gat	tta	acc	aag	aat	cta	acc	att	ctc	tat	gtg	att	ttt	tct	aac	gcg	291
Asp	Leu	Thr	Lys	Asn	Leu	Thr	Ile	Leu	Tyr	Val	Ile	Phe	Ser	Asn	Ala	
			80					85					90			
cct	tat	gtg	ggc	tta	tta	ggg	acg	gtt	tta	ggg	att	atg	gtg	att	ttc	339
Pro	Tyr	Val	Gly	Leu	Leu	Gly	Thr	Val	Leu	Gly	Ile	Met	Val	Ile	Phe	
		95					100					105				
tat	gac	atg	ggc	gtg	agc	ggc	ggg	atg	gac	gct	aaa	acg	atc	atg	gta	387
Tyr	Asp	Met	Gly	Val	Ser	Gly	Gly	Met	Asp	Ala	Lys	Thr	Ile	Met	Val	
	110					115					120					
ggt	ttg	tct	ttg	gct	tta	aaa	gcg	acc	gct	cta	ggg	ctt	gct	gtg	gcg	435
Gly	Leu	Ser	Leu	Ala	Leu	Lys	Ala	Thr	Ala	Leu	Gly	Leu	Ala	Val	Ala	
	125				130					135					140	

att ccc act ttg atc gct tat aat agc ttg ttg aga aaa tcc gat gtt 483
 Ile Pro Thr Leu Ile Ala Tyr Asn Ser Leu Leu Arg Lys Ser Asp Val
 145 150 155

ttg agc gaa aaa ttc agg atc atg aaa aaa tgaaaagcat cagaagaggc 533
 Leu Ser Glu Lys Phe Arg Ile Met Lys Lys
 160 165

gatgggc 540

<210> 320
 <211> 166
 <212> PRT
 <213> Helicobacter pylori

<400> 320
 Met Ser Val Ser His Val Ala Leu Ile Leu Arg Lys Leu Phe Tyr His
 1 5 10 15
 Arg Gln Gly Val Phe Met Gly Gly Phe Ser Val Gly Met Leu Lys Asp
 20 25 30
 Tyr Val Asp Ile Phe Val Phe Ala Val Leu Gly Val Ala Ser Phe Leu
 35 40 45
 Ala Leu Trp Phe Ala Ile Glu Arg Val Ile Phe Tyr Ser Lys Val Asp
 50 55 60
 Leu Lys Ala Tyr Asp Asp Ile Asp Ala Leu Asn Leu Asp Leu Thr Lys
 65 70 75 80
 Asn Leu Thr Ile Leu Tyr Val Ile Phe Ser Asn Ala Pro Tyr Val Gly
 85 90 95
 Leu Leu Gly Thr Val Leu Gly Ile Met Val Ile Phe Tyr Asp Met Gly
 100 105 110
 Val Ser Gly Gly Met Asp Ala Lys Thr Ile Met Val Gly Leu Ser Leu
 115 120 125
 Ala Leu Lys Ala Thr Ala Leu Gly Leu Ala Val Ala Ile Pro Thr Leu
 130 135 140
 Ile Ala Tyr Asn Ser Leu Leu Arg Lys Ser Asp Val Leu Ser Glu Lys
 145 150 155 160
 Phe Arg Ile Met Lys Lys
 165

<210> 321
 <211> 777
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (25)...(723)

<400> 321
 tcatgaatta aaccctagcg aaca atg aag ctt ttt gac tac gct cct ttg 51
 Met Lys Leu Phe Asp Tyr Ala Pro Leu
 1 5

agt ttg gct tgg cgg gag ttt ttg caa agc gaa ttt aaa aag cct tat 99
 Ser Leu Ala Trp Arg Glu Phe Leu Gln Ser Glu Phe Lys Lys Pro Tyr
 10 15 20 25

ttt tta gaa ata gaa aaa cgc tac cta gaa gcc cta aaa atc cct aaa	147
Phe Leu Glu Ile Glu Lys Arg Tyr Leu Glu Ala Leu Lys Ile Pro Lys	
30 35 40	
acc att ttc cct aaa agc tct aat ctg ttt tat gcg ctc aat cta acg	195
Thr Ile Phe Pro Lys Ser Ser Asn Leu Phe Tyr Ala Leu Asn Leu Thr	
45 50 55	
ccc cct tgt gcg gtt aaa atc atc ctt tta ggg caa gac ccc tac cat	243
Pro Pro Cys Ala Val Lys Ile Ile Leu Leu Gly Gln Asp Pro Tyr His	
60 65 70	
tcc acc tac cta gaa aat gat caa gaa ttg ccg gtg gcg atg ggg ttg	291
Ser Thr Tyr Leu Glu Asn Asp Gln Glu Leu Pro Val Ala Met Gly Leu	
75 80 85	
agc ttt agc gtg gaa aaa aac gcc cct att cct cca agt tta aaa aat	339
Ser Phe Ser Val Glu Lys Asn Ala Pro Ile Pro Pro Ser Leu Lys Asn	
90 95 100 105	
att ttt aaa gaa ttg cat gcg aat tta ggc gtg cct gtg cct tgt tgt	387
Ile Phe Lys Glu Leu His Ala Asn Leu Gly Val Pro Val Pro Cys Cys	
110 115 120	
ggg gat ttg agc gca tgg gct aaa agg ggc atg ctc tta ttg aac gcc	435
Gly Asp Leu Ser Ala Trp Ala Lys Arg Gly Met Leu Leu Leu Asn Ala	
125 130 135	
att tta agc gtg gaa aaa aac caa gcc gct tcg cac caa tat att ggc	483
Ile Leu Ser Val Glu Lys Asn Gln Ala Ala Ser His Gln Tyr Ile Gly	
140 145 150	
tgg gaa gct ttt agc gat caa ata ctg atg cgc ctt ttt gaa acg acc	531
Trp Glu Ala Phe Ser Asp Gln Ile Leu Met Arg Leu Phe Glu Thr Thr	
155 160 165	
gcc cct tta atc gtg gtg tta cta ggg aaa gtc gcc caa aaa aag atc	579
Ala Pro Leu Ile Val Val Leu Leu Gly Lys Val Ala Gln Lys Lys Ile	
170 175 180 185	
gcg tta atc ccc aaa aac aaa cac atc atc atc aca gcc cct cac cct	627
Ala Leu Ile Pro Lys Asn Lys His Ile Ile Ile Thr Ala Pro His Pro	
190 195 200	
agc cca cta tct agg ggg ttt tta ggg agt ggg gtt ttt aca agc gtt	675
Ser Pro Leu Ser Arg Gly Phe Leu Gly Ser Gly Val Phe Thr Ser Val	
205 210 215	
caa aaa gct tat aga gag gtt tat cgc aag gat ttt gat ttt agt tta	723
Gln Lys Ala Tyr Arg Glu Val Tyr Arg Lys Asp Phe Asp Phe Ser Leu	
220 225 230	
tgattgatgc ttaatgagac agaaccctt aagaatgcct ttatttaaga gcat	777

<210> 322

<211> 233

<212> PRT

<213> Helicobacter pylori

<400> 322

```

Met Lys Leu Phe Asp Tyr Ala Pro Leu Ser Leu Ala Trp Arg Glu Phe
 1          5          10          15
Leu Gln Ser Glu Phe Lys Lys Pro Tyr Phe Leu Glu Ile Glu Lys Arg
 20          25          30
Tyr Leu Glu Ala Leu Lys Ile Pro Lys Thr Ile Phe Pro Lys Ser Ser
 35          40          45
Asn Leu Phe Tyr Ala Leu Asn Leu Thr Pro Pro Cys Ala Val Lys Ile
 50          55          60
Ile Leu Leu Gly Gln Asp Pro Tyr His Ser Thr Tyr Leu Glu Asn Asp
 65          70          75          80
Gln Glu Leu Pro Val Ala Met Gly Leu Ser Phe Ser Val Glu Lys Asn
 85          90          95
Ala Pro Ile Pro Pro Ser Leu Lys Asn Ile Phe Lys Glu Leu His Ala
100          105          110
Asn Leu Gly Val Pro Val Pro Cys Cys Gly Asp Leu Ser Ala Trp Ala
115          120          125
Lys Arg Gly Met Leu Leu Leu Asn Ala Ile Leu Ser Val Glu Lys Asn
130          135          140
Gln Ala Ala Ser His Gln Tyr Ile Gly Trp Glu Ala Phe Ser Asp Gln
145          150          155          160
Ile Leu Met Arg Leu Phe Glu Thr Thr Ala Pro Leu Ile Val Val Leu
165          170          175
Leu Gly Lys Val Ala Gln Lys Lys Ile Ala Leu Ile Pro Lys Asn Lys
180          185          190
His Ile Ile Ile Thr Ala Pro His Pro Ser Pro Leu Ser Arg Gly Phe
195          200          205
Leu Gly Ser Gly Val Phe Thr Ser Val Gln Lys Ala Tyr Arg Glu Val
210          215          220
Tyr Arg Lys Asp Phe Asp Phe Ser Leu
225          230

```

<210> 323

<211> 1242

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (19) ... (1179)

<400> 323

```

aagaagaaat aaaaactc atg ggg ttt tta ttt gaa aaa tcg tta atg agt      51
                Met Gly Phe Leu Phe Glu Lys Ser Leu Met Ser
                1          5          10

ttt ttc gct cat cca atc aaa atc ctt aaa atc atc agt ttg att tta      99
Phe Phe Ala His Pro Ile Lys Ile Leu Lys Ile Ile Ser Leu Ile Leu
                15          20          25

agt ttt ttg gta agc ttt ttg gtt gct gaa aac gct cat gag cca gaa      147
Ser Phe Leu Val Ser Phe Leu Val Ala Glu Asn Ala His Glu Pro Glu
                30          35          40

gaa atc aag gct aaa gtg gct tat gtg aaa atc ccc caa tta gaa gat      195
Glu Ile Lys Ala Lys Val Ala Tyr Val Lys Ile Pro Gln Leu Glu Asp
                45          50          55

```

ttg gaa aac aac ccg gtt tat atc ggt caa att ata ggc gta act tat	243
Leu Glu Asn Asn Pro Val Tyr Ile Gly Gln Ile Ile Gly Val Thr Tyr	
60 65 70 75	
gat tta ttg ctg ttt gac gct gag ttt ttg gaa gcc aaa atc aaa gac	291
Asp Leu Leu Leu Phe Asp Ala Glu Phe Leu Glu Ala Lys Ile Lys Asp	
80 85 90	
ggg ttg gat aaa acc caa att gag ctt tta aac aag atg cct aaa tgg	339
Gly Leu Asp Lys Thr Gln Ile Glu Leu Leu Asn Lys Met Pro Lys Trp	
95 100 105	
aaa aag gtg gaa aaa gag ctt ttc aga gcg act tat tat tac aag att	387
Lys Lys Val Glu Lys Glu Leu Phe Arg Ala Thr Tyr Tyr Tyr Lys Ile	
110 115 120	
aag ggc ata aaa gcg att att ccg tcc tta gaa gtg agc gcg ttt tcc	435
Lys Gly Ile Lys Ala Ile Ile Pro Ser Leu Glu Val Ser Ala Phe Ser	
125 130 135	
aat aaa gac aaa tac ata gat cat tcc ata gcc cca aaa gtt act ttg	483
Asn Lys Asp Lys Tyr Ile Asp His Ser Ile Ala Pro Lys Val Thr Leu	
140 145 150 155	
cag gta acg gat ttg tcc aaa aac cct cgt tat gcg aat gtc atg gct	531
Gln Val Thr Asp Leu Ser Lys Asn Pro Arg Tyr Ala Asn Val Met Ala	
160 165 170	
aaa gat tta caa gtc ttg caa tac aaa acc aaa gat tat gac gat aaa	579
Lys Asp Leu Gln Val Leu Gln Tyr Lys Thr Lys Asp Tyr Asp Asp Lys	
175 180 185	
aac aat att ttg gtg atg gaa ata gcg ttc aaa gaa gcc act tgg gaa	627
Asn Asn Ile Leu Val Met Glu Ile Ala Phe Lys Glu Ala Thr Trp Glu	
190 195 200	
gat ttt cac atc aaa gaa gcg atc aag caa ggg ttt gat aac gcc tct	675
Asp Phe His Ile Lys Glu Ala Ile Lys Gln Gly Phe Asp Asn Ala Ser	
205 210 215	
tta aac cag atc aag gct aaa gaa ggg agc gtt ttt tat tat tgc gtg	723
Leu Asn Gln Ile Lys Ala Lys Glu Gly Ser Val Phe Tyr Tyr Cys Val	
220 225 230 235	
ttg cct aag act att caa aac ctt tct ttt gat tat ttc tcg ctt tca	771
Leu Pro Lys Thr Ile Gln Asn Leu Ser Phe Asp Tyr Phe Ser Leu Ser	
240 245 250	
aat aag caa ttt aaa acc tta tct ttt tca acc att ccc act caa gac	819
Asn Lys Gln Phe Lys Thr Leu Ser Phe Ser Thr Ile Pro Thr Gln Asp	
255 260 265	
act acc ggt att caa agc gat ctc atc cct aaa aac aat ttt tta gtc	867
Thr Thr Gly Ile Gln Ser Asp Leu Ile Pro Lys Asn Asn Phe Leu Val	
270 275 280	
ttt tct aat gtg gcg ttg ctc gct ttg tgc gtg ttt ttc ttg gtg ctg	915
Phe Ser Asn Val Ala Leu Leu Ala Leu Cys Val Phe Phe Leu Val Leu	
285 290 295	

ttt ttc att ttt ggg cgc aaa ctc att ttt tta ggg ctt ggg att ttg	963
Phe Phe Ile Phe Gly Arg Lys Leu Ile Phe Leu Gly Leu Gly Ile Leu	
300 305 310 315	
tgc tta ggg ttt gtt ttg tat cac ctt tta ttc acg caa aaa tca gcc	1011
Cys Leu Gly Phe Val Leu Tyr His Leu Phe Thr Gln Lys Ser Ala	
320 325 330	
cta ttg ctc gct cat aaa aaa atc cgc att ctg ccc acg caa aat tcc	1059
Leu Leu Leu Ala His Lys Lys Ile Arg Ile Leu Pro Thr Gln Asn Ser	
335 340 345	
acc att tta ggg ctt tct aaa aat gaa atg ccg att aaa atc tta ggc	1107
Thr Ile Leu Gly Leu Ser Lys Asn Glu Met Pro Ile Lys Ile Leu Gly	
350 355 360	
tcg cat gat gat tat tat aaa atc cta acg ccg cat gaa caa ata gga	1155
Ser His Asp Asp Tyr Tyr Lys Ile Leu Thr Pro His Glu Gln Ile Gly	
365 370 375	
tgg gtc aaa aaa gat gaa gtc aaa taaaaagtcc aatcgtttta gagcgattta	1209
Trp Val Lys Lys Asp Glu Val Lys	
380 385	

tagagcttta gtgacgcta taggactagc tgt	1242
-------------------------------------	------

<210> 324
 <211> 387
 <212> PRT
 <213> *Helicobacter pylori*

<400> 324																
Met Gly Phe Leu Phe Glu Lys Ser Leu Met Ser Phe Phe Ala His Pro																
1 5 10 15																
Ile Lys Ile Leu Lys Ile Ile Ser Leu Ile Leu Ser Phe Leu Val Ser																
20 25 30																
Phe Leu Val Ala Glu Asn Ala His Glu Pro Glu Glu Ile Lys Ala Lys																
35 40 45																
Val Ala Tyr Val Lys Ile Pro Gln Leu Glu Asp Leu Glu Asn Asn Pro																
50 55 60																
Val Tyr Ile Gly Gln Ile Ile Gly Val Thr Tyr Asp Leu Leu Leu Phe																
65 70 75 80																
Asp Ala Glu Phe Leu Glu Ala Lys Ile Lys Asp Gly Leu Asp Lys Thr																
85 90 95																
Gln Ile Glu Leu Leu Asn Lys Met Pro Lys Trp Lys Lys Val Glu Lys																
100 105 110																
Glu Leu Phe Arg Ala Thr Tyr Tyr Lys Ile Lys Gly Ile Lys Ala																
115 120 125																
Ile Ile Pro Ser Leu Glu Val Ser Ala Phe Ser Asn Lys Asp Lys Tyr																
130 135 140																
Ile Asp His Ser Ile Ala Pro Lys Val Thr Leu Gln Val Thr Asp Leu																
145 150 155 160																
Ser Lys Asn Pro Arg Tyr Ala Asn Val Met Ala Lys Asp Leu Gln Val																
165 170 175																
Leu Gln Tyr Lys Thr Lys Asp Tyr Asp Asp Lys Asn Asn Ile Leu Val																
180 185 190																
Met Glu Ile Ala Phe Lys Glu Ala Thr Trp Glu Asp Phe His Ile Lys																
195 200 205																

Glu Ala Ile Lys Gln Gly Phe Asp Asn Ala Ser Leu Asn Gln Ile Lys
 210 215 220
 Ala Lys Glu Gly Ser Val Phe Tyr Tyr Cys Val Leu Pro Lys Thr Ile
 225 230 235 240
 Gln Asn Leu Ser Phe Asp Tyr Phe Ser Leu Ser Asn Lys Gln Phe Lys
 245 250 255
 Thr Leu Ser Phe Ser Thr Ile Pro Thr Gln Asp Thr Thr Gly Ile Gln
 260 265 270
 Ser Asp Leu Ile Pro Lys Asn Asn Phe Leu Val Phe Ser Asn Val Ala
 275 280 285
 Leu Leu Ala Leu Cys Val Phe Phe Leu Val Leu Phe Phe Ile Phe Gly
 290 295 300
 Arg Lys Leu Ile Phe Leu Gly Leu Gly Ile Leu Cys Leu Gly Phe Val
 305 310 315 320
 Leu Tyr His Leu Leu Phe Thr Gln Lys Ser Ala Leu Leu Leu Ala His
 325 330 335
 Lys Lys Ile Arg Ile Leu Pro Thr Gln Asn Ser Thr Ile Leu Gly Leu
 340 345 350
 Ser Lys Asn Glu Met Pro Ile Lys Ile Leu Gly Ser His Asp Asp Tyr
 355 360 365
 Tyr Lys Ile Leu Thr Pro His Glu Gln Ile Gly Trp Val Lys Lys Asp
 370 375 380
 Glu Val Lys
 385

<210> 325
 <211> 1455
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (34)...(1395)

<400> 325
 ttctaattctc aaaaatgggt ggtggttatta aca atg aca aaa cga ctt ttt aaa 54
 Met Thr Lys Arg Leu Phe Lys
 1 5

 ggg ttg tta gcg gtt tct ctt gct gtg agt ttg cat ggt ggt gaa gtt 102
 Gly Leu Leu Ala Val Ser Leu Ala Val Ser Leu His Gly Gly Glu Val
 10 15 20

 aag gaa aaa aag ccg gtt aag ccg gtt aaa gaa gat ccg caa gaa tta 150
 Lys Glu Lys Lys Pro Val Lys Pro Val Lys Glu Asp Pro Gln Glu Leu
 25 30 35

 gcg gct aaa agg gtg gaa gcg ttc agt cgt ttc tct aat gtg gtt tca 198
 Ala Ala Lys Arg Val Glu Ala Phe Ser Arg Phe Ser Asn Val Val Ser
 40 45 50 55

 gaa att gaa aaa aaa tat gtg gat aaa atc agc att tct gag atc atg 246
 Glu Ile Glu Lys Lys Tyr Val Asp Lys Ile Ser Ile Ser Glu Ile Met
 60 65 70

 act aaa gcg att gaa ggc ttg ctc tct aat ttg gac gcg cat tca gcg 294
 Thr Lys Ala Ile Glu Gly Leu Leu Ser Asn Leu Asp Ala His Ser Ala
 75 80 85

tat ttg aat gaa aag aag ttt aag gaa ttt caa gcc caa acc gag ggc	342
Tyr Leu Asn Glu Lys Lys Phe Lys Glu Phe Gln Ala Gln Thr Glu Gly	
90 95 100	
gaa ttt ggg ggg ctt ggg atc acg gtg ggc atg cgc gat ggc gtt tta	390
Glu Phe Gly Gly Leu Gly Ile Thr Val Gly Met Arg Asp Gly Val Leu	
105 110 115	
acc gtt att gcc cct tta gaa ggc act cca gct tac aag gct ggg gtt	438
Thr Val Ile Ala Pro Leu Glu Gly Thr Pro Ala Tyr Lys Ala Gly Val	
120 125 130 135	
aag tca ggc gat aac att tta aaa atc aat aac gaa agc acg ctg agc	486
Lys Ser Gly Asp Asn Ile Leu Lys Ile Asn Asn Glu Ser Thr Leu Ser	
140 145 150	
atg agc att gat gat gcg atc aac ctc atg cgc ggc aag cca aaa acc	534
Met Ser Ile Asp Asp Ala Ile Asn Leu Met Arg Gly Lys Pro Lys Thr	
155 160 165	
cct att cag atc acc gtt gta aga aaa aac gag cca aaa cct tta gtg	582
Pro Ile Gln Ile Thr Val Val Arg Lys Asn Glu Pro Lys Pro Leu Val	
170 175 180	
ttt aac atc att aga gac atc att aaa ctc ccc tct gtc tat gtg aaa	630
Phe Asn Ile Ile Arg Asp Ile Ile Lys Leu Pro Ser Val Tyr Val Lys	
185 190 195	
aag att aaa gaa acc cct tat ctg tat gtg aga gtg agt ggt ttt gac	678
Lys Ile Lys Glu Thr Pro Tyr Leu Tyr Val Arg Val Ser Gly Phe Asp	
200 205 210 215	
aag aat gtt acc aaa tcg gtt tta gaa ggc tta aaa gct aac cct aag	726
Lys Asn Val Thr Lys Ser Val Leu Glu Gly Leu Lys Ala Asn Pro Lys	
220 225 230	
gct aag ggg atc gtg ttg gat tta agg ggc aat cct gga ggg cta tta	774
Ala Lys Gly Ile Val Leu Asp Leu Arg Gly Asn Pro Gly Gly Leu Leu	
235 240 245	
aac caa gcg gtg ggc ttg tct aac ctc ttc att aaa gag ggg gtt tta	822
Asn Gln Ala Val Gly Leu Ser Asn Leu Phe Ile Lys Glu Gly Val Leu	
250 255 260	
gtc tct caa aaa ggc aaa aat aaa gaa gaa aat tta gaa tac aag gct	870
Val Ser Gln Lys Gly Lys Asn Lys Glu Glu Asn Leu Glu Tyr Lys Ala	
265 270 275	
aac ggc aga gcc cct tat acc aat ttg cct att gcg gtg tta gtc aat	918
Asn Gly Arg Ala Pro Tyr Thr Asn Leu Pro Ile Ala Val Leu Val Asn	
280 285 290 295	
ggc ggt tca gcg agc gcg agc gag atc gtc gca ggg gca ctg caa gat	966
Gly Gly Ser Ala Ser Ala Ser Glu Ile Val Ala Gly Ala Leu Gln Asp	
300 305 310	
cac aaa cgg gcc gtg att atc ggt gaa aaa acc ttt ggt aag gga agc	1014
His Lys Arg Ala Val Ile Ile Gly Glu Lys Thr Phe Gly Lys Gly Ser	

315						320						325						
gtg	cag	atg	ctg	ctc	cct	gtc	aat	aaa	gac	gaa	gcc	att	aaa	atc	aca	1062		
Val	Gln	Met	Leu	Leu	Pro	Val	Asn	Lys	Asp	Glu	Ala	Ile	Lys	Ile	Thr			
330						335						340						
acc	gca	cgc	tac	tat	ttg	ccg	agc	ggg	cgt	acc	att	caa	gct	aag	ggg	1110		
Thr	Ala	Arg	Tyr	Tyr	Leu	Pro	Ser	Gly	Arg	Thr	Ile	Gln	Ala	Lys	Gly			
345						350						355						
atc	acg	cct	gat	att	gtg	att	tat	ccg	ggt	aaa	gtg	cca	gaa	aat	gaa	1158		
Ile	Thr	Pro	Asp	Ile	Val	Ile	Tyr	Pro	Gly	Lys	Val	Pro	Glu	Asn	Glu			
360						365						370						375
aac	aaa	ttc	agc	ttg	aaa	gaa	gcg	gat	cta	aaa	cac	cat	tta	gag	caa	1206		
Asn	Lys	Phe	Ser	Leu	Lys	Glu	Ala	Asp	Leu	Lys	His	His	Leu	Glu	Gln			
380						385						390						
gag	ctt	aaa	aag	att	gat	gat	aaa	acc	ccc	aat	tcc	aaa	gag	gcg	gat	1254		
Glu	Leu	Lys	Lys	Ile	Asp	Asp	Lys	Thr	Pro	Asn	Ser	Lys	Glu	Ala	Asp			
395						400						405						
aaa	gac	aag	aaa	aac	gaa	gag	gaa	aaa	gag	att	act	cct	aaa	atg	atc	1302		
Lys	Asp	Lys	Lys	Asn	Glu	Glu	Glu	Lys	Glu	Ile	Thr	Pro	Lys	Met	Ile			
410						415						420						
aac	gat	gat	att	cag	cta	aaa	acc	gct	att	gac	agc	ttg	aaa	acc	tgg	1350		
Asn	Asp	Asp	Ile	Gln	Leu	Lys	Thr	Ala	Ile	Asp	Ser	Leu	Lys	Thr	Trp			
425						430						435						
tct	atc	gtt	gat	gag	aaa	atg	gat	gaa	aaa	gcg	cct	aag	aag	aaa		1395		
Ser	Ile	Val	Asp	Glu	Lys	Met	Asp	Glu	Lys	Ala	Pro	Lys	Lys	Lys				
440						445						450						
taaaaactca tgggggttttt atttgaaaaa tcgttaatga gtttttttcgc tcatccaatc 1455																		

<210> 326

<211> 454

<212> PRT

<213> *Helicobacter pylori*

<400> 326

Met	Thr	Lys	Arg	Leu	Phe	Lys	Gly	Leu	Leu	Ala	Val	Ser	Leu	Ala	Val
1				5				10						15	
Ser	Leu	His	Gly	Gly	Glu	Val	Lys	Glu	Lys	Lys	Pro	Val	Lys	Pro	Val
			20					25					30		
Lys	Glu	Asp	Pro	Gln	Glu	Leu	Ala	Ala	Lys	Arg	Val	Glu	Ala	Phe	Ser
		35					40					45			
Arg	Phe	Ser	Asn	Val	Val	Ser	Glu	Ile	Glu	Lys	Lys	Tyr	Val	Asp	Lys
		50				55					60				
Ile	Ser	Ile	Ser	Glu	Ile	Met	Thr	Lys	Ala	Ile	Glu	Gly	Leu	Leu	Ser
		65			70					75					80
Asn	Leu	Asp	Ala	His	Ser	Ala	Tyr	Leu	Asn	Glu	Lys	Lys	Phe	Lys	Glu
				85					90					95	
Phe	Gln	Ala	Gln	Thr	Glu	Gly	Glu	Phe	Gly	Gly	Leu	Gly	Ile	Thr	Val
			100					105					110		
Gly	Met	Arg	Asp	Gly	Val	Leu	Thr	Val	Ile	Ala	Pro	Leu	Glu	Gly	Thr
		115					120					125			

Pro Ala Tyr Lys Ala Gly Val Lys Ser Gly Asp Asn Ile Leu Lys Ile
 130 135 140
 Asn Asn Glu Ser Thr Leu Ser Met Ser Ile Asp Asp Ala Ile Asn Leu
 145 150 155 160
 Met Arg Gly Lys Pro Lys Thr Pro Ile Gln Ile Thr Val Val Arg Lys
 165 170 175
 Asn Glu Pro Lys Pro Leu Val Phe Asn Ile Ile Arg Asp Ile Ile Lys
 180 185 190
 Leu Pro Ser Val Tyr Val Lys Lys Ile Lys Glu Thr Pro Tyr Leu Tyr
 195 200 205
 Val Arg Val Ser Gly Phe Asp Lys Asn Val Thr Lys Ser Val Leu Glu
 210 215 220
 Gly Leu Lys Ala Asn Pro Lys Ala Lys Gly Ile Val Leu Asp Leu Arg
 225 230 235 240
 Gly Asn Pro Gly Gly Leu Leu Asn Gln Ala Val Gly Leu Ser Asn Leu
 245 250 255
 Phe Ile Lys Glu Gly Val Leu Val Ser Gln Lys Gly Lys Asn Lys Glu
 260 265 270
 Glu Asn Leu Glu Tyr Lys Ala Asn Gly Arg Ala Pro Tyr Thr Asn Leu
 275 280 285
 Pro Ile Ala Val Leu Val Asn Gly Gly Ser Ala Ser Ala Ser Glu Ile
 290 295 300
 Val Ala Gly Ala Leu Gln Asp His Lys Arg Ala Val Ile Ile Gly Glu
 305 310 315 320
 Lys Thr Phe Gly Lys Gly Ser Val Gln Met Leu Leu Pro Val Asn Lys
 325 330 335
 Asp Glu Ala Ile Lys Ile Thr Thr Ala Arg Tyr Tyr Leu Pro Ser Gly
 340 345 350
 Arg Thr Ile Gln Ala Lys Gly Ile Thr Pro Asp Ile Val Ile Tyr Pro
 355 360 365
 Gly Lys Val Pro Glu Asn Glu Asn Lys Phe Ser Leu Lys Glu Ala Asp
 370 375 380
 Leu Lys His His Leu Glu Gln Glu Leu Lys Lys Ile Asp Asp Lys Thr
 385 390 395 400
 Pro Asn Ser Lys Glu Ala Asp Lys Asp Lys Lys Asn Glu Glu Glu Lys
 405 410 415
 Glu Ile Thr Pro Lys Met Ile Asn Asp Asp Ile Gln Leu Lys Thr Ala
 420 425 430
 Ile Asp Ser Leu Lys Thr Trp Ser Ile Val Asp Glu Lys Met Asp Glu
 435 440 445
 Lys Ala Pro Lys Lys Lys
 450

<210> 327
 <211> 1150
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (22)...(1098)

<400> 327
 gatataaaaag gttagttaat c atg gat ttt tta aaa gaa aac tta aac act 51
 Met Asp Phe Leu Lys Glu Asn Leu Asn Thr
 1 5 10

atc ata gag ggg gat tgt tta gaa aaa ttg aaa gac ttt cct aac aga 99

Ile	Ile	Glu	Gly	Asp	Cys	Leu	Glu	Lys	Leu	Lys	Asp	Phe	Pro	Asn	Arg		
				15					20					25			
agc	gtt	gat	ttt	atc	ttt	gct	gac	ccc	cca	tat	ttt	atg	caa	aca	gag	147	
Ser	Val	Asp	Phe	Ile	Phe	Ala	Asp	Pro	Pro	Tyr	Phe	Met	Gln	Thr	Glu		
			30					35					40				
ggg	gaa	ttg	aag	cgt	ttt	gaa	ggc	aca	aaa	ttt	caa	ggc	gtt	gag	gat	195	
Gly	Glu	Leu	Lys	Arg	Phe	Glu	Gly	Thr	Lys	Phe	Gln	Gly	Val	Glu	Asp		
		45					50					55					
tat	tgg	gat	aaa	ttt	ggc	tct	ttt	aag	gaa	tac	gat	gcc	ttt	tgt	ttg	243	
Tyr	Trp	Asp	Lys	Phe	Gly	Ser	Phe	Lys	Glu	Tyr	Asp	Ala	Phe	Cys	Leu		
	60					65					70						
ggg	tgg	ttg	aaa	gaa	tgc	caa	agg	att	tta	aaa	gat	aat	ggc	agt	att	291	
Gly	Trp	Leu	Lys	Glu	Cys	Gln	Arg	Ile	Leu	Lys	Asp	Asn	Gly	Ser	Ile		
	75				80					85					90		
tgt	gtg	ata	ggg	agt	ttt	caa	aat	att	ttt	aga	att	ggg	ttt	cat	ttg	339	
Cys	Val	Ile	Gly	Ser	Phe	Gln	Asn	Ile	Phe	Arg	Ile	Gly	Phe	His	Leu		
				95				100						105			
caa	aat	tta	ggg	ttt	tgg	ata	ctc	aat	gat	att	att	tgg	cac	aag	agt	387	
Gln	Asn	Leu	Gly	Phe	Trp	Ile	Leu	Asn	Asp	Ile	Ile	Trp	His	Lys	Ser		
			110					115					120				
aat	ccg	gtg	cct	aat	ttt	gct	ggc	aag	aga	tta	tgc	aac	gcc	cat	gag	435	
Asn	Pro	Val	Pro	Asn	Phe	Ala	Gly	Lys	Arg	Leu	Cys	Asn	Ala	His	Glu		
		125					130					135					
acg	ctt	att	tgg	tgt	gct	aaa	cac	aaa	aac	agc	aaa	gtt	gcc	ttt	aat	483	
Thr	Leu	Ile	Trp	Cys	Ala	Lys	His	Lys	Asn	Ser	Lys	Val	Ala	Phe	Asn		
	140					145					150						
tat	aaa	aca	atg	aag	tac	ctc	aat	aac	gac	aaa	caa	gaa	aaa	tcg	gtt	531	
Tyr	Lys	Thr	Met	Lys	Tyr	Leu	Asn	Asn	Asp	Lys	Gln	Glu	Lys	Ser	Val		
	155				160				165					170			
tgg	caa	atc	cct	att	tgc	atg	ggg	aac	gaa	aga	cta	aaa	gat	gcg	caa	579	
Trp	Gln	Ile	Pro	Ile	Cys	Met	Gly	Asn	Glu	Arg	Leu	Lys	Asp	Ala	Gln		
				175				180					185				
ggg	aaa	aaa	gtg	cat	tcc	acg	caa	aaa	cca	gaa	gag	ctt	tta	aaa	aaa	627	
Gly	Lys	Lys	Val	His	Ser	Thr	Gln	Lys	Pro	Glu	Ala	Leu	Leu	Lys	Lys		
			190					195					200				
atc	att	tta	agc	gag	act	aaa	cct	aaa	gat	att	att	tta	gat	ccc	ttt	675	
Ile	Ile	Leu	Ser	Ala	Thr	Lys	Pro	Lys	Asp	Ile	Ile	Leu	Asp	Pro	Phe		
		205					210					215					
ttt	ggc	aca	ggc	aca	aca	ggg	gct	gtg	gct	aaa	tcc	atg	aac	agg	tat	723	
Phe	Gly	Thr	Gly	Thr	Thr	Gly	Ala	Val	Ala	Lys	Ser	Met	Asn	Arg	Tyr		
	220					225					230						
ttt	att	ggg	att	gaa	aaa	gat	tct	ttt	tat	att	aaa	gaa	gag	gca	aaa	771	
Phe	Ile	Gly	Ile	Glu	Lys	Asp	Ser	Phe	Tyr	Ile	Lys	Glu	Ala	Ala	Lys		
	235				240					245					250		

cgc ctg aat aac act agg gat aaa agc gat ttt atc act aat tta gat 819
 Arg Leu Asn Asn Thr Arg Asp Lys Ser Asp Phe Ile Thr Asn Leu Asp
 255 260 265

 tta gaa act aaa ccc cca aaa ata cct atg agt ctt tta att tct aaa 867
 Leu Glu Thr Lys Pro Pro Lys Ile Pro Met Ser Leu Leu Ile Ser Lys
 270 275 280

 caa tta tta aaa atc ggg gat ttt tta tac tca cct aac aaa gaa aaa 915
 Gln Leu Leu Lys Ile Gly Asp Phe Leu Tyr Ser Pro Asn Lys Glu Lys
 285 290 295

 att tgt caa gtt tta gaa aac gga caa gtg agg gat aat gaa aac tat 963
 Ile Cys Gln Val Leu Glu Asn Gly Gln Val Arg Asp Asn Glu Asn Tyr
 300 305 310

 gaa act tct att cat aag atg agc gct aaa tat ttg aat aaa acc aac 1011
 Glu Thr Ser Ile His Lys Met Ser Ala Lys Tyr Leu Asn Lys Thr Asn
 315 320 325 330

 cat aat ggc tgg aaa ttt ttt tat gcg tat tac caa aat caa ttt tta 1059
 His Asn Gly Trp Lys Phe Phe Tyr Ala Tyr Tyr Gln Asn Gln Phe Leu
 335 340 345

 ttg cta gat gaa ttg cgt tat atc tgc caa aag gac tct taatggacta 1108
 Leu Leu Asp Glu Leu Arg Tyr Ile Cys Gln Lys Asp Ser
 350 355

 tcaaaccttt aacgagattt ttaatcgttt tgtctttgga ac 1150

<210> 328

<211> 359

<212> PRT

<213> *Helicobacter pylori*

<400> 328

Met Asp Phe Leu Lys Glu Asn Leu Asn Thr Ile Ile Glu Gly Asp Cys
 1 5 10 15
 Leu Glu Lys Leu Lys Asp Phe Pro Asn Arg Ser Val Asp Phe Ile Phe
 20 25 30
 Ala Asp Pro Pro Tyr Phe Met Gln Thr Glu Gly Glu Leu Lys Arg Phe
 35 40 45
 Glu Gly Thr Lys Phe Gln Gly Val Glu Asp Tyr Trp Asp Lys Phe Gly
 50 55 60
 Ser Phe Lys Glu Tyr Asp Ala Phe Cys Leu Gly Trp Leu Lys Glu Cys
 65 70 75 80
 Gln Arg Ile Leu Lys Asp Asn Gly Ser Ile Cys Val Ile Gly Ser Phe
 85 90 95
 Gln Asn Ile Phe Arg Ile Gly Phe His Leu Gln Asn Leu Gly Phe Trp
 100 105 110
 Ile Leu Asn Asp Ile Ile Trp His Lys Ser Asn Pro Val Pro Asn Phe
 115 120 125
 Ala Gly Lys Arg Leu Cys Asn Ala His Glu Thr Leu Ile Trp Cys Ala
 130 135 140
 Lys His Lys Asn Ser Lys Val Ala Phe Asn Tyr Lys Thr Met Lys Tyr
 145 150 155 160
 Leu Asn Asn Asp Lys Gln Glu Lys Ser Val Trp Gln Ile Pro Ile Cys
 165 170 175
 Met Gly Asn Glu Arg Leu Lys Asp Ala Gln Gly Lys Lys Val His Ser

			180					185				190			
Thr	Gln	Lys	Pro	Glu	Ala	Leu	Leu	Lys	Lys	Ile	Ile	Leu	Ser	Ala	Thr
			195					200				205			
Lys	Pro	Lys	Asp	Ile	Ile	Leu	Asp	Pro	Phe	Phe	Gly	Thr	Gly	Thr	Thr
			210					215				220			
Gly	Ala	Val	Ala	Lys	Ser	Met	Asn	Arg	Tyr	Phe	Ile	Gly	Ile	Glu	Lys
			225												240
Asp	Ser	Phe	Tyr	Ile	Lys	Glu	Ala	Ala	Lys	Arg	Leu	Asn	Asn	Thr	Arg
				245						250					255
Asp	Lys	Ser	Asp	Phe	Ile	Thr	Asn	Leu	Asp	Leu	Glu	Thr	Lys	Pro	Pro
			260						265					270	
Lys	Ile	Pro	Met	Ser	Leu	Leu	Ile	Ser	Lys	Gln	Leu	Leu	Lys	Ile	Gly
			275					280							
Asp	Phe	Leu	Tyr	Ser	Pro	Asn	Lys	Glu	Lys	Ile	Cys	Gln	Val	Leu	Glu
			290				295				300				
Asn	Gly	Gln	Val	Arg	Asp	Asn	Glu	Asn	Tyr	Glu	Thr	Ser	Ile	His	Lys
					310						315				320
Met	Ser	Ala	Lys	Tyr	Leu	Asn	Lys	Thr	Asn	His	Asn	Gly	Trp	Lys	Phe
				325					330					335	
Phe	Tyr	Ala	Tyr	Tyr	Gln	Asn	Gln	Phe	Leu	Leu	Leu	Asp	Glu	Leu	Arg
			340					345					350		
Tyr	Ile	Cys	Gln	Lys	Asp	Ser									
			355												

<210> 329
 <211> 1536
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (34)...(1497)

<400> 329	
tagaaaagat caaacaatta taaaaggata aaa atg gat cat tta aag cat ttg	54
	Met Asp His Leu Lys His Leu
	1 5
cag caa ttg caa aac att gaa agg atc gtg ctt tca ggc att gtg ttg	102
Gln Gln Leu Gln Asn Ile Glu Arg Ile Val Leu Ser Gly Ile Val Leu	
	10 15 20
gcc aat cat aag att gaa gag gtc cat agc gtt tta gag cct agc gat	150
Ala Asn His Lys Ile Glu Glu Val His Ser Val Leu Glu Pro Ser Asp	
	25 30 35
ttt tac tac ccg cct aac ggc tta ttt ttt gaa atc gct tta aaa ctg	198
Phe Tyr Tyr Pro Pro Asn Gly Leu Phe Phe Glu Ile Ala Leu Lys Leu	
	40 45 50 55
cat gaa gaa gat tgc ccc att gat gag aat ttt atc cgc caa aaa atg	246
His Glu Glu Asp Cys Pro Ile Asp Glu Asn Phe Ile Arg Gln Lys Met	
	60 65 70
cct aaa gac aag cag atc aaa gaa gaa gat cta gtc gct att ttt gcg	294
Pro Lys Asp Lys Gln Ile Lys Glu Glu Asp Leu Val Ala Ile Phe Ala	
	75 80 85

gca agc ccc ata gat aat att gaa gcc tat gtg gaa gag att aaa aac	342
Ala Ser Pro Ile Asp Asn Ile Glu Ala Tyr Val Glu Glu Ile Lys Asn	
90 95 100	
gct tcc att aaa cga aaa ctt ttt ggc ttg gct aac acc att aga gag	390
Ala Ser Ile Lys Arg Lys Leu Phe Gly Leu Ala Asn Thr Ile Arg Glu	
105 110 115	
caa gcc cta gaa agc gcg caa aaa tcc agc gat att tta ggc gct gtg	438
Gln Ala Leu Glu Ser Ala Gln Lys Ser Ser Asp Ile Leu Gly Ala Val	
120 125 130 135	
gag cga gaa gtc tat gcg tta ttg aat ggc agc acc ata gaa ggc ttt	486
Glu Arg Glu Val Tyr Ala Leu Leu Asn Gly Ser Thr Ile Glu Gly Phe	
140 145 150	
agg aat att aaa gaa gtg ctt gaa agc gca atg gat ctc att aca gaa	534
Arg Asn Ile Lys Glu Val Leu Glu Ser Ala Met Asp Leu Ile Thr Glu	
155 160 165	
aac caa aga aag ggg agt ttg gaa gtt act ggc ata ccg act ggc ttt	582
Asn Gln Arg Lys Gly Ser Leu Glu Val Thr Gly Ile Pro Thr Gly Phe	
170 175 180	
gtc caa ttg gat aac tat acg agc ggt ttc aat aag ggg agt tta gtc	630
Val Gln Leu Asp Asn Tyr Thr Ser Gly Phe Asn Lys Gly Ser Leu Val	
185 190 195	
att ata ggg gca agg ccg tct atg ggt aaa act agt ttg atg atg aac	678
Ile Ile Gly Ala Arg Pro Ser Met Gly Lys Thr Ser Leu Met Met Asn	
200 205 210 215	
atg gtc tta agc gcg ctc aat gac gat agg ggg gta gcg gtt ttt agt	726
Met Val Leu Ser Ala Leu Asn Asp Asp Arg Gly Val Ala Val Phe Ser	
220 225 230	
tta gaa atg tcc gca gag caa ctc gct tta agg gcg tta tcg gat ctc	774
Leu Glu Met Ser Ala Glu Gln Leu Ala Leu Arg Ala Leu Ser Asp Leu	
235 240 245	
acc tct att aac atg cat gat tta gaa agc ggg agg ctt gat gat gat	822
Thr Ser Ile Asn Met His Asp Leu Glu Ser Gly Arg Leu Asp Asp Asp	
250 255 260	
caa tgg gaa aat tta gcc aaa tgc ttt gat cac ctt tcg caa aaa aaa	870
Gln Trp Glu Asn Leu Ala Lys Cys Phe Asp His Leu Ser Gln Lys Lys	
265 270 275	
ctc ttt ttc tac gat aaa agt tat gtg agg ata gag caa atc cgc ttg	918
Leu Phe Phe Tyr Asp Lys Ser Tyr Val Arg Ile Glu Gln Ile Arg Leu	
280 285 290 295	
caa cta cga aag ctt aaa tcc caa cac aag gaa ttg ggt atc gct ttt	966
Gln Leu Arg Lys Leu Lys Ser Gln His Lys Glu Leu Gly Ile Ala Phe	
300 305 310	
att gac tat ttg cag ctc atg tca ggg agt aaa gcc act aaa gag cgc	1014.
Ile Asp Tyr Leu Gln Leu Met Ser Gly Ser Lys Ala Thr Lys Glu Arg	
315 320 325	

cat gag caa atc gct gaa att tca agg gag ctt aaa act tta gcc aga	1062
His Glu Gln Ile Ala Glu Ile Ser Arg Glu Leu Lys Thr Leu Ala Arg	
330 335 340	
gaa tta gaa atc cct atc ata gcg tta gtg caa ctc aac cgc agc cta	1110
Glu Leu Glu Ile Pro Ile Ile Ala Leu Val Gln Leu Asn Arg Ser Leu	
345 350 355	
gaa aac cga gac gat aaa cgg ccc att ctt tcg gat atc aaa gac agc	1158
Glu Asn Arg Asp Asp Lys Arg Pro Ile Leu Ser Asp Ile Lys Asp Ser	
360 365 370 375	
ggg ggg att gaa caa gac gct gat att gtt tta ttt tta tat aga ggc	1206
Gly Gly Ile Glu Gln Asp Ala Asp Ile Val Leu Phe Leu Tyr Arg Gly	
380 385 390	
tat atc tat caa atg agg gct gaa gac aac aaa ata gac aaa ctc aaa	1254
Tyr Ile Tyr Gln Met Arg Ala Glu Asp Asn Lys Ile Asp Lys Leu Lys	
395 400 405	
aaa gaa ggt aaa att gaa gag gcg caa gag ttg tac tta aaa gtt aat	1302
Lys Glu Gly Lys Ile Glu Glu Ala Gln Glu Leu Tyr Leu Lys Val Asn	
410 415 420	
gaa gaa agg cgt atc cac aag caa aat ggc agc att gaa gag gct gaa	1350
Glu Glu Arg Arg Ile His Lys Gln Asn Gly Ser Ile Glu Glu Ala Glu	
425 430 435	
atc att gtg gct aaa aac agg aat ggg gct aca gga acg gtt tat acg	1398
Ile Ile Val Ala Lys Asn Arg Asn Gly Ala Thr Gly Thr Val Tyr Thr	
440 445 450 455	
cgc ttt aac gct cct ttc acg cgc tat gaa gac atg ccc ata gat tcc	1446
Arg Phe Asn Ala Pro Phe Thr Arg Tyr Glu Asp Met Pro Ile Asp Ser	
460 465 470	
cat tta gaa gaa ggg caa gaa act aaa gtg gat tat gat ata gtt aca	1494
His Leu Glu Glu Gly Gln Glu Thr Lys Val Asp Tyr Asp Ile Val Thr	
475 480 485	
act tgaaagacaa aacttttcag ggggcgtttg aacttctta	1536
Thr	

<210> 330

<211> 488

<212> PRT

<213> Helicobacter pylori

<400> 330

Met Asp His Leu Lys His Leu Gln Gln Leu Gln Asn Ile Glu Arg Ile	
1 5 10 15	
Val Leu Ser Gly Ile Val Leu Ala Asn His Lys Ile Glu Glu Val His	
20 25 30	
Ser Val Leu Glu Pro Ser Asp Phe Tyr Tyr Pro Pro Asn Gly Leu Phe	
35 40 45	
Phe Glu Ile Ala Leu Lys Leu His Glu Glu Asp Cys Pro Ile Asp Glu	

50	Asn	Phe	Ile	Arg	Gln	Lys	Met	Pro	Lys	Asp	Lys	Gln	Ile	Lys	Glu	Glu
65	Asp	Leu	Val	Ala	Ile	Phe	Ala	Ala	Ser	Pro	Ile	Asp	Asn	Ile	Glu	Ala
					85					90					95	
	Tyr	Val	Glu	Glu	Ile	Lys	Asn	Ala	Ser	Ile	Lys	Arg	Lys	Leu	Phe	Gly
				100					105					110		
	Leu	Ala	Asn	Thr	Ile	Arg	Glu	Gln	Ala	Leu	Glu	Ser	Ala	Gln	Lys	Ser
			115					120					125			
	Ser	Asp	Ile	Leu	Gly	Ala	Val	Glu	Arg	Glu	Val	Tyr	Ala	Leu	Leu	Asn
		130				135						140				
	Gly	Ser	Thr	Ile	Glu	Gly	Phe	Arg	Asn	Ile	Lys	Glu	Val	Leu	Glu	Ser
145					150						155					160
	Ala	Met	Asp	Leu	Ile	Thr	Glu	Asn	Gln	Arg	Lys	Gly	Ser	Leu	Glu	Val
				165						170					175	
	Thr	Gly	Ile	Pro	Thr	Gly	Phe	Val	Gln	Leu	Asp	Asn	Tyr	Thr	Ser	Gly
			180						185					190		
	Phe	Asn	Lys	Gly	Ser	Leu	Val	Ile	Ile	Gly	Ala	Arg	Pro	Ser	Met	Gly
		195					200						205			
	Lys	Thr	Ser	Leu	Met	Met	Asn	Met	Val	Leu	Ser	Ala	Leu	Asn	Asp	Asp
		210				215						220				
	Arg	Gly	Val	Ala	Val	Phe	Ser	Leu	Glu	Met	Ser	Ala	Glu	Gln	Leu	Ala
225					230						235					240
	Leu	Arg	Ala	Leu	Ser	Asp	Leu	Thr	Ser	Ile	Asn	Met	His	Asp	Leu	Glu
				245						250					255	
	Ser	Gly	Arg	Leu	Asp	Asp	Asp	Gln	Trp	Glu	Asn	Leu	Ala	Lys	Cys	Phe
			260					265					270			
	Asp	His	Leu	Ser	Gln	Lys	Lys	Leu	Phe	Phe	Tyr	Asp	Lys	Ser	Tyr	Val
		275						280					285			
	Arg	Ile	Glu	Gln	Ile	Arg	Leu	Gln	Leu	Arg	Lys	Leu	Lys	Ser	Gln	His
		290				295						300				
	Lys	Glu	Leu	Gly	Ile	Ala	Phe	Ile	Asp	Tyr	Leu	Gln	Leu	Met	Ser	Gly
305					310						315					320
	Ser	Lys	Ala	Thr	Lys	Glu	Arg	His	Glu	Gln	Ile	Ala	Glu	Ile	Ser	Arg
				325						330					335	
	Glu	Leu	Lys	Thr	Leu	Ala	Arg	Glu	Leu	Glu	Ile	Pro	Ile	Ile	Ala	Leu
			340						345					350		
	Val	Gln	Leu	Asn	Arg	Ser	Leu	Glu	Asn	Arg	Asp	Asp	Lys	Arg	Pro	Ile
		355					360					365				
	Leu	Ser	Asp	Ile	Lys	Asp	Ser	Gly	Gly	Ile	Glu	Gln	Asp	Ala	Asp	Ile
		370				375						380				
	Val	Leu	Phe	Leu	Tyr	Arg	Gly	Tyr	Ile	Tyr	Gln	Met	Arg	Ala	Glu	Asp
385					390					395						400
	Asn	Lys	Ile	Asp	Lys	Leu	Lys	Lys	Glu	Gly	Lys	Ile	Glu	Glu	Ala	Gln
				405						410					415	
	Glu	Leu	Tyr	Leu	Lys	Val	Asn	Glu	Glu	Arg	Arg	Ile	His	Lys	Gln	Asn
			420						425					430		
	Gly	Ser	Ile	Glu	Glu	Ala	Glu	Ile	Ile	Val	Ala	Lys	Asn	Arg	Asn	Gly
		435					440						445			
	Ala	Thr	Gly	Thr	Val	Tyr	Thr	Arg	Phe	Asn	Ala	Pro	Phe	Thr	Arg	Tyr
		450				455						460				
	Glu	Asp	Met	Pro	Ile	Asp	Ser	His	Leu	Glu	Glu	Gly	Gln	Glu	Thr	Lys
465					470						475					480
	Val	Asp	Tyr	Asp	Ile	Val	Thr	Thr								
					485											

<210> 331
 <211> 1246

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (98)...(1207)

<400> 331

```
gaaacgcata aggggggttg ctatcgcttt aacccactat gaaaaaaaaat cccttaaact 60
ctttttaggg atttatttag gctcttcggt tgtgttg atg cta gtg att agc gtt 115
                               Met Leu Val Ile Ser Val
                               1           5
```

```
tta gcg ttt aac tat gaa aaa aac gaa aaa atc aaa atg ata cgc atg 163
Leu Ala Phe Asn Tyr Glu Lys Asn Glu Lys Ile Lys Met Ile Arg Met
                10                15                20
```

```
gac atg gac aaa atg gct tct aag atc gct agc gaa gtg att gcc ttg 211
Asp Met Asp Lys Met Ala Ser Lys Ile Ala Ser Glu Val Ile Ala Leu
                25                30                35
```

```
cac atg caa acg cat ggg gat tat caa aac gct tta aac gct ctc att 259
His Met Gln Thr His Gly Asp Tyr Gln Asn Ala Leu Asn Ala Leu Ile
                40                45                50
```

```
tca cgc tat aaa gac gct tcc ata gcc ctt ttt gat agt aaa aag cgt 307
Ser Arg Tyr Lys Asp Ala Ser Ile Ala Leu Phe Asp Ser Lys Lys Arg
                55                60                65                70
```

```
gtt ttg tat tct aat atc cct gaa agc gcc aat ttg att aaa aac cat 355
Val Leu Tyr Ser Asn Ile Pro Glu Ser Ala Asn Leu Ile Lys Asn His
                75                80                85
```

```
aaa gaa gcg ggc ttt ttt agt ttt agg gga gag tat tac cta ttg agc 403
Lys Glu Ala Gly Phe Phe Ser Phe Arg Gly Glu Tyr Tyr Leu Leu Ser
                90                95                100
```

```
gat gaa act ttc gct cac tta ggc gtg gct aaa atg ctt ttt aaa aat 451
Asp Glu Thr Phe Ala His Leu Gly Val Ala Lys Met Leu Phe Lys Asn
                105                110                115
```

```
tct aaa ccc ctt cat ttt tct tct ttg tat cgt aac att gtt tta gtg 499
Ser Lys Pro Leu His Phe Ser Ser Leu Tyr Arg Asn Ile Val Leu Val
                120                125                130
```

```
ttt gtt gta gcg ttt tta tgc gtg ata ggg gtt tct gtg ttt ttg ggg 547
Phe Val Val Ala Phe Leu Cys Val Ile Gly Val Ser Val Phe Leu Gly
                135                140                145                150
```

```
cgt ttg ttt tta aag ccc att agg aat gaa atc acc cgc att gat cat 595
Arg Leu Phe Leu Lys Pro Ile Arg Asn Glu Ile Thr Arg Ile Asp His
                155                160                165
```

```
ttt tta aaa aac acc acg cat gaa tta aac acc ccc atg agc gct tta 643
Phe Leu Lys Asn Thr Thr His Glu Leu Asn Thr Pro Met Ser Ala Leu
                170                175                180
```

```
gtc ttg tct tta aaa acc tta gaa gac aac caa caa cac cgc cgc att 691
Val Leu Ser Leu Lys Thr Leu Glu Asp Asn Gln Gln His Arg Arg Ile
```

185	190	195	
aaa atc gct atc cag cgc atg agt ttt tta tac cgc tcg ctc tcg tat			739
Lys Ile Ala Ile Gln Arg Met Ser Phe Leu Tyr Arg Ser Leu Ser Tyr			
200	205	210	
tta gtg atg caa gat att gag cgc gaa tct ttt gtg ctt tta gat tta			787
Leu Val Met Gln Asp Ile Glu Arg Glu Ser Phe Val Leu Leu Asp Leu			
215	220	225	230
aaa gcc ctg att att aaa gaa aac acg ctt ttt agc gag atg ata gac			835
Lys Ala Leu Ile Ile Lys Glu Asn Thr Leu Phe Ser Glu Met Ile Asp			
	235	240	245
tac cac aag ctg gaa ttt aaa agc gat tta gtg gaa gtg gaa ctt aaa			883
Tyr His Lys Leu Glu Phe Lys Ser Asp Leu Val Glu Val Glu Leu Lys			
	250	255	260
gct aaa gag cag gat ttc att tcg ctt tat agc aat ttg ctc atg aac			931
Ala Lys Glu Gln Asp Phe Ile Ser Leu Tyr Ser Asn Leu Leu Met Asn			
	265	270	275
gcg atc aaa tac agc gtc atg aat ggg tat atc cac ata gag cta acg			979
Ala Ile Lys Tyr Ser Val Met Asn Gly Tyr Ile His Ile Glu Leu Thr			
	280	285	290
cat gcg ttt ttg aaa gtg aaa aat tta ggg tat gaa atc cct aaa gac			1027
His Ala Phe Leu Lys Val Lys Asn Leu Gly Tyr Glu Ile Pro Lys Asp			
295	300	305	310
aag atc aca gaa tta agc gtt cgt tat gtg cgt ttc aat tct ggc gtg			1075
Lys Ile Thr Glu Leu Ser Val Arg Tyr Val Arg Phe Asn Ser Gly Val			
	315	320	325
ttg ggt tat ggt ata ggg tta ggt ttg gtg aaa aaa gtg tgc gaa aag			1123
Leu Gly Tyr Gly Ile Gly Leu Gly Leu Val Lys Lys Val Cys Glu Lys			
	330	335	340
tat aaa atg cgt tta gaa att cat agc gaa ccc tct tta aag gga tcg			1171
Tyr Lys Met Arg Leu Glu Ile His Ser Glu Pro Ser Leu Lys Gly Ser			
	345	350	355
ttt tat gaa aat tcg ttt tgc gtt caa ttt caa gga taaagatgct			1217
Phe Tyr Glu Asn Ser Phe Cys Val Gln Phe Gln Gly			
	360	365	370
ttcagtgtat gaaaaagtga atgctctag			1246
<210> 332			
<211> 370			
<212> PRT			
<213> Helicobacter pylori			
<400> 332			
Met Leu Val Ile Ser Val Leu Ala Phe Asn Tyr Glu Lys Asn Glu Lys			
1	5	10	15
Ile Lys Met Ile Arg Met Asp Met Asp Lys Met Ala Ser Lys Ile Ala			
	20	25	30
Ser Glu Val Ile Ala Leu His Met Gln Thr His Gly Asp Tyr Gln Asn			

		35				40				45					
Ala	Leu	Asn	Ala	Leu	Ile	Ser	Arg	Tyr	Lys	Asp	Ala	Ser	Ile	Ala	Leu
50						55				60					
Phe	Asp	Ser	Lys	Lys	Arg	Val	Leu	Tyr	Ser	Asn	Ile	Pro	Glu	Ser	Ala
65					70					75					80
Asn	Leu	Ile	Lys	Asn	His	Lys	Glu	Ala	Gly	Phe	Phe	Ser	Phe	Arg	Gly
			85						90					95	
Glu	Tyr	Tyr	Leu	Leu	Ser	Asp	Glu	Thr	Phe	Ala	His	Leu	Gly	Val	Ala
			100					105					110		
Lys	Met	Leu	Phe	Lys	Asn	Ser	Lys	Pro	Leu	His	Phe	Ser	Ser	Leu	Tyr
		115					120					125			
Arg	Asn	Ile	Val	Leu	Val	Phe	Val	Val	Ala	Phe	Leu	Cys	Val	Ile	Gly
130						135					140				
Val	Ser	Val	Phe	Leu	Gly	Arg	Leu	Phe	Leu	Lys	Pro	Ile	Arg	Asn	Glu
145					150					155					160
Ile	Thr	Arg	Ile	Asp	His	Phe	Leu	Lys	Asn	Thr	Thr	His	Glu	Leu	Asn
			165						170					175	
Thr	Pro	Met	Ser	Ala	Leu	Val	Leu	Ser	Leu	Lys	Thr	Leu	Glu	Asp	Asn
		180						185					190		
Gln	Gln	His	Arg	Arg	Ile	Lys	Ile	Ala	Ile	Gln	Arg	Met	Ser	Phe	Leu
		195				200						205			
Tyr	Arg	Ser	Leu	Ser	Tyr	Leu	Val	Met	Gln	Asp	Ile	Glu	Arg	Glu	Ser
210						215					220				
Phe	Val	Leu	Leu	Asp	Leu	Lys	Ala	Leu	Ile	Ile	Lys	Glu	Asn	Thr	Leu
225					230					235					240
Phe	Ser	Glu	Met	Ile	Asp	Tyr	His	Lys	Leu	Glu	Phe	Lys	Ser	Asp	Leu
			245						250					255	
Val	Glu	Val	Glu	Leu	Lys	Ala	Lys	Glu	Gln	Asp	Phe	Ile	Ser	Leu	Tyr
			260					265					270		
Ser	Asn	Leu	Leu	Met	Asn	Ala	Ile	Lys	Tyr	Ser	Val	Met	Asn	Gly	Tyr
		275					280					285			
Ile	His	Ile	Glu	Leu	Thr	His	Ala	Phe	Leu	Lys	Val	Lys	Asn	Leu	Gly
290						295					300				
Tyr	Glu	Ile	Pro	Lys	Asp	Lys	Ile	Thr	Glu	Leu	Ser	Val	Arg	Tyr	Val
305					310					315					320
Arg	Phe	Asn	Ser	Gly	Val	Leu	Gly	Tyr	Gly	Ile	Gly	Leu	Gly	Leu	Val
				325					330					335	
Lys	Lys	Val	Cys	Glu	Lys	Tyr	Lys	Met	Arg	Leu	Glu	Ile	His	Ser	Glu
			340					345					350		
Pro	Ser	Leu	Lys	Gly	Ser	Phe	Tyr	Glu	Asn	Ser	Phe	Cys	Val	Gln	Phe
		355					360					365			
Gln	Gly														
	370														

<210> 333
 <211> 703
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (60)...(665)

<400> 333
 gggatagttt taaaaatgat gaagagtttt taacattttc ttacgcttgg attgataaa 59
 atg ctg ccc aaa ctt aaa gac aca ggg agt ttt tat atc ttt aat acc 107
 Met Leu Pro Lys Leu Lys Asp Thr Gly Ser Phe Tyr Ile Phe Asn Thr
 1 5 10 15

cct ttt aat tgc gct tta ttt tta gcg tat ttg cac cat aaa aaa gtg	155
Pro Phe Asn Cys Ala Leu Phe Leu Ala Tyr Leu His His Lys Lys Val	
20 25 30	
cat ttt tta aat ttt atc act tgg gtt aaa aaa gat ggg ttt gcc aac	203
His Phe Leu Asn Phe Ile Thr Trp Val Lys Lys Asp Gly Phe Ala Asn	
35 40 45	
gcc aaa aag cgt tat aac cac gcg caa gaa agc att tta ttt tat agc	251
Ala Lys Lys Arg Tyr Asn His Ala Gln Glu Ser Ile Leu Phe Tyr Ser	
50 55 60	
atg cac aag aaa aac tac acc ttt aat gcc gat gag att cgc atc gct	299
Met His Lys Lys Asn Tyr Thr Phe Asn Ala Asp Glu Ile Arg Ile Ala	
65 70 75 80	
tat gaa tcc gct gaa cgc atc aaa cat gct caa agt aag ggg att tta	347
Tyr Glu Ser Ala Glu Arg Ile Lys His Ala Gln Ser Lys Gly Ile Leu	
85 90 95	
aaa aat aac aaa cgc tgg ttc cct aac cct aag ggc aaa tta tgc ctt	395
Lys Asn Asn Lys Arg Trp Phe Pro Asn Pro Lys Gly Lys Leu Cys Leu	
100 105 110	
gat gtg tgg gaa atc act tca caa agg cat gtt gaa aaa gag aag ggt	443
Asp Val Trp Glu Ile Thr Ser Gln Arg His Val Glu Lys Glu Lys Gly	
115 120 125	
aaa atc ctt aag ccc aaa cac ccc agc atc aaa cct aaa gcg ctc att	491
Lys Ile Leu Lys Pro Lys His Pro Ser Ile Lys Pro Lys Ala Leu Ile	
130 135 140	
gaa cgc atg ata aaa gct agc tct cac aaa aac gat ttg att tta gat	539
Glu Arg Met Ile Lys Ala Ser Ser His Lys Asn Asp Leu Ile Leu Asp	
145 150 155 160	
ttg ttt agc ggc agt ggc atg act agc tta gtg gct aaa agt ttg gag	587
Leu Phe Ser Gly Ser Gly Met Thr Ser Leu Val Ala Lys Ser Leu Glu	
165 170 175	
cgt aat ttt ata ggg tgt gag agc cat gct gaa tac gtg cat ggg agt	635
Arg Asn Phe Ile Gly Cys Glu Ser His Ala Glu Tyr Val His Gly Ser	
180 185 190	
ttg gaa atg ttt agg tat aat gaa tgc gaa taataaaagga tatttgacat	685
Leu Glu Met Phe Arg Tyr Asn Glu Cys Glu	
195 200	
gccaaaatta gaaaaaat	703
<210> 334	
<211> 202	
<212> PRT	
<213> Helicobacter pylori	
<400> 334	
Met Leu Pro Lys Leu Lys Asp Thr Gly Ser Phe Tyr Ile Phe Asn Thr	
1 5 10 15	

Pro	Phe	Asn	Cys	Ala	Leu	Phe	Leu	Ala	Tyr	Leu	His	His	Lys	Lys	Val
			20					25					30		
His	Phe	Leu	Asn	Phe	Ile	Thr	Trp	Val	Lys	Lys	Asp	Gly	Phe	Ala	Asn
		35					40					45			
Ala	Lys	Lys	Arg	Tyr	Asn	His	Ala	Gln	Glu	Ser	Ile	Leu	Phe	Tyr	Ser
		50				55					60				
Met	His	Lys	Lys	Asn	Tyr	Thr	Phe	Asn	Ala	Asp	Glu	Ile	Arg	Ile	Ala
					70					75					80
Tyr	Glu	Ser	Ala	Glu	Arg	Ile	Lys	His	Ala	Gln	Ser	Lys	Gly	Ile	Leu
				85					90					95	
Lys	Asn	Asn	Lys	Arg	Trp	Phe	Pro	Asn	Pro	Lys	Gly	Lys	Leu	Cys	Leu
			100					105					110		
Asp	Val	Trp	Glu	Ile	Thr	Ser	Gln	Arg	His	Val	Glu	Lys	Glu	Lys	Gly
		115					120					125			
Lys	Ile	Leu	Lys	Pro	Lys	His	Pro	Ser	Ile	Lys	Pro	Lys	Ala	Leu	Ile
		130				135					140				
Glu	Arg	Met	Ile	Lys	Ala	Ser	Ser	His	Lys	Asn	Asp	Leu	Ile	Leu	Asp
					150					155					160
Leu	Phe	Ser	Gly	Ser	Gly	Met	Thr	Ser	Leu	Val	Ala	Lys	Ser	Leu	Glu
				165					170					175	
Arg	Asn	Phe	Ile	Gly	Cys	Glu	Ser	His	Ala	Glu	Tyr	Val	His	Gly	Ser
			180					185					190		
Leu	Glu	Met	Phe	Arg	Tyr	Asn	Glu	Cys	Glu						
		195					200								

<210> 335
 <211> 1448
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (67)...(1404)

<400> 335
 agagtttctag gggcgtggcg tataagtcaa gcgaatatc tagcgaagaa aaacaagagg 60
 aataac atg aac gaa acg ctt tat tgc agt ttt tgc aaa aaa cca gaa 108
 Met Asn Glu Thr Leu Tyr Cys Ser Phe Cys Lys Lys Pro Glu
 1 5 10

tca aga gat ccc aaa aaa cgc cgc att att ttt gcg agc aat ctc aat 156
 Ser Arg Asp Pro Lys Lys Arg Arg Ile Ile Phe Ala Ser Asn Leu Asn
 15 20 25 30

aaa gat gtg tgc gtg tgc gaa tat tgt ata gat gtg atg cat ggg gaa 204
 Lys Asp Val Cys Val Cys Glu Tyr Cys Ile Asp Val Met His Gly Glu
 35 40 45

ttg cac aaa tac gac aat tct tta ttg gcg ctc aaa aga gac cga ttg 252
 Leu His Lys Tyr Asp Asn Ser Leu Leu Ala Leu Lys Arg Asp Arg Leu
 50 55 60

aga aga atg gaa tct agc gct tat gaa gaa gag ttt tta ctc tct tac 300
 Arg Arg Met Glu Ser Ser Ala Tyr Glu Glu Glu Phe Leu Leu Ser Tyr
 65 70 75

att cca gcc cct aaa gag ctt aag gcg gtt tta gac aat tat gtg ata 348
 Ile Pro Ala Pro Lys Glu Leu Lys Ala Val Leu Asp Asn Tyr Val Ile

80	85	90	
ggg caa gag cag gct Gly Gln Glu Gln Ala 95	aaa aag gtt ttt Lys Lys Val Phe 100	tcc gta gcc gtg tat aac cat Ser Val Ala Val Tyr Asn His 105	396
tac aaa cgc tta tct Tyr Lys Arg Leu Ser 115	ttt aaa gaa aaa ctc Phe Lys Glu Lys Leu 120	aaa aaa caa gac aac caa Lys Lys Gln Asp Asn Gln 125	444
gac agc aat gtg gag Asp Ser Asn Val Glu 130	tta gag cat tta gaa Leu Glu His Leu Glu 135	gaa gaa gtg gag ttg agc aag Glu Glu Val Glu Leu Ser Lys 140	492
tct aat att tta cta atc Ser Asn Ile Leu Leu Ile 145	ggc cct aca gga tca Gly Pro Thr Gly Ser 150	ggc aaa act tta atg Gly Lys Thr Leu Met 155	540
gcg caa act ctg gcc aag Ala Gln Thr Leu Ala Lys 160	cat ttg gat att cct His Leu Asp Ile Pro 165	atc gcc att agc gat Ile Ala Ile Ser Asp 170	588
gcg act agc ttg act Ala Thr Ser Leu Thr 175	gaa gcg ggc tat gtg Glu Ala Gly Tyr Val 180	ggc gaa gac gtg gaa aat Gly Glu Asp Val Glu Asn 185	636
att ctc aca aga ttg ttg Ile Leu Thr Arg Leu 195	caa gcg agc gac tgg Gln Ala Ser Asp Trp 200	aat gtc caa aaa gcc Asn Val Gln Lys Ala 205	684
caa aaa ggc att gtg ttt Gln Lys Gly Ile Val 210	att gat gag att gat Ile Asp Glu Ile Asp 215	aaa atc agc cgt ttg Lys Ile Ser Arg Leu 220	732
tca gaa aac cgc tct atc Ser Glu Asn Arg Ser 225	act aga gat gtt tct Thr Arg Asp Val Ser 230	ggc gag ggc gtt cag Gly Glu Gly Val Gln 235	780
caa gcg ttg ttg aaa atc Gln Ala Leu Leu Lys 240	gtt gaa ggt tct tta Val Glu Gly Ser Leu 245	gtg aat atc ccc ccc Val Asn Ile Pro Pro 250	828
aaa ggc ggc aga aag cac Lys Gly Gly Arg Lys 255	cct gag ggc aat ttc Pro Glu Gly Asn Phe 260	att att caa att gac acg Ile Ile Gln Ile Asp Thr 265	876
agc gat att tta ttc att Ser Asp Ile Leu Phe 275	tgt gct gga gcg ttt Cys Ala Gly Ala Phe 280	gat ggg tta gct gaa Asp Gly Leu Ala Glu 285	924
atc att aaa aaa cgc acc Ile Ile Lys Lys Arg 290	acg cag aat gtg ttg Thr Gln Asn Val Leu 295	ggc ttc act caa gaa Gly Phe Thr Gln Glu 300	972
aag atg agc aaa aaa gag Lys Met Ser Lys Lys 305	caa gaa gcg atc ttg Gln Glu Ala Ile Leu 310	cat tta gtc caa acc His Leu Val Gln Thr 315	1020
cat gac ctg gtt act tat cat gac ctg gtt act 1068	ggg ctt atc cct gag ctt atc cct gag ctt 1068	att ggc cgt ttg att ggc cgt ttg 1068	1068

His	Asp	Leu	Val	Thr	Tyr	Gly	Leu	Ile	Pro	Glu	Leu	Ile	Gly	Arg	Leu		
320						325					330						
ccg	gtt	tta	agc	acg	cta	gat	agc	atc	agt	tta	gaa	gcg	atg	gtg	gat	1116	
Pro	Val	Leu	Ser	Thr	Leu	Asp	Ser	Ile	Ser	Leu	Glu	Ala	Met	Val	Asp		
335					340					345					350		
att	tta	caa	aaa	cct	aaa	aac	gct	ctt	atc	aag	caa	tac	cag	cag	ctt	1164	
Ile	Leu	Gln	Lys	Pro	Lys	Asn	Ala	Leu	Ile	Lys	Gln	Tyr	Gln	Gln	Leu		
				355					360					365			
ttc	aaa	atg	gat	gag	gtg	gat	ttg	atc	ttt	gaa	gaa	gaa	gcc	att	aaa	1212	
Phe	Lys	Met	Asp	Glu	Val	Asp	Leu	Ile	Phe	Glu	Glu	Glu	Ala	Ile	Lys		
			370					375					380				
gaa	atc	gct	caa	ctc	gca	tta	gaa	aga	aaa	acc	ggg	gct	agg	ggc	tta	1260	
Glu	Ile	Ala	Gln	Leu	Ala	Leu	Glu	Arg	Lys	Thr	Gly	Ala	Arg	Gly	Leu		
		385					390					395					
agg	gcg	atc	att	gaa	gat	ttt	tgt	ttg	gat	att	atg	ttt	gat	tta	ccc	1308	
Arg	Ala	Ile	Ile	Glu	Asp	Phe	Cys	Leu	Asp	Ile	Met	Phe	Asp	Leu	Pro		
	400					405					410						
aag	ctt	aaa	gga	tcg	gaa	gtg	cgt	atc	act	aaa	gat	tgt	gtt	tta	aaa	1356	
Lys	Leu	Lys	Gly	Ser	Glu	Val	Arg	Ile	Thr	Lys	Asp	Cys	Val	Leu	Lys		
415					420					425					430		
cag	gct	gaa	cct	ttg	atc	att	gct	aaa	acg	cat	tct	aaa	att	ctt	cct	1404	
Gln	Ala	Glu	Pro	Leu	Ile	Ile	Ala	Lys	Thr	His	Ser	Lys	Ile	Leu	Pro		
			435					440						445			
taaggaacac	gcttataaat	ttaacgataa	aggattagaa	aggg												1448	

<210> 336

<211> 446

<212> PRT

<213> Helicobacter pylori

<400> 336

Met	Asn	Glu	Thr	Leu	Tyr	Cys	Ser	Phe	Cys	Lys	Lys	Pro	Glu	Ser	Arg		
1				5					10					15			
Asp	Pro	Lys	Lys	Arg	Arg	Ile	Ile	Phe	Ala	Ser	Asn	Leu	Asn	Lys	Asp		
			20					25					30				
Val	Cys	Val	Cys	Glu	Tyr	Cys	Ile	Asp	Val	Met	His	Gly	Glu	Leu	His		
	35					40					45						
Lys	Tyr	Asp	Asn	Ser	Leu	Leu	Ala	Leu	Lys	Arg	Asp	Arg	Leu	Arg	Arg		
	50				55					60							
Met	Glu	Ser	Ser	Ala	Tyr	Glu	Glu	Glu	Phe	Leu	Leu	Ser	Tyr	Ile	Pro		
65				70					75					80			
Ala	Pro	Lys	Glu	Leu	Lys	Ala	Val	Leu	Asp	Asn	Tyr	Val	Ile	Gly	Gln		
			85					90						95			
Glu	Gln	Ala	Lys	Lys	Val	Phe	Ser	Val	Ala	Val	Tyr	Asn	His	Tyr	Lys		
		100					105						110				
Arg	Leu	Ser	Phe	Lys	Glu	Lys	Leu	Lys	Lys	Gln	Asp	Asn	Gln	Asp	Ser		
		115				120					125						
Asn	Val	Glu	Leu	Glu	His	Leu	Glu	Glu	Val	Glu	Leu	Ser	Lys	Ser	Asn		
	130				135					140							
Ile	Leu	Leu	Ile	Gly	Pro	Thr	Gly	Ser	Gly	Lys	Thr	Leu	Met	Ala	Gln		
145					150					155					160		

Thr	Leu	Ala	Lys	His	Leu	Asp	Ile	Pro	Ile	Ala	Ile	Ser	Asp	Ala	Thr
				165					170					175	
Ser	Leu	Thr	Glu	Ala	Gly	Tyr	Val	Gly	Glu	Asp	Val	Glu	Asn	Ile	Leu
			180					185					190		
Thr	Arg	Leu	Leu	Gln	Ala	Ser	Asp	Trp	Asn	Val	Gln	Lys	Ala	Gln	Lys
		195					200					205			
Gly	Ile	Val	Phe	Ile	Asp	Glu	Ile	Asp	Lys	Ile	Ser	Arg	Leu	Ser	Glu
	210					215					220				
Asn	Arg	Ser	Ile	Thr	Arg	Asp	Val	Ser	Gly	Glu	Gly	Val	Gln	Gln	Ala
225					230					235					240
Leu	Leu	Lys	Ile	Val	Glu	Gly	Ser	Leu	Val	Asn	Ile	Pro	Pro	Lys	Gly
				245					250					255	
Gly	Arg	Lys	His	Pro	Glu	Gly	Asn	Phe	Ile	Gln	Ile	Asp	Thr	Ser	Asp
			260					265					270		
Ile	Leu	Phe	Ile	Cys	Ala	Gly	Ala	Phe	Asp	Gly	Leu	Ala	Glu	Ile	Ile
		275					280					285			
Lys	Lys	Arg	Thr	Thr	Gln	Asn	Val	Leu	Gly	Phe	Thr	Gln	Glu	Lys	Met
	290					295					300				
Ser	Lys	Lys	Glu	Gln	Glu	Ala	Ile	Leu	His	Leu	Val	Gln	Thr	His	Asp
305					310					315					320
Leu	Val	Thr	Tyr	Gly	Leu	Ile	Pro	Glu	Leu	Ile	Gly	Arg	Leu	Pro	Val
				325					330					335	
Leu	Ser	Thr	Leu	Asp	Ser	Ile	Ser	Leu	Glu	Ala	Met	Val	Asp	Ile	Leu
			340					345					350		
Gln	Lys	Pro	Lys	Asn	Ala	Leu	Ile	Lys	Gln	Tyr	Gln	Gln	Leu	Phe	Lys
		355					360					365			
Met	Asp	Glu	Val	Asp	Leu	Ile	Phe	Glu	Glu	Glu	Ala	Ile	Lys	Glu	Ile
	370					375					380				
Ala	Gln	Leu	Ala	Leu	Glu	Arg	Lys	Thr	Gly	Ala	Arg	Gly	Leu	Arg	Ala
385					390					395					400
Ile	Ile	Glu	Asp	Phe	Cys	Leu	Asp	Ile	Met	Phe	Asp	Leu	Pro	Lys	Leu
				405					410					415	
Lys	Gly	Ser	Glu	Val	Arg	Ile	Thr	Lys	Asp	Cys	Val	Leu	Lys	Gln	Ala
			420					425					430		
Glu	Pro	Leu	Ile	Ile	Ala	Lys	Thr	His	Ser	Lys	Ile	Leu	Pro		
		435					440					445			

<210> 337

<211> 911

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (34)...(858)

<400> 337

agtgttagaa	aaaactttgc	tttgaaattt	ggc	atg	aaa	gca	ggc	att	att	ggg	54
				Met	Lys	Ala	Gly	Ile	Ile	Gly	
				1				5			

tta	ggg	ctt	atg	ggg	ggg	agt	tta	ggg	cta	gcc	ttg	caa	gaa	tgg	ggg	102
Leu	Gly	Leu	Met	Gly	Gly	Ser	Leu	Gly	Leu	Ala	Leu	Gln	Glu	Trp	Gly	
		10					15					20				

cgt	ttt	aaa	agc	gtt	ata	ggc	tat	gat	cat	aac	gct	ttg	cat	gct	aaa	150
Arg	Phe	Lys	Ser	Val	Ile	Gly	Tyr	Asp	His	Asn	Ala	Leu	His	Ala	Lys	
	25					30					35					

ttg gct ttg act ttg ggg ctt gta gat gaa tgc gtg gga ttt gaa aag	198
Leu Ala Leu Thr Leu Gly Leu Val Asp Glu Cys Val Gly Phe Glu Lys	
40 45 50 55	
att tta gaa tgc gat gtg att ttt ttg gcc att ccg gtt gag ggc atc	246
Ile Leu Glu Cys Asp Val Ile Phe Leu Ala Ile Pro Val Glu Gly Ile	
60 65 70	
att gga tgt ctg aaa aaa atg acc tct atc aaa aaa agc gcg acc att	294
Ile Gly Cys Leu Lys Lys Met Thr Ser Ile Lys Lys Ser Ala Thr Ile	
75 80 85	
att gat tta ggg ggc gct aaa gcg caa atc att cgc aat atc cct aaa	342
Ile Asp Leu Gly Gly Ala Lys Ala Gln Ile Ile Arg Asn Ile Pro Lys	
90 95 100	
agc att cgt aag aat ttc atc gct gcg cac ccc atg tgc ggg aca gag	390
Ser Ile Arg Lys Asn Phe Ile Ala Ala His Pro Met Cys Gly Thr Glu	
105 110 115	
ttt tat ggc cct aaa gcg agc gtt aag ggg ctg tat gaa aac gct cta	438
Phe Tyr Gly Pro Lys Ala Ser Val Lys Gly Leu Tyr Glu Asn Ala Leu	
120 125 130 135	
gtg ata ttg tgc gat tta gaa gat tca ggg act gag caa gta gag atc	486
Val Ile Leu Cys Asp Leu Glu Asp Ser Gly Thr Glu Gln Val Glu Ile	
140 145 150	
gct aaa gaa atc ttt tta ggc gtt aaa gcg cgc ttg att aaa atg aaa	534
Ala Lys Glu Ile Phe Leu Gly Val Lys Ala Arg Leu Ile Lys Met Lys	
155 160 165	
tcc aat gag cat gac acc cat gtg gct tat atc agc cat tta ccc cat	582
Ser Asn Glu His Asp Thr His Val Ala Tyr Ile Ser His Leu Pro His	
170 175 180	
gtt ttg agc tat gcg tta gcc aat agc gtt tta aag caa aac gac cca	630
Val Leu Ser Tyr Ala Leu Ala Asn Ser Val Leu Lys Gln Asn Asp Pro	
185 190 195	
gag atg att tta tct tta gcg ggt ggg ggt ttt agg gat atg agc cgt	678
Glu Met Ile Leu Ser Leu Ala Gly Gly Gly Phe Arg Asp Met Ser Arg	
200 205 210 215	
ctg tcc aaa agc tcg cct tta atg tgg aaa gat att ttc aaa caa aac	726
Leu Ser Lys Ser Ser Pro Leu Met Trp Lys Asp Ile Phe Lys Gln Asn	
220 225 230	
cga gac aat gtc tta gaa gcg att aaa aaa tgc gaa aaa gaa atc gtg	774
Arg Asp Asn Val Leu Glu Ala Ile Lys Lys Cys Glu Lys Glu Ile Val	
235 240 245	
caa gct aag gcg tgg ata gaa aat aac gat tat gaa agc ctt gca gaa	822
Gln Ala Lys Ala Trp Ile Glu Asn Asn Asp Tyr Glu Ser Leu Ala Glu	
250 255 260	
tgg atg gcg caa gcg aac aaa ctc cag gag ttc atg taaagtaaaa	868
Trp Met Ala Gln Ala Asn Lys Leu Gln Glu Phe Met	

265

270

275

tgatgtaaaa taatttaaaa ttttttatat tgttggtttt agg

911

<210> 338

<211> 275

<212> PRT

<213> *Helicobacter pylori*

<400> 338

```

Met Lys Ala Gly Ile Ile Gly Leu Gly Leu Met Gly Gly Ser Leu Gly
 1          5          10          15
Leu Ala Leu Gln Glu Trp Gly Arg Phe Lys Ser Val Ile Gly Tyr Asp
          20          25          30
His Asn Ala Leu His Ala Lys Leu Ala Leu Thr Leu Gly Leu Val Asp
          35          40          45
Glu Cys Val Gly Phe Glu Lys Ile Leu Glu Cys Asp Val Ile Phe Leu
          50          55          60
Ala Ile Pro Val Glu Gly Ile Ile Gly Cys Leu Lys Lys Met Thr Ser
65          70          75          80
Ile Lys Lys Ser Ala Thr Ile Ile Asp Leu Gly Gly Ala Lys Ala Gln
          85          90          95
Ile Ile Arg Asn Ile Pro Lys Ser Ile Arg Lys Asn Phe Ile Ala Ala
          100          105          110
His Pro Met Cys Gly Thr Glu Phe Tyr Gly Pro Lys Ala Ser Val Lys
          115          120          125
Gly Leu Tyr Glu Asn Ala Leu Val Ile Leu Cys Asp Leu Glu Asp Ser
          130          135          140
Gly Thr Glu Gln Val Glu Ile Ala Lys Glu Ile Phe Leu Gly Val Lys
145          150          155          160
Ala Arg Leu Ile Lys Met Lys Ser Asn Glu His Asp Thr His Val Ala
          165          170          175
Tyr Ile Ser His Leu Pro His Val Leu Ser Tyr Ala Leu Ala Asn Ser
          180          185          190
Val Leu Lys Gln Asn Asp Pro Glu Met Ile Leu Ser Leu Ala Gly Gly
          195          200          205
Gly Phe Arg Asp Met Ser Arg Leu Ser Lys Ser Ser Pro Leu Met Trp
210          215          220
Lys Asp Ile Phe Lys Gln Asn Arg Asp Asn Val Leu Glu Ala Ile Lys
225          230          235          240
Lys Cys Glu Lys Glu Ile Val Gln Ala Lys Ala Trp Ile Glu Asn Asn
          245          250          255
Asp Tyr Glu Ser Leu Ala Glu Trp Met Ala Gln Ala Asn Lys Leu Gln
          260          265          270
Glu Phe Met
          275

```

<210> 339

<211> 304

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (73)...(267)

<400> 339

aataatttaa aattttttat attgttggtt ttaggggtgc gaggagcgaa atgggggtatt 60

```

tggattgttt tt atg gat tat agg ctg ttt cat atg gat agc atg gat tta 111
      Met Asp Tyr Arg Leu Phe His Met Asp Ser Met Asp Leu
        1             5             10

ccc agc aac cag caa aca acc ata aga gat tat ctt aaa ccc gga tct 159
Pro Ser Asn Gln Gln Thr Thr Ile Arg Asp Tyr Leu Lys Pro Gly Ser
      15             20             25

att gtt gtg ttt gcc ata att gta ata ata att tca tct cat ttc tcc 207
Ile Val Val Phe Ala Ile Ile Val Ile Ile Ile Ser Ser His Phe Ser
      30             35             40             45

aac gcc tat aaa acc ctt atc gct tct aat aaa aaa cca gtt tta agc 255
Asn Ala Tyr Lys Thr Leu Ile Ala Ser Asn Lys Lys Pro Val Leu Ser
              50             55             60

cat tta gaa att tgatttctta aaccttttta tcaaaaatac cggtgtt 304
His Leu Glu Ile
              65

```

<210> 340
 <211> 65
 <212> PRT
 <213> Helicobacter pylori

```

<400> 340
Met Asp Tyr Arg Leu Phe His Met Asp Ser Met Asp Leu Pro Ser Asn
  1             5             10             15
Gln Gln Thr Thr Ile Arg Asp Tyr Leu Lys Pro Gly Ser Ile Val Val
      20             25             30
Phe Ala Ile Ile Val Ile Ile Ile Ser Ser His Phe Ser Asn Ala Tyr
      35             40             45
Lys Thr Leu Ile Ala Ser Asn Lys Lys Pro Val Leu Ser His Leu Glu
  50             55             60
Ile
65

```

<210> 341
 <211> 271
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (34)...(237)

```

<400> 341
agctcacatt ttagaaaaat atttaaaggg aga atg atg caa aat agc gtt aaa 54
      Met Met Gln Asn Ser Val Lys
        1             5

aaa tta gaa tat gaa gag cgt ttc aat gac gct ctt ttg aaa tta caa 102
Lys Leu Glu Tyr Glu Glu Arg Phe Asn Asp Ala Leu Leu Lys Leu Gln
      10             15             20

gca tgc caa gaa gaa aag cag gta acg agt tgt ttg aaa tgc gag cag 150
Ala Cys Gln Glu Glu Lys Gln Val Thr Ser Cys Leu Lys Cys Glu Gln

```

25	30	35	
gtt ttg aat tgc aag atc cgc aac agc tat gtg gat gcg gct tat gag			198
Val Leu Asn Cys Lys Ile Arg Asn Ser Tyr Val Asp Ala Ala Tyr Glu			
40	45	50	55
agc atg agt tta ggc gaa cgg ggc ggg ttt gat ttc aat taaatgggat			247
Ser Met Ser Leu Gly Glu Arg Gly Gly Phe Asp Phe Asn			
	60	65	
taaaatggct agtaatacta cctt			271
<210> 342			
<211> 68			
<212> PRT			
<213> Helicobacter pylori			
<400> 342			
Met Met Gln Asn Ser Val Lys Lys Leu Glu Tyr Glu Glu Arg Phe Asn			
1	5	10	15
Asp Ala Leu Leu Lys Leu Gln Ala Cys Gln Glu Glu Lys Gln Val Thr			
	20	25	30
Ser Cys Leu Lys Cys Glu Gln Val Leu Asn Cys Lys Ile Arg Asn Ser			
	35	40	45
Tyr Val Asp Ala Ala Tyr Glu Ser Met Ser Leu Gly Glu Arg Gly Gly			
	50	55	60
Phe Asp Phe Asn			
65			
<210> 343			
<211> 572			
<212> DNA			
<213> Helicobacter pylori			
<220>			
<221> CDS			
<222> (27)...(524)			
<400> 343			
aaaaggcttt ttaaaaggac acacca atg agc gaa cca tta gaa aca tta gac			53
	Met Ser Glu Pro Leu Glu Thr Leu Asp		
	1	5	
aag gat aaa caa gct atg agt gaa gca att aaa aaa gat att gaa aaa			101
Lys Asp Lys Gln Ala Met Ser Glu Ala Ile Lys Lys Asp Ile Glu Lys			
10	15	20	25
gac aaa gaa aac ctc gca cga gtc aaa gca gac aaa aaa gtc aaa gcc			149
Asp Lys Glu Asn Leu Ala Arg Val Lys Ala Asp Lys Lys Val Lys Ala			
	30	35	40
gat gaa agt gaa aaa ggc tac gaa aaa gac gat gac aaa aaa gcc gag			197
Asp Glu Ser Glu Lys Gly Tyr Glu Lys Asp Asp Asp Lys Lys Ala Glu			
	45	50	55
aat ctt gac aaa gaa atc gct aaa gac aaa gct agc cct aac gat aat			245
Asn Leu Asp Lys Glu Ile Ala Lys Asp Lys Ala Ser Pro Asn Asp Asn			
	60	65	70

gag ctt tat gaa gag gac gat aga gtt aaa cga gac aaa gaa aga gac 293
 Glu Leu Tyr Glu Glu Asp Asp Arg Val Lys Arg Asp Lys Glu Arg Asp
 75 80 85
 gat gcc ttg cgt gat aaa gaa aaa gcc aaa gat gac gca tgc atg gta 341
 Asp Ala Leu Arg Asp Lys Glu Lys Ala Lys Asp Asp Ala Cys Met Val
 90 95 100 105
 aga gcg gac gat gac acc ata gag gac gat gag gaa tat ggt gat gat 389
 Arg Ala Asp Asp Asp Thr Ile Glu Asp Asp Glu Glu Tyr Gly Asp Asp
 110 115 120
 gat aag tta aga gac gaa ata ctc ggt gtt atg gag gag tta tgc gat 437
 Asp Lys Leu Arg Asp Glu Ile Leu Gly Val Met Glu Glu Leu Cys Asp
 125 130 135
 acc ctt aat gat aac ctt aac ttc aaa aaa gtc gtc tgt atg ggc ggt 485
 Thr Leu Asn Asp Asn Leu Asn Phe Lys Lys Val Val Cys Met Gly Gly
 140 145 150
 aag gtt tca att gcg ttc aaa ttt cta att ttt tgc tct taatctttta 534
 Lys Val Ser Ile Ala Phe Lys Phe Leu Ile Phe Cys Ser
 155 160 165

gaaaaaattc aaactctaag gatctatctt ttcgtag 572

<210> 344
 <211> 166
 <212> PRT
 <213> Helicobacter pylori

<400> 344
 Met Ser Glu Pro Leu Glu Thr Leu Asp Lys Asp Lys Gln Ala Met Ser
 1 5 10 15
 Glu Ala Ile Lys Lys Asp Ile Glu Lys Asp Lys Glu Asn Leu Ala Arg
 20 25 30
 Val Lys Ala Asp Lys Lys Val Lys Ala Asp Glu Ser Glu Lys Gly Tyr
 35 40 45
 Glu Lys Asp Asp Asp Lys Lys Ala Glu Asn Leu Asp Lys Glu Ile Ala
 50 55 60
 Lys Asp Lys Ala Ser Pro Asn Asp Asn Glu Leu Tyr Glu Glu Asp Asp
 65 70 75 80
 Arg Val Lys Arg Asp Lys Glu Arg Asp Asp Ala Leu Arg Asp Lys Glu
 85 90 95
 Lys Ala Lys Asp Asp Ala Cys Met Val Arg Ala Asp Asp Asp Thr Ile
 100 105 110
 Glu Asp Asp Glu Glu Tyr Gly Asp Asp Asp Lys Leu Arg Asp Glu Ile
 115 120 125
 Leu Gly Val Met Glu Glu Leu Cys Asp Thr Leu Asn Asp Asn Leu Asn
 130 135 140
 Phe Lys Lys Val Val Cys Met Gly Gly Lys Val Ser Ile Ala Phe Lys
 145 150 155 160
 Phe Leu Ile Phe Cys Ser
 165

<210> 345
 <211> 2327

<212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (82)...(2283)

```

<400> 345
caacaagcta accaaagcat tgaagaagct ttacagaatg tcccgggtct gcaaattagg 60
aatgcgacag gtgtaggggc t atg cct act atc caa atc cgt ggc ttt gga 111
                        Met Pro Thr Ile Gln Ile Arg Gly Phe Gly
                        1                      5                      10

gct ggg ggt tca ggg cat agc gat gcg acg ctg atg tta gtc aat ggt 159
Ala Gly Gly Ser Gly His Ser Asp Ala Thr Leu Met Leu Val Asn Gly
                        15                      20                      25

att cct gtt tat atg gcc ccc tac gct cac att gag cta gac att ttc 207
Ile Pro Val Tyr Met Ala Pro Tyr Ala His Ile Glu Leu Asp Ile Phe
                        30                      35                      40

ccc gtt acc ttt caa gcc att gat cgc att gat gtg atc aag ggt gga 255
Pro Val Thr Phe Gln Ala Ile Asp Arg Ile Asp Val Ile Lys Gly Gly
                        45                      50                      55

ggc agc gtg caa tac ggg cct aac act tat ggg ggt att gtc aat atc 303
Gly Ser Val Gln Tyr Gly Pro Asn Thr Tyr Gly Gly Ile Val Asn Ile
                        60                      65                      70

atc act aag cct atc cct aat caa tgg gaa aac caa gcg gct gaa agg 351
Ile Thr Lys Pro Ile Pro Asn Gln Trp Glu Asn Gln Ala Ala Glu Arg
                        75                      80                      85                      90

atc act tat tgg gct aag gct aga aac gct ggg ttt gcc gct cct cct 399
Ile Thr Tyr Trp Ala Lys Ala Arg Asn Ala Gly Phe Ala Ala Pro Pro
                        95                      100                      105

gat aaa acc ggc gat cct tct ttc atc aag tct tta ggc aac aac ctc 447
Asp Lys Thr Gly Asp Pro Ser Phe Ile Lys Ser Leu Gly Asn Asn Leu
                        110                      115                      120

ctc tat aac act tat gtg agg agt gga ggg atg atc aat aag cat gtg 495
Leu Tyr Asn Thr Tyr Val Arg Ser Gly Gly Met Ile Asn Lys His Val
                        125                      130                      135

ggg atc caa gcg caa gct aac tgg gtt aga gga caa ggc ttt agg gac 543
Gly Ile Gln Ala Gln Ala Asn Trp Val Arg Gly Gln Gly Phe Arg Asp
                        140                      145                      150

aat agc ccc tct aac att tca aac tat tgg cta gat gga gtc tat gac 591
Asn Ser Pro Ser Asn Ile Ser Asn Tyr Trp Leu Asp Gly Val Tyr Asp
                        155                      160                      165                      170

atc aat gaa aac aat ggg att aaa gcc tat tac caa tac tac gat ttt 639
Ile Asn Glu Asn Asn Gly Ile Lys Ala Tyr Tyr Gln Tyr Tyr Asp Phe
                        175                      180                      185

gct atc gct caa cca gga tca ctc agc gag caa gat tac aaa ata aac 687
Ala Ile Ala Gln Pro Gly Ser Leu Ser Glu Gln Asp Tyr Lys Ile Asn

```


190					195					200						
cgc	ttc	gct	aat	ttg	cgc	ccc	tta	aac	caa	aaa	ggc	ggg	cgt	tca	caa	735
Arg	Phe	Ala	Asn	Leu	Arg	Pro	Leu	Asn	Gln	Lys	Gly	Gly	Arg	Ser	Gln	
		205					210					215				
cgc	ttt	ggg	gct	gtg	tat	gaa	aac	cgc	ttc	ggg	gat	tta	gac	aaa	gtg	783
Arg	Phe	Gly	Ala	Val	Tyr	Glu	Asn	Arg	Phe	Gly	Asp	Leu	Asp	Lys	Val	
		220					225					230				
ggc	ggg	act	ttt	agc	ttc	act	tac	tat	ggg	cag	ttg	atg	act	agg	gat	831
Gly	Gly	Thr	Phe	Ser	Phe	Thr	Tyr	Tyr	Gly	Gln	Leu	Met	Thr	Arg	Asp	
		235					240					245				
ttt	caa	gtg	agc	tct	agc	tac	aat	agc	gct	aac	atg	gtt	act	tgt	ttt	879
Phe	Gln	Val	Ser	Ser	Ser	Tyr	Asn	Ser	Ala	Asn	Met	Val	Thr	Cys	Phe	
				255					260					265		
agc	gaa	gcg	gca	tgc	agg	gcg	gca	gga	ctt	ccg	gca	ggg	tat	aac	ttg	927
Ser	Glu	Ala	Ala	Cys	Arg	Ala	Ala	Gly	Leu	Pro	Ala	Gly	Tyr	Asn	Leu	
				270					275					280		
gct	gtg	cct	tat	tat	gcc	act	aac	tac	aat	ggc	tgg	gca	gaa	gta	gaa	975
Ala	Val	Pro	Tyr	Tyr	Ala	Thr	Asn	Tyr	Asn	Gly	Trp	Ala	Glu	Val	Glu	
				285					290					295		
aac	cct	gtg	cgc	tcc	att	aac	aac	gct	ttt	gag	cct	aaa	gtg	aat	ttg	1023
Asn	Pro	Val	Arg	Ser	Ile	Asn	Asn	Ala	Phe	Glu	Pro	Lys	Val	Asn	Leu	
				300					305					310		
atc	gtc	aat	acc	ggg	aaa	gtc	aag	caa	acc	ttt	atc	atg	ggc	ttg	cgt	1071
Ile	Val	Asn	Thr	Gly	Lys	Val	Lys	Gln	Thr	Phe	Ile	Met	Gly	Leu	Arg	
				315					320					325		
ttc	atg	acc	acc	act	ttt	tta	cag	cgc	caa	tac	tta	aac	acc	aat	gaa	1119
Phe	Met	Thr	Thr	Thr	Phe	Leu	Gln	Arg	Gln	Tyr	Leu	Asn	Thr	Asn	Glu	
				335					340					345		
tgc	gcc	acc	aaa	acg	agc	ggt	gag	ggg	gca	gga	ttc	ttg	tgt	gag	ggc	1167
Cys	Ala	Thr	Lys	Thr	Ser	Gly	Glu	Gly	Ala	Gly	Phe	Leu	Cys	Glu	Gly	
				350					355					360		
gct	aat	gtg	atg	agc	ggt	tgg	aaa	cct	cac	atc	aag	cat	ggc	gtt	tat	1215
Ala	Asn	Val	Met	Ser	Gly	Trp	Lys	Pro	His	Ile	Lys	His	Gly	Val	Tyr	
				365					370					375		
aga	aac	tgg	aat	aac	tgg	cgt	aac	aat	tac	aca	gcg	gtt	tat	ttg	agc	1263
Arg	Asn	Trp	Asn	Asn	Trp	Arg	Asn	Asn	Tyr	Thr	Ala	Val	Tyr	Leu	Ser	
				380					385					390		
gat	cgc	att	gaa	gct	tgg	gat	ggg	cgc	ttt	ttc	atc	gtg	cct	ggt	ttg	1311
Asp	Arg	Ile	Glu	Ala	Trp	Asp	Gly	Arg	Phe	Phe	Ile	Val	Pro	Gly	Leu	
				395					400					405		
cgc	tac	gct	ttt	gtg	caa	tac	aac	aac	gaa	aat	gcg	tct	aac	tgg	atg	1359
Arg	Tyr	Ala	Phe	Val	Gln	Tyr	Asn	Asn	Glu	Asn	Ala	Ser	Asn	Trp	Met	
				415					420					425		
caa	atc	cct	gag	aag	gat	tta	aga	aaa	atc	aag	cac	atg	aac	aat	tgg	1407

Gln	Ile	Pro	Glu	Lys	Asp	Leu	Arg	Lys	Ile	Lys	His	Met	Asn	Asn	Trp	
			430					435					440			
atg	ccc	tca	acc	aac	att	ggc	ttt	atc	ccc	gtg	caa	ggc	gat	cac	aat	1455
Met	Pro	Ser	Thr	Asn	Ile	Gly	Phe	Ile	Pro	Val	Gln	Gly	Asp	His	Asn	
		445				450						455				
gtg	ctt	acc	tac	ttt	aac	tac	caa	cgc	tct	ttc	gtc	ccg	cct	caa	tta	1503
Val	Leu	Thr	Tyr	Phe	Asn	Tyr	Gln	Arg	Ser	Phe	Val	Pro	Pro	Gln	Leu	
	460					465					470					
gac	gtt	ttg	agc	tat	gga	gga	gcg	gag	tat	ttt	acc	cag	cac	ttt	gac	1551
Asp	Val	Leu	Ser	Tyr	Gly	Gly	Ala	Glu	Tyr	Phe	Thr	Gln	His	Phe	Asp	
475					480				485						490	
acg	gtg	gaa	gca	gga	gcg	cgc	tac	acc	tat	aag	gat	aaa	ttc	agc	ttc	1599
Thr	Val	Glu	Ala	Gly	Ala	Arg	Tyr	Thr	Tyr	Lys	Asp	Lys	Phe	Ser	Phe	
				495					500					505		
aat	gcg	gac	tac	ttc	agg	att	tgg	gcg	cgc	gat	ttt	gcc	acc	ggg	cag	1647
Asn	Ala	Asp	Tyr	Phe	Arg	Ile	Trp	Ala	Arg	Asp	Phe	Ala	Thr	Gly	Gln	
			510				515						520			
tat	tca	gtc	tat	aca	agc	ggc	ccc	atg	aag	ggc	aat	gtg	cgc	ccc	att	1695
Tyr	Ser	Val	Tyr	Thr	Ser	Gly	Pro	Met	Lys	Gly	Asn	Val	Arg	Pro	Ile	
		525					530					535				
aat	ggc	tat	tct	caa	ggc	gtg	gag	ctg	gaa	ttg	tat	tac	agg	cct	att	1743
Asn	Gly	Tyr	Ser	Gln	Gly	Val	Glu	Leu	Glu	Leu	Tyr	Tyr	Arg	Pro	Ile	
	540					545					550					
aga	ggg	ttg	caa	ttc	cat	gcc	gct	ttc	aac	tac	att	gac	act	cgt	gta	1791
Arg	Gly	Leu	Gln	Phe	His	Ala	Ala	Phe	Asn	Tyr	Ile	Asp	Thr	Arg	Val	
555					560				565						570	
acc	agc	cat	ggc	cct	tta	acc	gac	ttg	aac	ggg	gat	gtg	cta	aaa	ggg	1839
Thr	Ser	His	Gly	Pro	Leu	Thr	Asp	Leu	Asn	Gly	Asp	Val	Leu	Lys	Gly	
				575					580					585		
act	agc	tat	aac	aag	cat	ttc	cct	ttt	gta	agc	cct	ttc	caa	ttc	att	1887
Thr	Ser	Tyr	Asn	Lys	His	Phe	Pro	Phe	Val	Ser	Pro	Phe	Gln	Phe	Ile	
			590					595					600			
ctt	gac	gct	cgt	tac	aat	tgg	cgt	aaa	acc	acc	atc	ggc	att	tct	agc	1935
Leu	Asp	Ala	Arg	Tyr	Asn	Trp	Arg	Lys	Thr	Thr	Ile	Gly	Ile	Ser	Ser	
		605					610					615				
tat	ttt	tac	agc	cgt	gct	tat	agc	ggg	att	agc	aac	agt	gca	gca	gga	1983
Tyr	Phe	Tyr	Ser	Arg	Ala	Tyr	Ser	Gly	Ile	Ser	Asn	Ser	Ala	Ala	Gly	
	620					625					630					
ggc	tat	tat	ggg	atg	caa	tat	tat	agt	ggg	ggg	aac	aac	tat	gaa	agc	2031
Gly	Tyr	Tyr	Gly	Met	Gln	Tyr	Tyr	Ser	Gly	Gly	Asn	Asn	Tyr	Glu	Ser	
635					640				645					650		
gtt	ctt	aat	agc	ggc	tat	caa	tgc	gaa	gct	tgg	tgt	atg	acc	caa	cat	2079
Val	Leu	Asn	Ser	Gly	Tyr	Gln	Cys	Glu	Ala	Trp	Cys	Met	Thr	Gln	His	
				655					660					665		

gaa ggg ctc ttg cct tgg tat tgg gtg tgg aat atc caa gtg agc caa	2127
Glu Gly Leu Leu Pro Trp Tyr Trp Val Trp Asn Ile Gln Val Ser Gln	
670 675 680	

att ttc tgg gaa aac ggg aga cac aga gtt aca gga agc ttg caa atc	2175
Ile Phe Trp Glu Asn Gly Arg His Arg Val Thr Gly Ser Leu Gln Ile	
685 690 695	

aat aat atc ttc aac atg aag tat tat ttt aca ggg att ggc tct agc	2223
Asn Asn Ile Phe Asn Met Lys Tyr Tyr Phe Thr Gly Ile Gly Ser Ser	
700 705 710	

cct gca ggc ttg caa cct gcg cct gga aga tcg gtt aca gcg tat ttg	2271
Pro Ala Gly Leu Gln Pro Ala Pro Gly Arg Ser Val Thr Ala Tyr Leu	
715 720 725 730	

aac tac act ttc taaaggcttt aaaaaggagg gggttattgc gcgatgatga	2323
Asn Tyr Thr Phe	

gccg	2327
------	------

<210> 346
 <211> 734
 <212> PRT
 <213> Helicobacter pylori

<400> 346

Met Pro Thr Ile Gln Ile Arg Gly Phe Gly Ala Gly Gly Ser Gly His	
1 5 10 15	
Ser Asp Ala Thr Leu Met Leu Val Asn Gly Ile Pro Val Tyr Met Ala	
20 25 30	
Pro Tyr Ala His Ile Glu Leu Asp Ile Phe Pro Val Thr Phe Gln Ala	
35 40 45	
Ile Asp Arg Ile Asp Val Ile Lys Gly Gly Gly Ser Val Gln Tyr Gly	
50 55 60	
Pro Asn Thr Tyr Gly Gly Ile Val Asn Ile Ile Thr Lys Pro Ile Pro	
65 70 75 80	
Asn Gln Trp Glu Asn Gln Ala Ala Glu Arg Ile Thr Tyr Trp Ala Lys	
85 90 95	
Ala Arg Asn Ala Gly Phe Ala Ala Pro Pro Asp Lys Thr Gly Asp Pro	
100 105 110	
Ser Phe Ile Lys Ser Leu Gly Asn Asn Leu Leu Tyr Asn Thr Tyr Val	
115 120 125	
Arg Ser Gly Gly Met Ile Asn Lys His Val Gly Ile Gln Ala Gln Ala	
130 135 140	
Asn Trp Val Arg Gly Gln Gly Phe Arg Asp Asn Ser Pro Ser Asn Ile	
145 150 155 160	
Ser Asn Tyr Trp Leu Asp Gly Val Tyr Asp Ile Asn Glu Asn Asn Gly	
165 170 175	
Ile Lys Ala Tyr Tyr Gln Tyr Tyr Asp Phe Ala Ile Ala Gln Pro Gly	
180 185 190	
Ser Leu Ser Glu Gln Asp Tyr Lys Ile Asn Arg Phe Ala Asn Leu Arg	
195 200 205	
Pro Leu Asn Gln Lys Gly Gly Arg Ser Gln Arg Phe Gly Ala Val Tyr	
210 215 220	
Glu Asn Arg Phe Gly Asp Leu Asp Lys Val Gly Gly Thr Phe Ser Phe	
225 230 235 240	
Thr Tyr Tyr Gly Gln Leu Met Thr Arg Asp Phe Gln Val Ser Ser Ser	

Ala Pro Gly Arg Ser Val Thr Ala Tyr Leu Asn Tyr Thr Phe
725 730

<210> 347
<211> 232
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (37)...(204)

<400> 347
cattggagat tgtgccattc tttgatttta tctaaa atg tct tta ggg gca gtg 54
Met Ser Leu Gly Ala Val
1 5
att aag ctt att ttt tgt tat aaa tta gag ggg gta ata tta gat tta 102
Ile Lys Leu Ile Phe Cys Tyr Lys Leu Glu Gly Val Ile Leu Asp Leu
10 15 20
aag cgc atc aat ttc aaa tcc tat tat ccc aat aat aaa aat gca tta 150
Lys Arg Ile Asn Phe Lys Ser Tyr Tyr Pro Asn Asn Lys Asn Ala Leu
25 30 35
ttt atc aac aat aaa aaa atc cat tat cta gtg cct caa agg ttc ata 198
Phe Ile Asn Asn Lys Lys Ile His Tyr Leu Val Pro Gln Arg Phe Ile
40 45 50
ttg ctt taaacttgct atggacgatt agaaatcg 232
Leu Leu
55

<210> 348
<211> 56
<212> PRT
<213> Helicobacter pylori

<400> 348
Met Ser Leu Gly Ala Val Ile Lys Leu Ile Phe Cys Tyr Lys Leu Glu
1 5 10 15
Gly Val Ile Leu Asp Leu Lys Arg Ile Asn Phe Lys Ser Tyr Tyr Pro
20 25 30
Asn Asn Lys Asn Ala Leu Phe Ile Asn Asn Lys Lys Ile His Tyr Leu
35 40 45
Val Pro Gln Arg Phe Ile Leu Leu
50 55

<210> 349
<211> 1142
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (24)...(1094)

<400> 349

```
cttttagaat tagggcttaa agc atg aaa gct agt att tat gat ttc act cta 53
      Met Lys Ala Ser Ile Tyr Asp Phe Thr Leu
      1              5              10

aag gaa ttg agc cag ctt tta aaa cca agc ttt agg gct aaa cag ctt 101
Lys Glu Leu Ser Gln Leu Leu Lys Pro Ser Phe Arg Ala Lys Gln Leu
      15              20              25

tat ttg tgg ctc tat gcg aag tat aaa aca agc ttt aag gac atg caa 149
Tyr Leu Trp Leu Tyr Ala Lys Tyr Lys Thr Ser Phe Lys Asp Met Gln
      30              35              40

aat aat ttt tca aaa gat ttt atc gct tat ttg gag cga gaa ttt gct 197
Asn Asn Phe Ser Lys Asp Phe Ile Ala Tyr Leu Glu Arg Glu Phe Ala
      45              50              55

ttg cgc acg ata gaa atc acg cat gtg agg gag agc gtt gat ggc tct 245
Leu Arg Thr Ile Glu Ile Thr His Val Arg Glu Ser Val Asp Gly Ser
      60              65              70

aaa aaa tac ctt ttt aaa tct tta aga gac aac cac act ttt gaa gcg 293
Lys Lys Tyr Leu Phe Lys Ser Leu Arg Asp Asn His Thr Phe Glu Ala
      75              80              85              90

gtg ttg ttg aaa atg aag gat aaa aag att gat gca gaa acg aac gct 341
Val Leu Leu Lys Met Lys Asp Lys Lys Ile Asp Ala Glu Thr Asn Ala
      95              100              105

att tta gag agg gaa aaa tac acc gta tgc gtg tct tgt caa atc ggc 389
Ile Leu Glu Arg Glu Lys Tyr Thr Val Cys Val Ser Cys Gln Ile Gly
      110              115              120

tgt caa gtg ggt tgc tcg ttt tgt ttc act caa aaa ggc ggt ttt gta 437
Cys Gln Val Gly Cys Ser Phe Cys Phe Thr Gln Lys Gly Gly Phe Val
      125              130              135

agg aac tta aaa gcg agc gag atc atc caa caa gcc cta ctc att aaa 485
Arg Asn Leu Lys Ala Ser Glu Ile Ile Gln Gln Ala Leu Leu Ile Lys
      140              145              150

gaa gac aac aac ctc ccc ctt gaa aaa gcg ctc aac att gtt ttt atg 533
Glu Asp Asn Asn Leu Pro Leu Glu Lys Ala Leu Asn Ile Val Phe Met
      155              160              165              170

gga atg ggc gag cct tta aac aat tta gat gag gtg tgt aaa gcg att 581
Gly Met Gly Glu Pro Leu Asn Asn Leu Asp Glu Val Cys Lys Ala Ile
      175              180              185

gag att ttc aat acc ggc atg caa att tcg cct aaa aga atc acc att 629
Glu Ile Phe Asn Thr Gly Met Gln Ile Ser Pro Lys Arg Ile Thr Ile
      190              195              200

tcc act agc ggc gta gcc gat aaa atc cct att tta gcg ggc aaa aac 677
Ser Thr Ser Gly Val Ala Asp Lys Ile Pro Ile Leu Ala Gly Lys Asn
      205              210              215

tta ggc gtg caa tta gcc ata tcc tta cac gcc gta gat gac aaa acg 725
Leu Gly Val Gln Leu Ala Ile Ser Leu His Ala Val Asp Asp Lys Thr
```

220	225	230	
cgc tcg tct tta atg ccc ttg aat aaa aaa tac aat att gaa tgc gtt			773
Arg Ser Ser Leu Met Pro Leu Asn Lys Lys Tyr Asn Ile Glu Cys Val			
235	240	245	250
ttg aat gaa gtg agg aaa tgg cct tta gag cag cgc aaa aga gtg atg			821
Leu Asn Glu Val Arg Lys Trp Pro Leu Glu Gln Arg Lys Arg Val Met			
	255	260	265
ttt gaa tac ctt ttg atc aaa gat ttg aac gat agc cta gac tgc gct			869
Phe Glu Tyr Leu Leu Ile Lys Asp Leu Asn Asp Ser Leu Asp Cys Ala			
	270	275	280
aaa aaa ctt tta aaa ctt tta aac ggc att aaa tcc aaa gtg aat ttg			917
Lys Lys Leu Leu Lys Leu Leu Asn Gly Ile Lys Ser Lys Val Asn Leu			
	285	290	295
atc tta ttc aac ccg cat gaa ggc tct aag ttt gaa cgc cct agc tta			965
Ile Leu Phe Asn Pro His Glu Gly Ser Lys Phe Glu Arg Pro Ser Leu			
	300	305	310
gag aac gct aga atg ttt gcg gat ttt tta aac tct aaa ggc tta tta			1013
Glu Asn Ala Arg Met Phe Ala Asp Phe Leu Asn Ser Lys Gly Leu Leu			
	315	320	330
tgc acc att aga gag tct aaa gcc ttg gat att gaa gcg gct tgc ggg			1061
Cys Thr Ile Arg Glu Ser Lys Ala Leu Asp Ile Glu Ala Ala Cys Gly			
	335	340	345
cag ttg agg gag aaa aaa ctc tct cag caa att tgaaaaacttt tttgtggtgt			1114
Gln Leu Arg Glu Lys Lys Leu Ser Gln Gln Ile			
	350	355	
ttgtcttttt tctaattgggg ggtgttgg			1142
<210> 350			
<211> 357			
<212> PRT			
<213> Helicobacter pylori			
<400> 350			
Met Lys Ala Ser Ile Tyr Asp Phe Thr Leu Lys Glu Leu Ser Gln Leu			
1 5 10 15			
Leu Lys Pro Ser Phe Arg Ala Lys Gln Leu Tyr Leu Trp Leu Tyr Ala			
20 25 30			
Lys Tyr Lys Thr Ser Phe Lys Asp Met Gln Asn Asn Phe Ser Lys Asp			
35 40 45			
Phe Ile Ala Tyr Leu Glu Arg Glu Phe Ala Leu Arg Thr Ile Glu Ile			
50 55 60			
Thr His Val Arg Glu Ser Val Asp Gly Ser Lys Lys Tyr Leu Phe Lys			
65 70 75 80			
Ser Leu Arg Asp Asn His Thr Phe Glu Ala Val Leu Leu Lys Met Lys			
85 90 95			
Asp Lys Lys Ile Asp Ala Glu Thr Asn Ala Ile Leu Glu Arg Glu Lys			
100 105 110			
Tyr Thr Val Cys Val Ser Cys Gln Ile Gly Cys Gln Val Gly Cys Ser			
115 120 125			
Phe Cys Phe Thr Gln Lys Gly Gly Phe Val Arg Asn Leu Lys Ala Ser			

130		135		140
Glu Ile Ile Gln Gln Ala Leu Leu Ile Lys Glu Asp Asn Asn Leu Pro				
145		150		155
Leu Glu Lys Ala Leu Asn Ile Val Phe Met Gly Met Gly Glu Pro Leu				
	165		170	175
Asn Asn Leu Asp Glu Val Cys Lys Ala Ile Glu Ile Phe Asn Thr Gly				
	180		185	190
Met Gln Ile Ser Pro Lys Arg Ile Thr Ile Ser Thr Ser Gly Val Ala				
	195		200	205
Asp Lys Ile Pro Ile Leu Ala Gly Lys Asn Leu Gly Val Gln Leu Ala				
	210		215	220
Ile Ser Leu His Ala Val Asp Asp Lys Thr Arg Ser Ser Leu Met Pro				
225		230		235
Leu Asn Lys Lys Tyr Asn Ile Glu Cys Val Leu Asn Glu Val Arg Lys				
	245		250	255
Trp Pro Leu Glu Gln Arg Lys Arg Val Met Phe Glu Tyr Leu Leu Ile				
	260		265	270
Lys Asp Leu Asn Asp Ser Leu Asp Cys Ala Lys Lys Leu Leu Lys Leu				
	275		280	285
Leu Asn Gly Ile Lys Ser Lys Val Asn Leu Ile Leu Phe Asn Pro His				
	290		295	300
Glu Gly Ser Lys Phe Glu Arg Pro Ser Leu Glu Asn Ala Arg Met Phe				
305		310		315
Ala Asp Phe Leu Asn Ser Lys Gly Leu Leu Cys Thr Ile Arg Glu Ser				
	325		330	335
Lys Ala Leu Asp Ile Glu Ala Ala Cys Gly Gln Leu Arg Glu Lys Lys				
	340		345	350
Leu Ser Gln Gln Ile				
	355			

<210> 351

<211> 990

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (1)...(987)

<400> 351

atg ccc att ctt ttt gat tgt aac gct att gct tca caa gtt tta aaa	48
Met Pro Ile Leu Phe Asp Cys Asn Ala Ile Ala Ser Gln Val Leu Lys	
1 5 10 15	
gat gaa gcg agc gcg ctt tta gaa agc gtt gga caa ttc caa aaa ccc	96
Asp Glu Ala Ser Ala Leu Leu Glu Ser Val Gly Gln Phe Gln Lys Pro	
20 25 30	
aac gat tta gaa gcg att gtc aaa ctc att tta aaa agc caa gaa aat	144
Asn Asp Leu Glu Ala Ile Val Lys Leu Ile Leu Lys Ser Gln Glu Asn	
35 40 45	
ggg ggt aag ctt gtg ata gtg ggt gtg ggt aag agc gct tta gtg gcg	192
Gly Gly Lys Leu Val Ile Val Gly Val Gly Lys Ser Ala Leu Val Ala	
50 55 60	
caa aaa atc gtt gct tcc atg cta agc acc ggt aac agg agc gcg ttt	240
Gln Lys Ile Val Ala Ser Met Leu Ser Thr Gly Asn Arg Ser Ala Phe	

65					70					75					80	
tta	cac	ccc	aca	gaa	gcc	atg	cat	ggg	gat	ttg	ggc	atg	gtg	gaa	aaa	288
Leu	His	Pro	Thr	Glu	Ala	Met	His	Gly	Asp	Leu	Gly	Met	Val	Glu	Lys	
				85					90					95		
aac	gat	gtg	ggt	tta	atg	att	agc	tat	ggg	ggc	gag	tct	tta	gaa	tta	336
Asn	Asp	Val	Val	Leu	Met	Ile	Ser	Tyr	Gly	Gly	Glu	Ser	Leu	Glu	Leu	
			100					105					110			
ttg	aat	ctg	gtg	agc	cat	tta	aaa	cgc	ttg	agc	cat	aaa	atc	atc	act	384
Leu	Asn	Leu	Val	Ser	His	Leu	Lys	Arg	Leu	Ser	His	Lys	Ile	Ile	Thr	
		115					120					125				
ttc	act	aaa	agc	cct	aat	agc	tcg	ctc	tct	aaa	ctc	ggc	gat	tat	tat	432
Phe	Thr	Lys	Ser	Pro	Asn	Ser	Ser	Leu	Ser	Lys	Leu	Gly	Asp	Tyr	Tyr	
	130					135					140					
ttg	agc	ttg	aaa	att	caa	aaa	gaa	gct	tgc	ccg	att	aac	acc	gct	cca	480
Leu	Ser	Leu	Lys	Ile	Gln	Lys	Glu	Ala	Cys	Pro	Ile	Asn	Thr	Ala	Pro	
145					150					155					160	
acg	act	tct	acc	acc	cta	act	cta	gcg	tta	ggc	gat	ggt	tta	atg	gca	528
Thr	Thr	Ser	Thr	Thr	Leu	Thr	Leu	Ala	Leu	Gly	Asp	Val	Leu	Met	Ala	
				165					170					175		
tgc	ttg	atg	cga	gcg	aaa	aac	ttt	agc	caa	gaa	gat	ttt	gcc	tcc	ttt	576
Cys	Leu	Met	Arg	Ala	Lys	Asn	Phe	Ser	Gln	Glu	Asp	Phe	Ala	Ser	Phe	
			180					185					190			
cat	ccg	ggc	ggg	ctt	tta	ggc	aaa	aaa	ctt	ttt	gtc	aag	ggt	aaa	gat	624
His	Pro	Gly	Gly	Leu	Leu	Gly	Lys	Lys	Leu	Phe	Val	Lys	Val	Lys	Asp	
		195					200					205				
tta	ctg	caa	acc	acg	aac	ctc	ccc	cta	atc	gct	cct	agc	aca	agt	ttt	672
Leu	Leu	Gln	Thr	Thr	Asn	Leu	Pro	Leu	Ile	Ala	Pro	Ser	Thr	Ser	Phe	
	210					215					220					
aaa	gac	gcg	ctc	ata	gaa	atg	agt	gaa	aaa	cgc	tta	ggc	agc	gcg	att	720
Lys	Asp	Ala	Leu	Ile	Glu	Met	Ser	Glu	Lys	Arg	Leu	Gly	Ser	Ala	Ile	
225					230					235					240	
tta	gtc	aat	gaa	gct	aac	gag	ctt	gtg	ggg	gtg	tta	agc	gat	ggc	gat	768
Leu	Val	Asn	Glu	Ala	Asn	Glu	Leu	Val	Gly	Val	Leu	Ser	Asp	Gly	Asp	
			245					250						255		
gtc	cgt	agg	gcg	tta	tta	aaa	ggg	gtg	agt	tta	aag	agc	gaa	gtg	agg	816
Val	Arg	Arg	Ala	Leu	Leu	Lys	Gly	Val	Ser	Leu	Lys	Ser	Glu	Val	Arg	
			260					265					270			
cat	ttt	gcc	act	tta	aaa	cct	aaa	agc	ttt	aag	aat	tta	gac	gct	ctt	864
His	Phe	Ala	Thr	Leu	Lys	Pro	Lys	Ser	Phe	Lys	Asn	Leu	Asp	Ala	Leu	
		275					280					285				
ctt	tta	gaa	gcg	ttg	gaa	ttt	tta	gag	cgc	cat	aag	atc	cag	ctt	tta	912
Leu	Leu	Glu	Ala	Leu	Glu	Phe	Leu	Glu	Arg	His	Lys	Ile	Gln	Leu	Leu	
	290					295					300					
gtg	tgc	gta	gat	gat	cat	aat	aag	ggt	tta	ggg	gtc	ttg	cac	ttg	cac	960

Val Cys Val Asp Asp His Asn Lys Val Leu Gly Val Leu His Leu His
 305 310 315 320

caa ctt tta gaa tta ggg ctt aaa gca tga
 Gln Leu Leu Glu Leu Gly Leu Lys Ala
 325

990

<210> 352
 <211> 329
 <212> PRT
 <213> Helicobacter pylori

<400> 352
 Met Pro Ile Leu Phe Asp Cys Asn Ala Ile Ala Ser Gln Val Leu Lys
 1 5 10 15
 Asp Glu Ala Ser Ala Leu Leu Glu Ser Val Gly Gln Phe Gln Lys Pro
 20 25 30
 Asn Asp Leu Glu Ala Ile Val Lys Leu Ile Leu Lys Ser Gln Glu Asn
 35 40 45
 Gly Gly Lys Leu Val Ile Val Gly Val Gly Lys Ser Ala Leu Val Ala
 50 55 60
 Gln Lys Ile Val Ala Ser Met Leu Ser Thr Gly Asn Arg Ser Ala Phe
 65 70 75 80
 Leu His Pro Thr Glu Ala Met His Gly Asp Leu Gly Met Val Glu Lys
 85 90 95
 Asn Asp Val Val Leu Met Ile Ser Tyr Gly Gly Glu Ser Leu Glu Leu
 100 105 110
 Leu Asn Leu Val Ser His Leu Lys Arg Leu Ser His Lys Ile Ile Thr
 115 120 125
 Phe Thr Lys Ser Pro Asn Ser Ser Leu Ser Lys Leu Gly Asp Tyr Tyr
 130 135 140
 Leu Ser Leu Lys Ile Gln Lys Glu Ala Cys Pro Ile Asn Thr Ala Pro
 145 150 155 160
 Thr Thr Ser Thr Thr Leu Thr Leu Ala Leu Gly Asp Val Leu Met Ala
 165 170 175
 Cys Leu Met Arg Ala Lys Asn Phe Ser Gln Glu Asp Phe Ala Ser Phe
 180 185 190
 His Pro Gly Gly Leu Leu Gly Lys Lys Leu Phe Val Lys Val Lys Asp
 195 200 205
 Leu Leu Gln Thr Thr Asn Leu Pro Leu Ile Ala Pro Ser Thr Ser Phe
 210 215 220
 Lys Asp Ala Leu Ile Glu Met Ser Glu Lys Arg Leu Gly Ser Ala Ile
 225 230 235 240
 Leu Val Asn Glu Ala Asn Glu Leu Val Gly Val Leu Ser Asp Gly Asp
 245 250 255
 Val Arg Arg Ala Leu Leu Lys Gly Val Ser Leu Lys Ser Glu Val Arg
 260 265 270
 His Phe Ala Thr Leu Lys Pro Lys Ser Phe Lys Asn Leu Asp Ala Leu
 275 280 285
 Leu Leu Glu Ala Leu Glu Phe Leu Glu Arg His Lys Ile Gln Leu Leu
 290 295 300
 Val Cys Val Asp Asp His Asn Lys Val Leu Gly Val Leu His Leu His
 305 310 315 320
 Gln Leu Leu Glu Leu Gly Leu Lys Ala
 325

<210> 353

<211> 991
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (64)...(939)

```

<400> 353
tccttaaaac atttgaagta taatacactc ttatgggtcaa atattaagtt taggaaaagc 60
tgc atg tgg agt ttc att caa aaa atc ttt aag gct tta atc atc gca 108
  Met Trp Ser Phe Ile Gln Lys Ile Phe Lys Ala Leu Ile Ile Ala
    1          5          10          15

cct tta gat ttt atc acg aag tat ttc aag tcg ttt gtg ctg tta ctc 156
Pro Leu Asp Phe Ile Thr Lys Tyr Phe Lys Ser Phe Val Leu Leu Leu
          20          25          30

att gta tta gtc ttt ttt agc gct aaa gaa agc gcg cca agc gcc ccg 204
Ile Val Leu Val Phe Phe Ser Ala Lys Glu Ser Ala Pro Ser Ala Pro
          35          40          45

cct aat ctc gct aaa ctc tat tta aat ggg gcg att ttt agc acc gag 252
Pro Asn Leu Ala Lys Leu Tyr Leu Asn Gly Ala Ile Phe Ser Thr Glu
          50          55          60

gat ttt gac aaa gaa gtg gat aaa atc cta aaa acc cct agc att aag 300
Asp Phe Asp Lys Glu Val Asp Lys Ile Leu Lys Thr Pro Ser Ile Lys
          65          70          75

ggc gtt ttg ctt ttg att gac tct cct ggt ggg gcg gtg tca gcg agc 348
Gly Val Leu Leu Leu Ile Asp Ser Pro Gly Gly Ala Val Ser Ala Ser
          80          85          90          95

gtg gaa ttg agc gaa aaa atc gct gat ttg aag caa aaa atg ccc gtt 396
Val Glu Leu Ser Glu Lys Ile Ala Asp Leu Lys Gln Lys Met Pro Val
          100          105          110

tta gcg tat gct agg ggg gtt atg gcg agc ggg agc tat tat gcg ggc 444
Leu Ala Tyr Ala Arg Gly Val Met Ala Ser Gly Ser Tyr Tyr Ala Gly
          115          120          125

atg caa gcg agc gaa gtt tat gcc tct aaa gcg agt ttg ata gga tcc 492
Met Gln Ala Ser Glu Val Tyr Ala Ser Lys Ala Ser Leu Ile Gly Ser
          130          135          140

att ggg gtg att ttt tca ggt gcg aat gtg gaa aat ttg ctc aat aaa 540
Ile Gly Val Ile Phe Ser Gly Ala Asn Val Glu Asn Leu Leu Asn Lys
          145          150          155

gtc ggc gta gcc act caa ggc gtg cat gcg ggc gaa tac aaa gaa ata 588
Val Gly Val Ala Thr Gln Gly Val His Ala Gly Glu Tyr Lys Glu Ile
          160          165          170          175

ggc act ttc acc aga gcg tgg aaa ccc aac gaa aaa gat ttt ttg caa 636
Gly Thr Phe Thr Arg Ala Trp Lys Pro Asn Glu Lys Asp Phe Leu Gln
          180          185          190

aat tta gtc aat gag caa tac caa atg ttt gtg aat gat gtc gca aaa 684

```

Asn	Leu	Val	Asn	Glu	Gln	Tyr	Gln	Met	Phe	Val	Asn	Asp	Val	Ala	Lys		
			195					200					205				
gct	agg	aaa	tta	gac	gct	aag	gat	tat	aag	gat	ttt	gct	gaa	ggg	aag	732	
Ala	Arg	Lys	Leu	Asp	Ala	Lys	Asp	Tyr	Lys	Asp	Phe	Ala	Glu	Gly	Lys		
		210					215					220					
gtc	ttt	agc	gct	caa	aag	gct	ctg	aaa	tta	aaa	ctc	att	gat	aaa	atc	780	
Val	Phe	Ser	Ala	Gln	Lys	Ala	Leu	Lys	Leu	Lys	Leu	Ile	Asp	Lys	Ile		
	225					230					235						
agc	acg	att	aag	caa	gcg	caa	gat	cgc	tta	atg	gaa	ttg	agt	aag	gtt	828	
Ser	Thr	Ile	Lys	Gln	Ala	Gln	Asp	Arg	Leu	Met	Glu	Leu	Ser	Lys	Val		
240					245					250					255		
aaa	aaa	gct	tat	tgg	cta	gaa	aaa	agc	cct	atg	gag	cgc	ttc	att	gaa	876	
Lys	Lys	Ala	Tyr	Trp	Leu	Glu	Lys	Ser	Pro	Met	Glu	Arg	Phe	Ile	Glu		
				260					265					270			
aaa	gcc	acg	caa	tca	gcc	aca	aac	atc	atc	aca	caa	gcc	ttt	ggc	tat	924	
Lys	Ala	Thr	Gln	Ser	Ala	Thr	Asn	Ile	Ile	Thr	Gln	Ala	Phe	Gly	Tyr		
			275					280					285				
caa	tta	tta	atg	aga	taa	agatg	ttt	aga	atttatt	tt	aaaaa	attc	aag	ctagaga		979	
Gln	Leu	Leu	Met	Arg													
			290														
ctctaaaggc	tt															991	
<210> 354																	
<211> 292																	
<212> PRT																	
<213> Helicobacter pylori																	
<400> 354																	
Met	Trp	Ser	Phe	Ile	Gln	Lys	Ile	Phe	Lys	Ala	Leu	Ile	Ile	Ala	Pro		
1				5				10						15			
Leu	Asp	Phe	Ile	Thr	Lys	Tyr	Phe	Lys	Ser	Phe	Val	Leu	Leu	Leu	Ile		
		20					25					30					
Val	Leu	Val	Phe	Phe	Ser	Ala	Lys	Glu	Ser	Ala	Pro	Ser	Ala	Pro	Pro		
	35					40					45						
Asn	Leu	Ala	Lys	Leu	Tyr	Leu	Asn	Gly	Ala	Ile	Phe	Ser	Thr	Glu	Asp		
50				55				60									
Phe	Asp	Lys	Glu	Val	Asp	Lys	Ile	Leu	Lys	Thr	Pro	Ser	Ile	Lys	Gly		
65				70				75						80			
Val	Leu	Leu	Leu	Ile	Asp	Ser	Pro	Gly	Gly	Ala	Val	Ser	Ala	Ser	Val		
			85					90						95			
Glu	Leu	Ser	Glu	Lys	Ile	Ala	Asp	Leu	Lys	Gln	Lys	Met	Pro	Val	Leu		
		100						105					110				
Ala	Tyr	Ala	Arg	Gly	Val	Met	Ala	Ser	Gly	Ser	Tyr	Tyr	Ala	Gly	Met		
	115					120						125					
Gln	Ala	Ser	Glu	Val	Tyr	Ala	Ser	Lys	Ala	Ser	Leu	Ile	Gly	Ser	Ile		
	130					135					140						
Gly	Val	Ile	Phe	Ser	Gly	Ala	Asn	Val	Glu	Asn	Leu	Leu	Asn	Lys	Val		
145				150				155						160			
Gly	Val	Ala	Thr	Gln	Gly	Val	His	Ala	Gly	Glu	Tyr	Lys	Glu	Ile	Gly		
			165					170					175				
Thr	Phe	Thr	Arg	Ala	Trp	Lys	Pro	Asn	Glu	Lys	Asp	Phe	Leu	Gln	Asn		
			180					185					190				

Leu	Val	Asn	Glu	Gln	Tyr	Gln	Met	Phe	Val	Asn	Asp	Val	Ala	Lys	Ala
		195					200					205			
Arg	Lys	Leu	Asp	Ala	Lys	Asp	Tyr	Lys	Asp	Phe	Ala	Glu	Gly	Lys	Val
	210					215					220				
Phe	Ser	Ala	Gln	Lys	Ala	Leu	Lys	Leu	Lys	Leu	Ile	Asp	Lys	Ile	Ser
225					230					235					240
Thr	Ile	Lys	Gln	Ala	Gln	Asp	Arg	Leu	Met	Glu	Leu	Ser	Lys	Val	Lys
			245						250					255	
Lys	Ala	Tyr	Trp	Leu	Glu	Lys	Ser	Pro	Met	Glu	Arg	Phe	Ile	Glu	Lys
		260					265						270		
Ala	Thr	Gln	Ser	Ala	Thr	Asn	Ile	Ile	Thr	Gln	Ala	Phe	Gly	Tyr	Gln
		275				280						285			
Leu	Leu	Met	Arg												
	290														

<210> 355
 <211> 1114
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (37)...(1050)

<400> 355 cgagctatca caacaaatca atttgttagga acaagc atg ttt ttt aaa act tat															54	
										Met	Phe	Phe	Lys	Thr	Tyr	
										1				5		
caa aaa tta ttg ggt gcg agc tgt ttg acg ttg tat tta gcg ggc tgt															102	
Gln	Lys	Leu	Leu	Gly	Ala	Ser	Cys	Leu	Thr	Leu	Tyr	Leu	Ala	Gly	Cys	
			10					15					20			
ggg agt gat agt agc gag cca ttg gtg gga att gaa aaa aat agc ttc															150	
Gly	Ser	Asp	Ser	Ser	Glu	Pro	Leu	Val	Gly	Ile	Glu	Lys	Asn	Ser	Phe	
		25					30					35				
aat tct acc gtg aaa atc att tct aaa acc gac aac ata gaa atc caa															198	
Asn	Ser	Thr	Val	Lys	Ile	Ile	Ser	Lys	Thr	Asp	Asn	Ile	Glu	Ile	Gln	
		40				45				50						
gac ttg aag ctc aat cgt ggc aat tgt gag cat gat caa aat ttc ttg															246	
Asp	Leu	Lys	Leu	Asn	Arg	Gly	Asn	Cys	Glu	His	Asp	Gln	Asn	Phe	Leu	
		55			60					65					70	
gta aag tta atc caa gaa aca gcc aat aca tac ctg ttt gca tca gaa															294	
Val	Lys	Leu	Ile	Gln	Glu	Thr	Ala	Asn	Thr	Tyr	Leu	Phe	Ala	Ser	Glu	
				75				80						85		
aaa gaa aaa gcg atc aaa aac cac caa gca aaa atc gca aga ctt caa															342	
Lys	Glu	Lys	Ala	Ile	Lys	Asn	His	Gln	Ala	Lys	Ile	Ala	Arg	Leu	Gln	
			90					95					100			
aaa gat tta gaa gaa ctc aca cag cat gtg caa caa tcc aat aat ctt															390	
Lys	Asp	Leu	Glu	Glu	Leu	Thr	Gln	His	Val	Gln	Gln	Ser	Asn	Asn	Leu	
		105					110					115				
gat aaa ttg tta gaa aat gga gga cta ttc gtt agt ggc cat gat tat															438	

Asp	Lys	Leu	Leu	Glu	Asn	Gly	Gly	Leu	Phe	Val	Ser	Gly	His	Asp	Tyr	
120						125					130					
aaa	tat	aca	aaa	gat	gat	aac	cca	ata	tat	gtt	gtt	aag	agg	atg	ctt	486
Lys	Tyr	Thr	Lys	Asp	Asp	Asn	Pro	Ile	Tyr	Val	Val	Lys	Arg	Met	Leu	
135					140					145					150	
gat	aac	ctt	gat	agc	tat	aaa	tat	gaa	tca	gac	gac	gtg	cta	gac	gtg	534
Asp	Asn	Leu	Asp	Ser	Tyr	Lys	Tyr	Glu	Ser	Asp	Asp	Val	Leu	Asp	Val	
				155				160						165		
cca	tat	gag	aag	cta	ttg	gaa	ata	agc	att	gct	att	gaa	gac	act	aaa	582
Pro	Tyr	Glu	Lys	Leu	Leu	Glu	Ile	Ser	Ile	Ala	Ile	Glu	Asp	Thr	Lys	
			170					175					180			
aac	ccc	aaa	gac	tac	cct	tat	atc	aac	ctt	aaa	gaa	ctc	aaa	aaa	tta	630
Asn	Pro	Lys	Asp	Tyr	Pro	Tyr	Ile	Asn	Leu	Lys	Glu	Leu	Lys	Lys	Leu	
		185					190					195				
ata	gat	agt	att	att	gat	gat	cat	ggg	tat	atg	gcc	gat	ggc	ttt	ttg	678
Ile	Asp	Ser	Ile	Ile	Asp	Asp	His	Gly	Tyr	Met	Ala	Asp	Gly	Phe	Leu	
	200				205						210					
aat	gaa	tat	tct	aat	agg	gta	tca	aaa	aaa	ggg	ctc	caa	atc	ctt	gct	726
Asn	Glu	Tyr	Ser	Asn	Arg	Val	Ser	Lys	Lys	Gly	Leu	Gln	Ile	Leu	Ala	
215					220					225					230	
aaa	cta	aaa	tcc	atg	tgg	cct	agc	gta	ggg	aaa	ttt	tat	ttc	gcc	tct	774
Lys	Leu	Lys	Ser	Met	Trp	Pro	Ser	Val	Gly	Lys	Phe	Tyr	Phe	Ala	Ser	
				235				240						245		
ttg	aaa	gag	gct	atc	cca	agg	cat	gcc	aaa	gaa	gtt	act	gac	aag	atg	822
Leu	Lys	Glu	Ala	Ile	Pro	Arg	His	Ala	Lys	Glu	Val	Thr	Asp	Lys	Met	
			250					255					260			
att	agc	tct	gaa	gaa	aaa	tct	atc	aaa	gcc	aat	caa	gtc	aaa	ctc	act	870
Ile	Ser	Ser	Glu	Glu	Lys	Ser	Ile	Lys	Ala	Asn	Gln	Val	Lys	Leu	Thr	
		265					270					275				
gaa	gcg	aag	caa	gat	att	gac	aaa	atg	gaa	aaa	atc	att	aaa	gat	tta	918
Glu	Ala	Lys	Gln	Asp	Ile	Asp	Lys	Met	Glu	Lys	Ile	Ile	Lys	Asp	Leu	
	280					285					290					
gaa	agc	aag	aaa	aac	acc	tta	tca	gtg	tat	tta	aaa	ttt	gga	gaa	agt	966
Glu	Ser	Lys	Lys	Asn	Thr	Leu	Ser	Val	Tyr	Leu	Lys	Phe	Gly	Glu	Ser	
295					300					305					310	
ttc	aca	gcg	cat	tat	aag	tgt	caa	aat	ctc	ata	gaa	gtt	gga	gtc	aaa	1014
Phe	Thr	Ala	His	Tyr	Lys	Cys	Gln	Asn	Leu	Ile	Glu	Val	Gly	Val	Lys	
				315					320					325		
acc	gat	aaa	ggc	tcc	tgg	act	ttc	aac	ttt	aac	aga	taa	aat	caggc		1060
Thr	Asp	Lys	Gly	Ser	Trp	Thr	Phe	Asn	Phe	Asn	Arg					
			330					335								
aaatatggac	aatagcacag	acagagcaaa	aatccttata	gaagagctta	aaat											1114
<210>	356															
<211>	338															

<212> PRT

<213> Helicobacter pylori

<400> 356

Met	Phe	Phe	Lys	Thr	Tyr	Gln	Lys	Leu	Leu	Gly	Ala	Ser	Cys	Leu	Thr
1				5					10					15	
Leu	Tyr	Leu	Ala	Gly	Cys	Gly	Ser	Asp	Ser	Ser	Glu	Pro	Leu	Val	Gly
			20					25					30		
Ile	Glu	Lys	Asn	Ser	Phe	Asn	Ser	Thr	Val	Lys	Ile	Ile	Ser	Lys	Thr
		35					40					45			
Asp	Asn	Ile	Glu	Ile	Gln	Asp	Leu	Lys	Leu	Asn	Arg	Gly	Asn	Cys	Glu
	50					55					60				
His	Asp	Gln	Asn	Phe	Leu	Val	Lys	Leu	Ile	Gln	Glu	Thr	Ala	Asn	Thr
65					70					75					80
Tyr	Leu	Phe	Ala	Ser	Glu	Lys	Glu	Lys	Ala	Ile	Lys	Asn	His	Gln	Ala
				85					90					95	
Lys	Ile	Ala	Arg	Leu	Gln	Lys	Asp	Leu	Glu	Glu	Leu	Thr	Gln	His	Val
			100					105					110		
Gln	Gln	Ser	Asn	Asn	Leu	Asp	Lys	Leu	Leu	Glu	Asn	Gly	Gly	Leu	Phe
		115					120					125			
Val	Ser	Gly	His	Asp	Tyr	Lys	Tyr	Thr	Lys	Asp	Asp	Asn	Pro	Ile	Tyr
	130					135					140				
Val	Val	Lys	Arg	Met	Leu	Asp	Asn	Leu	Asp	Ser	Tyr	Lys	Tyr	Glu	Ser
145					150					155					160
Asp	Asp	Val	Leu	Asp	Val	Pro	Tyr	Glu	Lys	Leu	Leu	Glu	Ile	Ser	Ile
				165					170					175	
Ala	Ile	Glu	Asp	Thr	Lys	Asn	Pro	Lys	Asp	Tyr	Pro	Tyr	Ile	Asn	Leu
			180					185					190		
Lys	Glu	Leu	Lys	Lys	Leu	Ile	Asp	Ser	Ile	Ile	Asp	Asp	His	Gly	Tyr
		195					200					205			
Met	Ala	Asp	Gly	Phe	Leu	Asn	Glu	Tyr	Ser	Asn	Arg	Val	Ser	Lys	Lys
	210					215					220				
Gly	Leu	Gln	Ile	Leu	Ala	Lys	Leu	Lys	Ser	Met	Trp	Pro	Ser	Val	Gly
225					230					235					240
Lys	Phe	Tyr	Phe	Ala	Ser	Leu	Lys	Glu	Ala	Ile	Pro	Arg	His	Ala	Lys
				245					250					255	
Glu	Val	Thr	Asp	Lys	Met	Ile	Ser	Ser	Glu	Glu	Lys	Ser	Ile	Lys	Ala
			260					265					270		
Asn	Gln	Val	Lys	Leu	Thr	Glu	Ala	Lys	Gln	Asp	Ile	Asp	Lys	Met	Glu
		275					280					285			
Lys	Ile	Lys	Asp	Leu	Glu	Ser	Lys	Lys	Asn	Thr	Leu	Ser	Val	Tyr	
	290				295					300					
Leu	Lys	Phe	Gly	Glu	Ser	Phe	Thr	Ala	His	Tyr	Lys	Cys	Gln	Asn	Leu
305					310					315					320
Ile	Glu	Val	Gly	Val	Lys	Thr	Asp	Lys	Gly	Ser	Trp	Thr	Phe	Asn	Phe
				325					330					335	
Asn	Arg														

<210> 357

<211> 847

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (94)...(807)

<400> 357

```
gccttgacgc atgtttttga agtttatcct aaagtcaata tttttttaaa aatccttcac 60
aaagaagggg cttaccacaa gcttatttct cgc atg tgt ttg gtc aaa gac aag 114
                               Met Cys Leu Val Lys Asp Lys
                               1                               5

ctc aaa gac att atc agc gtc aaa agc gcg ctt tct ttt tcg tta aaa 162
Leu Lys Asp Ile Ile Ser Val Lys Ser Ala Leu Ser Phe Ser Leu Lys
                               10                               15                               20

ggg gat ttt gac tgc cct tta gaa gaa aac tcg ctc ttt aaa gcc ctc 210
Gly Asp Phe Asp Cys Pro Leu Glu Glu Asn Ser Leu Phe Lys Ala Leu
                               25                               30                               35

caa att tta aag aat ttt tta aaa tca aaa aat ttc tct cat tct gtc 258
Gln Ile Leu Lys Asn Phe Leu Lys Ser Lys Asn Phe Ser His Ser Val
                               40                               45                               50                               55

atc aaa tcc cta gac acc cta gcg att gaa gtg gaa aaa aac atc ccc 306
Ile Lys Ser Leu Asp Thr Leu Ala Ile Glu Val Glu Lys Asn Ile Pro
                               60                               65                               70

act caa gcc gga tta ggc ggt ggg agc act gat gct ggg ggg cta ttg 354
Thr Gln Ala Gly Leu Gly Gly Gly Ser Thr Asp Ala Gly Gly Leu Leu
                               75                               80                               85

tat cat tta aat cag att ttt gac tgg cgt ttg agt tta gaa gag ctt 402
Tyr His Leu Asn Gln Ile Phe Asp Trp Arg Leu Ser Leu Glu Glu Leu
                               90                               95                               100

tat agc atg gga tct tta gtg ggc gcg gac acc aat ttt ttc atc tcg 450
Tyr Ser Met Gly Ser Leu Val Gly Ala Asp Thr Asn Phe Phe Ile Ser
                               105                               110                               115

caa tac aaa agc act aac gcc act tct tat ggc gaa gtc att gaa aat 498
Gln Tyr Lys Ser Thr Asn Ala Thr Ser Tyr Gly Glu Val Ile Glu Asn
                               120                               125                               130                               135

ttt gaa gaa gag cct tta gaa aat cgc cta gaa atc tat gca cca aat 546
Phe Glu Glu Glu Pro Leu Glu Asn Arg Leu Glu Ile Tyr Ala Pro Asn
                               140                               145                               150

cat gtt ttt tgc agc acc aaa gcc gtt tat caa gct tat aag cct gaa 594
His Val Phe Cys Ser Thr Lys Ala Val Tyr Gln Ala Tyr Lys Pro Glu
                               155                               160                               165

act tgt ttt tct caa gct aaa gaa tgg ctt aaa aag ccg agt ttg gaa 642
Thr Cys Phe Ser Gln Ala Lys Glu Trp Leu Lys Lys Pro Ser Leu Glu
                               170                               175                               180

tgc cta aaa act tat gat aga aac gga tta aac gac ctt tta aag ccg 690
Cys Leu Lys Thr Tyr Asp Arg Asn Gly Leu Asn Asp Leu Leu Lys Pro
                               185                               190                               195

gct tta ctc act aac caa gcc tta aaa gat ata gaa agc gaa cta ggc 738
Ala Leu Leu Thr Asn Gln Ala Leu Lys Asp Ile Glu Ser Glu Leu Gly
                               200                               205                               210                               215

aag gag tgg ttt ttt agc ggg agc ggg agc gcg ttt ttt agg cta aag 786
```


Lys Glu Trp Phe Phe Ser Gly Ser Gly Ser Ala Phe Phe Arg Leu Lys
 220 225 230

cct atg caa aaa ggg ggc gaa tgaaactcat tgccagcaac aaaaaagcct 837
 Pro Met Gln Lys Gly Gly Glu
 235

attttgacta 847

<210> 358
 <211> 238
 <212> PRT
 <213> Helicobacter pylori

<400> 358
 Met Cys Leu Val Lys Asp Lys Leu Lys Asp Ile Ile Ser Val Lys Ser
 1 5 10 15
 Ala Leu Ser Phe Ser Leu Lys Gly Asp Phe Asp Cys Pro Leu Glu Glu
 20 25 30
 Asn Ser Leu Phe Lys Ala Leu Gln Ile Leu Lys Asn Phe Leu Lys Ser
 35 40 45
 Lys Asn Phe Ser His Ser Val Ile Lys Ser Leu Asp Thr Leu Ala Ile
 50 55 60
 Glu Val Glu Lys Asn Ile Pro Thr Gln Ala Gly Leu Gly Gly Gly Ser
 65 70 75 80
 Thr Asp Ala Gly Gly Leu Leu Tyr His Leu Asn Gln Ile Phe Asp Trp
 85 90 95
 Arg Leu Ser Leu Glu Glu Leu Tyr Ser Met Gly Ser Leu Val Gly Ala
 100 105 110
 Asp Thr Asn Phe Phe Ile Ser Gln Tyr Lys Ser Thr Asn Ala Thr Ser
 115 120 125
 Tyr Gly Glu Val Ile Glu Asn Phe Glu Glu Glu Pro Leu Glu Asn Arg
 130 135 140
 Leu Glu Ile Tyr Ala Pro Asn His Val Phe Cys Ser Thr Lys Ala Val
 145 150 155 160
 Tyr Gln Ala Tyr Lys Pro Glu Thr Cys Phe Ser Gln Ala Lys Glu Trp
 165 170 175
 Leu Lys Lys Pro Ser Leu Glu Cys Leu Lys Thr Tyr Asp Arg Asn Gly
 180 185 190
 Leu Asn Asp Leu Leu Lys Pro Ala Leu Leu Thr Asn Gln Ala Leu Lys
 195 200 205
 Asp Ile Glu Ser Glu Leu Gly Lys Glu Trp Phe Phe Ser Gly Ser Gly
 210 215 220
 Ser Ala Phe Phe Arg Leu Lys Pro Met Gln Lys Gly Gly Glu
 225 230 235

<210> 359
 <211> 1092
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (28)...(1047)

<400> 359
 tgaaactatc catttaaagg tgtgaaa atg gca aat tta gaa aat tta gac tgg 54
 Met Ala Asn Leu Glu Asn Leu Asp Trp

1										5										
aaa	aat	tta	ggc	ttt	agc	tac	att	aaa	acg	gat	ttt	cgc	ttc	atc	gcc	102				
Lys	Asn	Leu	Gly	Phe	Ser	Tyr	Ile	Lys	Thr	Asp	Phe	Arg	Phe	Ile	Ala					
10					15					20					25					
act	tat	aaa	aac	ggc	tct	tgg	tcg	caa	ggc	gga	ttg	gtg	agc	gaa	aac	150				
Thr	Tyr	Lys	Asn	Gly	Ser	Trp	Ser	Gln	Gly	Gly	Leu	Val	Ser	Glu	Asn					
				30					35					40						
atg	tta	caa	ctc	agc	gaa	ggc	tcg	ccg	gtc	ttg	cac	tac	ggg	cag	gct	198				
Met	Leu	Gln	Leu	Ser	Glu	Gly	Ser	Pro	Val	Leu	His	Tyr	Gly	Gln	Ala					
			45					50					55							
tgt	ttt	gaa	ggc	ttg	aag	gct	tac	cgc	tct	caa	aag	ggg	aaa	gct	tta	246				
Cys	Phe	Glu	Gly	Leu	Lys	Ala	Tyr	Arg	Ser	Gln	Lys	Gly	Lys	Ala	Leu					
		60					65					70								
ctc	ttt	cgc	cct	tta	gaa	aac	gcc	aaa	cgc	ttg	caa	act	tca	tgc	gaa	294				
Leu	Phe	Arg	Pro	Leu	Glu	Asn	Ala	Lys	Arg	Leu	Gln	Thr	Ser	Cys	Glu					
	75					80					85									
aga	ctg	ctc	atg	ccc	aaa	gtg	agc	gaa	gag	ctg	ttt	tta	agg	gca	tgc	342				
Arg	Leu	Leu	Met	Pro	Lys	Val	Ser	Glu	Glu	Leu	Phe	Leu	Arg	Ala	Cys					
	90				95					100					105					
gct	gaa	gtg	gtg	aaa	gcg	aat	caa	aaa	tgg	ctc	gct	cct	tat	aaa	agc	390				
Ala	Glu	Val	Val	Lys	Ala	Asn	Gln	Lys	Trp	Leu	Ala	Pro	Tyr	Lys	Ser					
				110					115					120						
ggg	gcg	agt	ttg	tat	ttg	cgc	cct	ttt	gtc	ata	ggc	gta	ggg	gat	aat	438				
Gly	Ala	Ser	Leu	Tyr	Leu	Arg	Pro	Phe	Val	Ile	Gly	Val	Gly	Asp	Asn					
			125					130					135							
ttg	ggg	gtg	aag	ccg	gct	aat	gaa	tac	ctt	ttt	atc	gtg	ttt	tgt	gcg	486				
Leu	Gly	Val	Lys	Pro	Ala	Asn	Glu	Tyr	Leu	Phe	Ile	Val	Phe	Cys	Ala					
		140					145					150								
cct	gtg	ggg	gcg	tat	ttt	aag	ggg	ggt	ata	gaa	aaa	ggg	ggg	gct	agg	534				
Pro	Val	Gly	Ala	Tyr	Phe	Lys	Gly	Gly	Ile	Glu	Lys	Gly	Gly	Ala	Arg					
	155					160					165									
ttt	atc	act	acg	att	ttt	gat	agg	gcc	gcg	cct	aaa	ggc	acc	ggt	ggg	582				
Phe	Ile	Thr	Thr	Ile	Phe	Asp	Arg	Ala	Ala	Pro	Lys	Gly	Thr	Gly	Gly					
	170				175					180					185					
gtg	aaa	gtg	gga	ggg	aat	tac	gct	gca	agc	ctg	tta	gcc	cat	aaa	atg	630				
Val	Lys	Val	Gly	Gly	Asn	Tyr	Ala	Ala	Ser	Leu	Leu	Ala	His	Lys	Met					
				190					195					200						
gcc	aca	gag	caa	ggc	tat	gat	gat	tgc	att	tat	tta	gac	cct	act	acg	678				
Ala	Thr	Glu	Gln	Gly	Tyr	Asp	Asp	Cys	Ile	Tyr	Leu	Asp	Pro	Thr	Thr					
			205					210					215							
cac	act	aaa	att	gaa	gaa	gtg	ggg	gcg	gcg	aat	ttt	ttt	ggc	atc	acg	726				
His	Thr	Lys	Ile	Glu	Glu	Val	Gly	Ala	Ala	Asn	Phe	Phe	Gly	Ile	Thr					
		220					225					230								
cat	gat	gat	gcc	ttt	atc	acc	ccg	cat	tcg	cca	agc	att	ctg	cca	agc	774				

His	Asp	Asp	Ala	Phe	Ile	Thr	Pro	His	Ser	Pro	Ser	Ile	Leu	Pro	Ser		
235						240					245						
att	acc	aaa	aaa	agc	ttg	atg	gtt	ttg	gct	aaa	gaa	tat	ttg	aac	ctc	822	
Ile	Thr	Lys	Lys	Ser	Leu	Met	Val	Leu	Ala	Lys	Glu	Tyr	Leu	Asn	Leu		
250					255				260					265			
aaa	gta	gaa	gag	agg	gaa	atc	cta	atg	gat	gag	ttg	gat	gcg	ttt	aaa	870	
Lys	Val	Glu	Glu	Arg	Glu	Ile	Leu	Met	Asp	Glu	Leu	Asp	Ala	Phe	Lys		
				270					275					280			
gaa	gct	gga	gcg	tgc	ggg	aca	gct	gcg	atc	att	acg	ccc	att	aaa	gaa	918	
Glu	Ala	Gly	Ala	Cys	Gly	Thr	Ala	Ala	Ile	Ile	Thr	Pro	Ile	Lys	Glu		
			285					290					295				
atc	gtg	cac	aac	aac	aag	tct	tat	ttt	ttt	gaa	gcg	ccg	ggc	cat	att	966	
Ile	Val	His	Asn	Asn	Lys	Ser	Tyr	Phe	Phe	Glu	Ala	Pro	Gly	His	Ile		
		300					305					310					
act	aaa	cga	ctc	tat	gat	ttg	ctt	tta	tcc	atc	caa	caa	ggc	gaa	caa	1014	
Thr	Lys	Arg	Leu	Tyr	Asp	Leu	Leu	Leu	Ser	Ile	Gln	Gln	Gly	Glu	Gln		
	315					320					325						
gaa	gcc	ccc	aaa	gat	tgg	att	ttt	gaa	gtt	ggc	taaaagggtta aaatttatag					1067	
Glu	Ala	Pro	Lys	Asp	Trp	Ile	Phe	Glu	Val	Gly							
330					335				340								
ctgtatgccg cataaaataa gggcg																1092	

<210> 360

<211> 340

<212> PRT

<213> *Helicobacter pylori*

<400> 360

Met	Ala	Asn	Leu	Glu	Asn	Leu	Asp	Trp	Lys	Asn	Leu	Gly	Phe	Ser	Tyr		
1				5					10					15			
Ile	Lys	Thr	Asp	Phe	Arg	Phe	Ile	Ala	Thr	Tyr	Lys	Asn	Gly	Ser	Trp		
			20					25					30				
Ser	Gln	Gly	Gly	Leu	Val	Ser	Glu	Asn	Met	Leu	Gln	Leu	Ser	Glu	Gly		
		35					40				45						
Ser	Pro	Val	Leu	His	Tyr	Gly	Gln	Ala	Cys	Phe	Glu	Gly	Leu	Lys	Ala		
	50					55					60						
Tyr	Arg	Ser	Gln	Lys	Gly	Lys	Ala	Leu	Leu	Phe	Arg	Pro	Leu	Glu	Asn		
65					70					75					80		
Ala	Lys	Arg	Leu	Gln	Thr	Ser	Cys	Glu	Arg	Leu	Leu	Met	Pro	Lys	Val		
			85					90						95			
Ser	Glu	Glu	Leu	Phe	Leu	Arg	Ala	Cys	Ala	Glu	Val	Val	Lys	Ala	Asn		
			100					105					110				
Gln	Lys	Trp	Leu	Ala	Pro	Tyr	Lys	Ser	Gly	Ala	Ser	Leu	Tyr	Leu	Arg		
		115					120					125					
Pro	Phe	Val	Ile	Gly	Val	Gly	Asp	Asn	Leu	Gly	Val	Lys	Pro	Ala	Asn		
		130				135					140						
Glu	Tyr	Leu	Phe	Ile	Val	Phe	Cys	Ala	Pro	Val	Gly	Ala	Tyr	Phe	Lys		
145					150					155					160		
Gly	Gly	Ile	Glu	Lys	Gly	Gly	Ala	Arg	Phe	Ile	Thr	Thr	Ile	Phe	Asp		
				165					170					175			
Arg	Ala	Ala	Pro	Lys	Gly	Thr	Gly	Gly	Val	Lys	Val	Gly	Gly	Asn	Tyr		
			180					185					190				

aac att aga gaa tac gcc cta aat ggg gct ttg cat tac gct aat gcg	390
Asn Ile Arg Glu Tyr Ala Leu Asn Gly Ala Leu His Tyr Ala Asn Ala	
105 110 115 120	
att tta cac cac acg agc tac act gaa tgc atc gcc ata ggc att aca	438
Ile Leu His His Thr Ser Tyr Thr Glu Cys Ile Ala Ile Gly Ile Thr	
125 130 135	
ggc tat aaa gac aat aag ggc ggc ata tgc tct caa atc gct gtc tat	486
Gly Tyr Lys Asp Asn Lys Gly Gly Ile Cys Ser Gln Ile Ala Val Tyr	
140 145 150	
tat gtg aat aaa agc aat cta ggc atg ggg ata gat gtt tca aaa ggc	534
Tyr Val Asn Lys Ser Asn Leu Gly Met Gly Ile Asp Val Ser Lys Gly	
155 160 165	
gag caa ggt tat agc gat ctc tcc ttt tta agc cgt aag cat ttt aac	582
Glu Gln Gly Tyr Ser Asp Leu Ser Phe Leu Ser Arg Lys His Phe Asn	
170 175 180	
gac ttt att aaa cga gta gac acc ctt tct tta agc gat gaa gat tta	630
Asp Phe Ile Lys Arg Val Asp Thr Leu Ser Leu Ser Asp Glu Asp Leu	
185 190 195 200	
gag cgc att aga gaa aag aaa aac caa gaa ata gaa gac tgc tta atg	678
Glu Arg Ile Arg Glu Lys Lys Asn Gln Glu Ile Glu Asp Cys Leu Met	
205 210 215	
cgg ctc aac aac aat att tac aac aaa gaa aag aat ttt tta agc gaa	726
Arg Leu Asn Asn Asn Ile Tyr Asn Lys Glu Lys Asn Phe Leu Ser Glu	
220 225 230	
cac aat cgg gta tat tta gtg att gcg agc att atc gct aat tta ggc	774
His Asn Arg Val Tyr Leu Val Ile Ala Ser Ile Ile Ala Asn Leu Gly	
235 240 245	
atc cct aat ttg gta acc ccc cta aac aaa gaa gat cta aaa tcc agc	822
Ile Pro Asn Leu Val Thr Pro Leu Asn Lys Glu Asp Leu Lys Ser Ser	
250 255 260	
gat gag gtc cat caa aga gat ggc gac atc atg ctc aga aaa atc caa	870
Asp Glu Val His Gln Arg Asp Gly Asp Ile Met Leu Arg Lys Ile Gln	
265 270 275 280	
tcc ttt tta gag aat aag gat ttg tct cca gag aaa agg caa agc att	918
Ser Phe Leu Glu Asn Lys Asp Leu Ser Pro Glu Lys Arg Gln Ser Ile	
285 290 295	
att tct tca tta gag act tta tta aga aac gaa aac aac aac aaa gcc	966
Ile Ser Ser Leu Glu Thr Leu Leu Arg Asn Glu Asn Asn Asn Lys Ala	
300 305 310	
act aat ggc gaa agc tgt ttg aag cgt tgt ttt agt gag att gtg gat	1014
Thr Asn Gly Glu Ser Cys Leu Lys Arg Cys Phe Ser Glu Ile Val Asp	
315 320 325	
agt ttg ggc att tat tat aaa atc ggt ctt agc acg gat ttt acc ggt	1062
Ser Leu Gly Ile Tyr Tyr Lys Ile Gly Leu Ser Thr Asp Phe Thr Gly	

330	335	340	
aaa ttg ttc aat gaa atg tat cgc tgg ctg ggt ttc acg aaa gac caa	1110		
Lys Leu Phe Asn Glu Met Tyr Arg Trp Leu Gly Phe Thr Lys Asp Gln			
345 350 355 360			
tta aac gat gtg gtg ctc aca ccc cct tat gtc gcc acg ctt tta gct	1158		
Leu Asn Asp Val Val Leu Thr Pro Pro Tyr Val Ala Thr Leu Leu Ala			
365 370 375			
aga ctt tct aaa gtc aat aag gat agt ttc gtg tgg gat ttt gcc acc	1206		
Arg Leu Ser Lys Val Asn Lys Asp Ser Phe Val Trp Asp Phe Ala Thr			
380 385 390			
gga agc gct ggg cta tta gtc gca agc atg aat ttg atg ata gaa gac	1254		
Gly Ser Ala Gly Leu Leu Val Ala Ser Met Asn Leu Met Ile Glu Asp			
395 400 405			
gct aaa aag cgt atc act agt cca gag gaa tta gag caa aaa atc gcc	1302		
Ala Lys Lys Arg Ile Thr Ser Pro Glu Glu Leu Glu Gln Lys Ile Ala			
410 415 420			
cac att aaa gcc aag caa ctt tta ggg ata gaa atc tta tcg gat atc	1350		
His Ile Lys Ala Lys Gln Leu Leu Gly Ile Glu Ile Leu Ser Asp Ile			
425 430 435 440			
cat act tta gcg gtg tta aac atg att tta atg ggc gat ggg agc agt	1398		
His Thr Leu Ala Val Leu Asn Met Ile Leu Met Gly Asp Gly Ser Ser			
445 450 455			
caa atc tta aac caa gac ggc ttg agc ggt ttt gat ggc aaa gtc aat	1446		
Gln Ile Leu Asn Gln Asp Gly Leu Ser Gly Phe Asp Gly Lys Val Asn			
460 465 470			
aac gaa gcg ttt aag gct aat gcc ttt gtt tta aac ccg cct tat tcc	1494		
Asn Glu Ala Phe Lys Ala Asn Ala Phe Val Leu Asn Pro Pro Tyr Ser			
475 480 485			
gct agc ggt aat ggc atg gtg ttt gtg gag cag gct tta gaa aaa atg	1542		
Ala Ser Gly Asn Gly Met Val Phe Val Glu Gln Ala Leu Glu Lys Met			
490 495 500			
caa agc ggt tat gcg agc gtg atc atc caa tca agc gcc ggc agt ggt	1590		
Gln Ser Gly Tyr Ala Ser Val Ile Ile Gln Ser Ser Ala Gly Ser Gly			
505 510 515 520			
aaa gcc aaa gaa tac aat gta agg att ttg gaa aaa cac acg ctt tta	1638		
Lys Ala Lys Glu Tyr Asn Val Arg Ile Leu Glu Lys His Thr Leu Leu			
525 530 535			
gcg agc att aaa atg cct tta gat tta ttc atc ggt aaa agc agc gtt	1686		
Ala Ser Ile Lys Met Pro Leu Asp Leu Phe Ile Gly Lys Ser Ser Val			
540 545 550			
caa acc cat atc tat gtt ttt agg gtc aat gaa aag cat gac gct aag	1734		
Gln Thr His Ile Tyr Val Phe Arg Val Asn Glu Lys His Asp Ala Lys			
555 560 565			
caa agg gtg aaa ttt att aat ttc agt aac gac ggc tac gct aga gcg	1782		

Gln	Arg	Val	Lys	Phe	Ile	Asn	Phe	Ser	Asn	Asp	Gly	Tyr	Ala	Arg	Ala		
570						575					580						
aat	cgc	aaa	aaa	gcc	aaa	gcc	agc	cac	aat	tta	aaa	gac	acg	cat	aac	1830	
Asn	Arg	Lys	Lys	Ala	Lys	Ala	Ser	His	Asn	Leu	Lys	Asp	Thr	His	Asn		
585					590					595					600		
gcc	aaa	gag	cgc	tac	aac	gaa	gtc	gtg	gat	tta	gtc	cat	att	ggc	caa	1878	
Ala	Lys	Glu	Arg	Tyr	Asn	Glu	Val	Val	Asp	Leu	Val	His	Ile	Gly	Gln		
				605					610					615			
tca	tgt	ttg	aaa	ttt	cta	agc	gaa	gat	gac	tat	tat	gaa	aac	acc	ata	1926	
Ser	Cys	Leu	Lys	Phe	Leu	Ser	Glu	Asp	Asp	Tyr	Tyr	Glu	Asn	Thr	Ile		
			620					625					630				
gat	ccc	aaa	aac	ggg	agc	gat	tgg	aac	caa	aac	aaa	ccc	act	gac	acc	1974	
Asp	Pro	Lys	Asn	Gly	Ser	Asp	Trp	Asn	Gln	Asn	Lys	Pro	Thr	Asp	Thr		
		635					640					645					
aaa	ccc	gaa	tta	gag	gat	ttt	aaa	aga	acg	ata	gcc	gat	tac	ctt	tct	2022	
Lys	Pro	Glu	Leu	Glu	Asp	Phe	Lys	Arg	Thr	Ile	Ala	Asp	Tyr	Leu	Ser		
	650					655					660						
tat	gaa	gta	agc	ttg	att	tta	aaa	aac	caa	atg	ccc	cca	aag	cga		2067	
Tyr	Glu	Val	Ser	Leu	Ile	Leu	Lys	Asn	Gln	Met	Pro	Pro	Lys	Arg			
665					670					675							
taggccccct	taatagccaa	ctcaacgcta	ttaagtgggg	cgag												2111	

<210> 362

<211> 679

<212> PRT

<213> Helicobacter pylori

<400> 362

Met	Asn	Lys	Val	Gln	Ser	Ile	Asp	Pro	Leu	Ile	Ala	Asp	Lys	Phe	Asn		
1				5					10					15			
Asn	Glu	Leu	Arg	Ser	Tyr	Asn	Leu	Glu	Tyr	Lys	Leu	Glu	Gln	Glu	Ser		
		20					25						30				
Leu	Asn	Lys	Glu	Ile	Asp	Glu	Ala	Leu	Lys	Asn	Tyr	Ala	Ser	Lys	Asn		
	35						40					45					
Gly	Gly	Leu	Gly	Gly	Asn	Arg	Pro	Asp	Val	Lys	Leu	Leu	Leu	Asn	Thr		
50					55						60						
Gln	Asp	Pro	Asn	Arg	Arg	Val	Pro	Ile	Leu	Ile	Glu	Tyr	Lys	Gly	Leu		
65				70					75					80			
Lys	Asp	Lys	Leu	Ile	Lys	Leu	Asp	Lys	Asn	Lys	Leu	Val	Glu	Asn	Phe		
			85					90					95				
Lys	Asn	His	Glu	Pro	His	Tyr	Lys	Asn	Ile	Arg	Glu	Tyr	Ala	Leu	Asn		
	100						105						110				
Gly	Ala	Leu	His	Tyr	Ala	Asn	Ala	Ile	Leu	His	His	Thr	Ser	Tyr	Thr		
	115					120						125					
Glu	Cys	Ile	Ala	Ile	Gly	Ile	Thr	Gly	Tyr	Lys	Asp	Asn	Lys	Gly	Gly		
	130				135						140						
Ile	Cys	Ser	Gln	Ile	Ala	Val	Tyr	Tyr	Val	Asn	Lys	Ser	Asn	Leu	Gly		
145				150					155					160			
Met	Gly	Ile	Asp	Val	Ser	Lys	Gly	Glu	Gln	Gly	Tyr	Ser	Asp	Leu	Ser		
			165					170						175			
Phe	Leu	Ser	Arg	Lys	His	Phe	Asn	Asp	Phe	Ile	Lys	Arg	Val	Asp	Thr		
		180					185						190				

Leu	Ser	Leu	Ser	Asp	Glu	Asp	Leu	Glu	Arg	Ile	Arg	Glu	Lys	Lys	Asn
		195					200					205			
Gln	Glu	Ile	Glu	Asp	Cys	Leu	Met	Arg	Leu	Asn	Asn	Asn	Ile	Tyr	Asn
		210				215					220				
Lys	Glu	Lys	Asn	Phe	Leu	Ser	Glu	His	Asn	Arg	Val	Tyr	Leu	Val	Ile
225					230					235					240
Ala	Ser	Ile	Ile	Ala	Asn	Leu	Gly	Ile	Pro	Asn	Leu	Val	Thr	Pro	Leu
				245					250					255	
Asn	Lys	Glu	Asp	Leu	Lys	Ser	Ser	Asp	Glu	Val	His	Gln	Arg	Asp	Gly
			260					265					270		
Asp	Ile	Met	Leu	Arg	Lys	Ile	Gln	Ser	Phe	Leu	Glu	Asn	Lys	Asp	Leu
		275					280					285			
Ser	Pro	Glu	Lys	Arg	Gln	Ser	Ile	Ile	Ser	Ser	Leu	Glu	Thr	Leu	Leu
	290					295					300				
Arg	Asn	Glu	Asn	Asn	Asn	Lys	Ala	Thr	Asn	Gly	Glu	Ser	Cys	Leu	Lys
305					310					315					320
Arg	Cys	Phe	Ser	Glu	Ile	Val	Asp	Ser	Leu	Gly	Ile	Tyr	Tyr	Lys	Ile
				325					330					335	
Gly	Leu	Ser	Thr	Asp	Phe	Thr	Gly	Lys	Leu	Phe	Asn	Glu	Met	Tyr	Arg
			340					345					350		
Trp	Leu	Gly	Phe	Thr	Lys	Asp	Gln	Leu	Asn	Asp	Val	Val	Leu	Thr	Pro
		355					360					365			
Pro	Tyr	Val	Ala	Thr	Leu	Leu	Ala	Arg	Leu	Ser	Lys	Val	Asn	Lys	Asp
	370					375					380				
Ser	Phe	Val	Trp	Asp	Phe	Ala	Thr	Gly	Ser	Ala	Gly	Leu	Leu	Val	Ala
385					390					395					400
Ser	Met	Asn	Leu	Met	Ile	Glu	Asp	Ala	Lys	Lys	Arg	Ile	Thr	Ser	Pro
				405					410					415	
Glu	Glu	Leu	Glu	Gln	Lys	Ile	Ala	His	Ile	Lys	Ala	Lys	Gln	Leu	Leu
			420					425					430		
Gly	Ile	Glu	Ile	Leu	Ser	Asp	Ile	His	Thr	Leu	Ala	Val	Leu	Asn	Met
		435					440					445			
Ile	Leu	Met	Gly	Asp	Gly	Ser	Gln	Ile	Leu	Asn	Gln	Asp	Gly	Leu	
		450				455				460					
Ser	Gly	Phe	Asp	Gly	Lys	Val	Asn	Asn	Glu	Ala	Phe	Lys	Ala	Asn	Ala
465					470					475					480
Phe	Val	Leu	Asn	Pro	Pro	Tyr	Ser	Ala	Ser	Gly	Asn	Gly	Met	Val	Phe
				485					490					495	
Val	Glu	Gln	Ala	Leu	Glu	Lys	Met	Gln	Ser	Gly	Tyr	Ala	Ser	Val	Ile
			500					505					510		
Ile	Gln	Ser	Ser	Ala	Gly	Ser	Gly	Lys	Ala	Lys	Glu	Tyr	Asn	Val	Arg
		515					520					525			
Ile	Leu	Glu	Lys	His	Thr	Leu	Leu	Ala	Ser	Ile	Lys	Met	Pro	Leu	Asp
		530				535					540				
Leu	Phe	Ile	Gly	Lys	Ser	Ser	Val	Gln	Thr	His	Ile	Tyr	Val	Phe	Arg
545					550					555					560
Val	Asn	Glu	Lys	His	Asp	Ala	Lys	Gln	Arg	Val	Lys	Phe	Ile	Asn	Phe
				565					570					575	
Ser	Asn	Asp	Gly	Tyr	Ala	Arg	Ala	Asn	Arg	Lys	Lys	Ala	Lys	Ala	Ser
			580					585					590		
His	Asn	Leu	Lys	Asp	Thr	His	Asn	Ala	Lys	Glu	Arg	Tyr	Asn	Glu	Val
		595					600					605			
Val	Asp	Leu	Val	His	Ile	Gly	Gln	Ser	Cys	Leu	Lys	Phe	Leu	Ser	Glu
		610				615					620				
Asp	Asp	Tyr	Tyr	Glu	Asn	Thr	Ile	Asp	Pro	Lys	Asn	Gly	Ser	Asp	Trp
625					630					635					640
Asn	Gln	Asn	Lys	Pro	Thr	Asp	Thr	Lys	Pro	Glu	Leu	Glu	Asp	Phe	Lys
				645					650					655	
Arg	Thr	Ile	Ala	Asp	Tyr	Leu	Ser	Tyr	Glu	Val	Ser	Leu	Ile	Leu	Lys

Asn Gln Met Pro Pro Lys Arg

```
<210> 363
<211> 644
<212> DNA
<213> Helicobacter pylori
```

<400> 363																		
atccttttgat		ttcaaaggct		taaa		atg		tat	gtg	gtg	tta	gaa	ggc	ggt	gat	51		
						Met		Tyr	Val	Val	Leu	Glu	Gly	Val	Asp			
						1					5							
ggc		gcg	ggc	aaa	agc	act	caa	gta	gaa	tta	tta	aaa	gac	cgg	ttt	aaa	99	
Gly		Ala	Gly	Lys	Ser	Thr	Gln	Val	Glu	Leu	Leu	Lys	Asp	Arg	Phe	Lys		
10						15					20							
aac		gcc	ctt	ttt	acc	aaa	gag	cca	ggg	ggg	acg	aga	atg	ggc	gag	agt	147	
Asn		Ala	Leu	Phe	Thr	Lys	Glu	Pro	Gly	Gly	Thr	Arg	Met	Gly	Glu	Ser		
					30					35								
tta		agg	cgt	atc	gct	ttg	aat	gaa	aac	att	agc	gaa	ttg	gct	aga	gcg	195	
Leu		Arg	Arg	Ile	Ala	Leu	Asn	Glu	Asn	Ile	Ser	Glu	Leu	Ala	Arg	Ala		
				45					50									
ttt		tta	ttc	tta	agc	gat	agg	gct	gag	cat	aca	gaa	agc	gtg	ata	aaa	243	
Phe		Leu	Phe	Leu	Ser	Asp	Arg	Ala	Glu	His	Thr	Glu	Ser	Val	Ile	Lys		
			60					65										
ccg		gca	ttg	aaa	gaa	aaa	aag	ctc	atc	att	agc	gac	agg	agc	ttg	atc	291	
Pro		Ala	Leu	Lys	Glu	Lys	Lys	Leu	Ile	Ile	Ser	Asp	Arg	Ser	Leu	Ile		
		75					80						85					
tct		ggc	atg	gct	tat	agc	caa	ttt	tca	agc	tta	gaa	tta	aac	ctg	ctt	339	
Ser		Gly	Met	Ala	Tyr	Ser	Gln	Phe	Ser	Ser	Leu	Glu	Leu	Asn	Leu	Leu		
90						95					100						105	
gcc		acc	caa	agc	gtc	ttg	cct	gca	aaa	atc	att	ctt	tta	ctc	ata	gac	387	
Ala		Thr	Gln	Ser	Val	Leu	Pro	Ala	Lys	Ile	Ile	Leu	Leu	Leu	Ile	Asp		
				110						115						120		
aaa		gag	ggc	tta	aaa	cag	cgc	tta	agc	ctt	aaa	agt	tta	gat	aaa	ata	435	
Lys		Glu	Gly	Leu	Lys	Gln	Arg	Leu	Ser	Leu	Lys	Ser	Leu	Asp	Lys	Ile		
				125					130						135			
gaa		aac	caa	ggc	ata	gaa	aaa	tta	ctt	cat	atc	cag	caa	aag	ctc	aaa	483	
Glu		Asn	Gln	Gly	Ile	Glu	Lys	Leu	Leu	His	Ile	Gln	Gln	Lys	Leu	Lys		
			140					145						150				
acc		cac	gct	tat	gcg	tta	caa	gaa	aaa	ttt	ggg	tgc	gaa	gtt	ttg	gaa	531	
Thr		His	Ala	Tyr	Ala	Leu	Gln	Glu	Lys	Phe	Gly	Cys	Glu	Val	Leu	Glu		
		155					160						165					

tta gac gct aaa gaa agc gtt aaa aac ttg cac gaa aaa atc gcc gct 579
 Leu Asp Ala Lys Glu Ser Val Lys Asn Leu His Glu Lys Ile Ala Ala
 170 175 180 185

ttt ata aaa tgc gct gtt taacctgttt gaagctttct tttaagcctc 627
 Phe Ile Lys Cys Ala Val
 190

tttgcccaaa ttgcttg 644

<210> 364
 <211> 191
 <212> PRT
 <213> Helicobacter pylori

<400> 364
 Met Tyr Val Val Leu Glu Gly Val Asp Gly Ala Gly Lys Ser Thr Gln
 1 5 10 15
 Val Glu Leu Leu Lys Asp Arg Phe Lys Asn Ala Leu Phe Thr Lys Glu
 20 25 30
 Pro Gly Gly Thr Arg Met Gly Glu Ser Leu Arg Arg Ile Ala Leu Asn
 35 40 45
 Glu Asn Ile Ser Glu Leu Ala Arg Ala Phe Leu Phe Leu Ser Asp Arg
 50 55 60
 Ala Glu His Thr Glu Ser Val Ile Lys Pro Ala Leu Lys Glu Lys Lys
 65 70 75 80
 Leu Ile Ile Ser Asp Arg Ser Leu Ile Ser Gly Met Ala Tyr Ser Gln
 85 90 95
 Phe Ser Ser Leu Glu Leu Asn Leu Leu Ala Thr Gln Ser Val Leu Pro
 100 105 110
 Ala Lys Ile Ile Leu Leu Leu Ile Asp Lys Glu Gly Leu Lys Gln Arg
 115 120 125
 Leu Ser Leu Lys Ser Leu Asp Lys Ile Glu Asn Gln Gly Ile Glu Lys
 130 135 140
 Leu Leu His Ile Gln Gln Lys Leu Lys Thr His Ala Tyr Ala Leu Gln
 145 150 155 160
 Glu Lys Phe Gly Cys Glu Val Leu Glu Leu Asp Ala Lys Glu Ser Val
 165 170 175
 Lys Asn Leu His Glu Lys Ile Ala Ala Phe Ile Lys Cys Ala Val
 180 185 190

<210> 365
 <211> 620
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (23) ... (583)

<400> 365
 gcaaatttta taaaggacat tc atg aaa ttg gtt tta ggc atc agt gga gcg 52
 Met Lys Leu Val Leu Gly Ile Ser Gly Ala
 1 5 10
 agc ggg ata ccc cta gcc ttg cgg ttt tta gaa aaa tta ccc aaa gaa 100
 Ser Gly Ile Pro Leu Ala Leu Arg Phe Leu Glu Lys Leu Pro Lys Glu
 15 20 25

att gaa gtt ttt gtc gtg gcg tct aaa aac gcg cat gtc gtg gcg tta	148
Ile Glu Val Phe Val Val Ala Ser Lys Asn Ala His Val Val Ala Leu	
30 35 40	
gaa gaa tct aat att aac ctt aaa aac gcc atg aaa gat tta cgg cct	196
Glu Glu Ser Asn Ile Asn Leu Lys Asn Ala Met Lys Asp Leu Arg Pro	
45 50 55	
agt ggt act ttt ttc aac gag caa gac atc cat gcg agc atc gct tca	244
Ser Gly Thr Phe Phe Asn Glu Gln Asp Ile His Ala Ser Ile Ala Ser	
60 65 70	
ggg agt tat ggt atc cat aaa atg gcg atc att cca gcg agc atg gac	292
Gly Ser Tyr Gly Ile His Lys Met Ala Ile Ile Pro Ala Ser Met Asp	
75 80 85 90	
atg gtg gct aaa atc gcg cat ggc ttt ggg ggg gat ttg att tct agg	340
Met Val Ala Lys Ile Ala His Gly Phe Gly Gly Asp Leu Ile Ser Arg	
95 100 105	
agt gcg tct gtg atg ctt aaa gaa aag cgc ccc tta ctc att gcc cct	388
Ser Ala Ser Val Met Leu Lys Glu Lys Arg Pro Leu Leu Ile Ala Pro	
110 115 120	
aga gaa atg cct tta agc gct atc atg tta gaa aat ttg ctc aaa ctc	436
Arg Glu Met Pro Leu Ser Ala Ile Met Leu Glu Asn Leu Leu Lys Leu	
125 130 135	
tcc cat tct aat gca atc att gcg ccg ccg atg atg act tat tac acc	484
Ser His Ser Asn Ala Ile Ile Ala Pro Pro Met Met Thr Tyr Tyr Thr	
140 145 150	
cag agc aag act tta gaa gcg atg caa gat ttt tta gtg ggg aag tgg	532
Gln Ser Lys Thr Leu Glu Ala Met Gln Asp Phe Leu Val Gly Lys Trp	
155 160 165 170	
ttt gac agc tta ggg ata gaa aat gac tta tac cca cga tgg gga atg	580
Phe Asp Ser Leu Gly Ile Glu Asn Asp Leu Tyr Pro Arg Trp Gly Met	
175 180 185	
aac tgatgcaaaa aatcggcatt tacccgggca cttttga	620
Asn	

<210> 366

<211> 187

<212> PRT

<213> *Helicobacter pylori*

<400> 366

Met Lys Leu Val Leu Gly Ile Ser Gly Ala Ser Gly Ile Pro Leu Ala	
1 5 10 15	
Leu Arg Phe Leu Glu Lys Leu Pro Lys Glu Ile Glu Val Phe Val Val	
20 25 30	
Ala Ser Lys Asn Ala His Val Val Ala Leu Glu Glu Ser Asn Ile Asn	
35 40 45	
Leu Lys Asn Ala Met Lys Asp Leu Arg Pro Ser Gly Thr Phe Phe Asn	

50		55		60
Glu Gln Asp Ile His	Ala Ser Ile Ala Ser Gly Ser Tyr Gly Ile His			
65	70	75	80	
Lys Met Ala Ile Ile	Pro Ala Ser Met Asp Met Val Ala Lys Ile Ala			
	85	90	95	
His Gly Phe Gly Gly	Asp Leu Ile Ser Arg Ser Ala Ser Val Met Leu			
	100	105	110	
Lys Glu Lys Arg Pro	Leu Leu Ile Ala Pro Arg Glu Met Pro Leu Ser			
	115	120	125	
Ala Ile Met Leu Glu	Asn Leu Leu Lys Leu Ser His Ser Asn Ala Ile			
	130	135	140	
Ile Ala Pro Pro Met	Met Thr Tyr Tyr Thr Gln Ser Lys Thr Leu Glu			
145	150	155	160	
Ala Met Gln Asp Phe	Leu Val Gly Lys Trp Phe Asp Ser Leu Gly Ile			
	165	170	175	
Glu Asn Asp Leu Tyr	Pro Arg Trp Gly Met Asn			
	180	185		

<210> 367
 <211> 341
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (13)...(309)

<400> 367
 ctccctgaag cg atg ctc gca tgg atg tct tgc tcg ttg aaa aaa gta cca 51
 Met Leu Ala Trp Met Ser Cys Ser Leu Lys Lys Val Pro
 1 5 10

cta ggc cgt aaa tct ttc atg gcg ttt tta agg tta ata tta gat tct 99
 Leu Gly Arg Lys Ser Phe Met Ala Phe Leu Arg Leu Ile Leu Asp Ser
 15 20 25

tct aac gcc acg aca tgc gcg ttt tta gac gcc acg aca aaa act tca 147
 Ser Asn Ala Thr Thr Cys Ala Phe Leu Asp Ala Thr Thr Lys Thr Ser
 30 35 40 45

att tct ttg ggt aat ttt tct aaa aac cgc aag gct agg ggt atc ccg 195
 Ile Ser Leu Gly Asn Phe Ser Lys Asn Arg Lys Ala Arg Gly Ile Pro
 50 55 60

ctc gct cca ctg atg cct aaa acc aat ttc atg aat gtc ctt tat aag 243
 Leu Ala Pro Leu Met Pro Lys Thr Asn Phe Met Asn Val Leu Tyr Lys
 65 70 75

att tgc gct tta gag ctg ctc aac act ttt gct ttg agt att tta ttg 291
 Ile Cys Ala Leu Glu Leu Leu Asn Thr Phe Ala Leu Ser Ile Leu Leu
 80 85 90

ctt tct aaa ttt ttc gct tgaatgattt gattaagcgc gccattttct 339
 Leu Ser Lys Phe Phe Ala
 95

ag 341

<210> 368
 <211> 99
 <212> PRT
 <213> Helicobacter pylori

<400> 368
 Met Leu Ala Trp Met Ser Cys Ser Leu Lys Lys Val Pro Leu Gly Arg
 1 5 10 15
 Lys Ser Phe Met Ala Phe Leu Arg Leu Ile Leu Asp Ser Ser Asn Ala
 20 25 30
 Thr Thr Cys Ala Phe Leu Asp Ala Thr Thr Lys Thr Ser Ile Ser Leu
 35 40 45
 Gly Asn Phe Ser Lys Asn Arg Lys Ala Arg Gly Ile Pro Leu Ala Pro
 50 55 60
 Leu Met Pro Lys Thr Asn Phe Met Asn Val Leu Tyr Lys Ile Cys Ala
 65 70 75 80
 Leu Glu Leu Leu Asn Thr Phe Ala Leu Ser Ile Leu Leu Leu Ser Lys
 85 90 95
 Phe Phe Ala

<210> 369
 <211> 858
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (85)...(822)

<400> 369
 ggcgccaacg attttaatga tcctcattgt gatttttagtg gttgtcaagc ctttttaaag 60
 acaagccatg aaaaaagaaa agtc atg aaa aaa gaa aag cat ctc aag caa 111
 Met Lys Lys Glu Lys His Leu Lys Gln
 1 5
 gaa aaa atc atc aac atg ttt gat gat ata gcc agc tct tac gat caa 159
 Glu Lys Ile Ile Asn Met Phe Asp Asp Ile Ala Ser Ser Tyr Asp Gln 25
 10 15 20
 gcc aac cgc ttg atg agt ttt ggc tta gac gtt aaa tgg cga gaa agg 207
 Ala Asn Arg Leu Met Ser Phe Gly Leu Asp Val Lys Trp Arg Glu Arg 40
 30 35 40
 gct tgc gag cat gcg ttt tta ttt tta gaa aac aag aaa gcg tta agg 255
 Ala Cys Glu His Ala Phe Leu Phe Leu Glu Asn Lys Lys Ala Leu Arg 55
 45 50 55
 ctt gtg gat gtg gca tgc ggg acg ggg gat atg ctt gtg gct tgg caa 303
 Leu Val Asp Val Ala Cys Gly Thr Gly Asp Met Leu Val Ala Trp Gln 70
 60 65 70
 aaa agc gct ctc aat tgc ggt ata gag ttt aag gaa tgt ttg ggg att 351
 Lys Ser Ala Leu Asn Cys Gly Ile Glu Phe Lys Glu Cys Leu Gly Ile 85
 75 80 85
 gac ccc tct aat aac atg ctt gaa tta gcc atc aaa aaa tgt gaa gag 399
 Asp Pro Ser Asn Asn Met Leu Glu Leu Ala Ile Lys Lys Cys Glu Glu

90	95	100	105	
ctt gaa aac aaa gct tct ttc atc caa gct caa gcc aaa gat tta aaa				447
Leu Glu Asn Lys Ala Ser Phe Ile Gln Ala Gln Ala Lys Asp Leu Lys	110	115	120	
ggc gtt gaa aat aac agc gtg gat atc ctc tct att gcg tat ggc ttg				495
Gly Val Glu Asn Asn Ser Val Asp Ile Leu Ser Ile Ala Tyr Gly Leu	125	130	135	
cgt aat gtc gtg gaa aga caa gag gcc tta aaa gag ttt ttt agg gtg				543
Arg Asn Val Val Glu Arg Gln Glu Ala Leu Lys Glu Phe Phe Arg Val	140	145	150	
tta aaa ccc agg ggc gtt tta gtg att tta gaa ttt tta aaa aaa gac				591
Leu Lys Pro Arg Gly Val Leu Val Ile Leu Glu Phe Leu Lys Lys Asp	155	160	165	
aac ccc aca tgg ctg gat aaa atc tca ggg ttt tac acg aat aag gtt				639
Asn Pro Thr Trp Leu Asp Lys Ile Ser Gly Phe Tyr Thr Asn Lys Val	170	175	180	185
ttg cct tta gtg gga ggg gct atc agt aag aat tat ggt gct tat tct				687
Leu Pro Leu Val Gly Gly Ala Ile Ser Lys Asn Tyr Gly Ala Tyr Ser	190	195	200	
tat tta ccg caa tcc att gag ggg ttt ttg agt tta gag ggt ttg aag				735
Tyr Leu Pro Gln Ser Ile Glu Gly Phe Leu Ser Leu Glu Gly Leu Lys	205	210	215	
cat gaa tta aga aac gca ggg ttt gag att tta agg act gaa gat tct				783
His Glu Leu Arg Asn Ala Gly Phe Glu Ile Leu Arg Thr Glu Asp Ser	220	225	230	
atc gct caa att tca acg acc atg ctt gtt aaa aaa aac taaaggaatg				832
Ile Ala Gln Ile Ser Thr Thr Met Leu Val Lys Lys Asn	235	240	245	
ttatgcaaga tgaattatgtt gaaacc				858

<210> 370

<211> 246

<212> PRT

<213> Helicobacter pylori

<400> 370

Met Lys Lys Glu Lys His Leu Lys Gln Glu Lys Ile Ile Asn Met Phe																
1 5 10 15																
Asp Asp Ile Ala Ser Ser Tyr Asp Gln Ala Asn Arg Leu Met Ser Phe																
20 25 30																
Gly Leu Asp Val Lys Trp Arg Glu Arg Ala Cys Glu His Ala Phe Leu																
35 40 45																
Phe Leu Glu Asn Lys Lys Ala Leu Arg Leu Val Asp Val Ala Cys Gly																
50 55 60																
Thr Gly Asp Met Leu Val Ala Trp Gln Lys Ser Ala Leu Asn Cys Gly																
65 70 75 80																
Ile Glu Phe Lys Glu Cys Leu Gly Ile Asp Pro Ser Asn Asn Met Leu																
85 90 95																
Glu Leu Ala Ile Lys Lys Cys Glu Glu Leu Glu Asn Lys Ala Ser Phe																

			100					105				110			
Ile	Gln	Ala	Gln	Ala	Lys	Asp	Leu	Lys	Gly	Val	Glu	Asn	Asn	Ser	Val
		115					120					125			
Asp	Ile	Leu	Ser	Ile	Ala	Tyr	Gly	Leu	Arg	Asn	Val	Val	Glu	Arg	Gln
		130				135					140				
Glu	Ala	Leu	Lys	Glu	Phe	Phe	Arg	Val	Leu	Lys	Pro	Arg	Gly	Val	Leu
145					150					155					160
Val	Ile	Leu	Glu	Phe	Leu	Lys	Lys	Asp	Asn	Pro	Thr	Trp	Leu	Asp	Lys
				165				170						175	
Ile	Ser	Gly	Phe	Tyr	Thr	Asn	Lys	Val	Leu	Pro	Leu	Val	Gly	Gly	Ala
			180					185					190		
Ile	Ser	Lys	Asn	Tyr	Gly	Ala	Tyr	Ser	Tyr	Leu	Pro	Gln	Ser	Ile	Glu
		195				200						205			
Gly	Phe	Leu	Ser	Leu	Glu	Gly	Leu	Lys	His	Glu	Leu	Arg	Asn	Ala	Gly
	210				215					220					
Phe	Glu	Ile	Leu	Arg	Thr	Glu	Asp	Ser	Ile	Ala	Gln	Ile	Ser	Thr	Thr
225					230					235					240
Met	Leu	Val	Lys	Lys	Asn										
				245											

<210> 371
 <211> 1443
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (57) ... (1403)

<400> 371
 aaaattctga gattttatat attttatatt tatcgttagg ttttaggttt aaagtt atg 59
 Met
 1

ggg agg aat caa gga gct tat ttg gat ccg tct gaa tcg att ttg atg 107
 Gly Arg Asn Gln Gly Ala Tyr Leu Asp Pro Ser Glu Ser Ile Leu Met
 5 10 15

ttg atg gtt gct ttt tta ttg gtg ctg ttg aac gct ttt ttt gtg ctt 155
 Leu Met Val Ala Phe Leu Leu Val Leu Leu Asn Ala Phe Phe Val Leu
 20 25 30

tca gag ttt gcc ctt gtg aaa gtg cgt aaa acc cgc tta gaa gag ctg 203
 Ser Glu Phe Ala Leu Val Lys Val Arg Lys Thr Arg Leu Glu Glu Leu
 35 40 45

gtt aaa atc ggt aat tcc aac gct aaa ctc gct tta aag atg agt caa 251
 Val Lys Ile Gly Asn Ser Asn Ala Lys Leu Ala Leu Lys Met Ser Gln
 50 55 60 65

aga cta gac act tat ttg agc gcg acg cag tta ggc atc acc ctt tct 299
 Arg Leu Asp Thr Tyr Leu Ser Ala Thr Gln Leu Gly Ile Thr Leu Ser
 70 75 80

tca tta gct tta ggc tgg gtg ggt gag ccc gct atc gca aaa ttg tta 347
 Ser Leu Ala Leu Gly Trp Val Gly Glu Pro Ala Ile Ala Lys Leu Leu
 85 90 95

gcc gcg ctg ttt gag tct atg gat ttg aga gaa aat cct att ttt atc	395
Ala Ala Leu Phe Glu Ser Met Asp Leu Arg Glu Asn Pro Ile Phe Ile	
100 105 110	
cat tca atg agc gtg gtc ata gcg ttt tta agc atc act ttt ttg cat	443
His Ser Met Ser Val Val Ile Ala Phe Leu Ser Ile Thr Phe Leu His	
115 120 125	
gtc gtg ttg ggc gag att gtg cct aaa tct tta gcg atc gct aaa tct	491
Val Val Leu Gly Glu Ile Val Pro Lys Ser Leu Ala Ile Ala Lys Ser	
130 135 140 145	
gaa aaa gcc acc ctt ttt gcc gca cgc cct ttg cat gtg ttt tgg gtg	539
Glu Lys Ala Thr Leu Phe Ala Ala Arg Pro Leu His Val Phe Trp Val	
150 155 160	
gtg ttt tat ccg gtg gtg cgt ttg ttt gat gtg atc gct cat ttt ttt	587
Val Phe Tyr Pro Val Val Arg Leu Phe Asp Val Ile Ala His Phe Phe	
165 170 175	
ttg aaa aag atg ggc atc aat cct aaa gag cat gac ggc acg cat tct	635
Leu Lys Lys Met Gly Ile Asn Pro Lys Glu His Asp Gly Thr His Ser	
180 185 190	
gaa gaa gag tta aaa atc att gtg ggc gag agt ttg aga gag ggc att	683
Glu Glu Glu Leu Lys Ile Ile Val Gly Glu Ser Leu Arg Glu Gly Ile	
195 200 205	
att gat tca gtg gag ggc gaa atc att aaa aac gca gtg gat ttt tct	731
Ile Asp Ser Val Glu Gly Glu Ile Ile Lys Asn Ala Val Asp Phe Ser	
210 215 220 225	
gac acg agc gct aaa gaa atc atg acc cca cga aaa gac atg gtg tgt	779
Asp Thr Ser Ala Lys Glu Ile Met Thr Pro Arg Lys Asp Met Val Cys	
230 235 240	
ttg gat gaa gaa aac agc tat gaa gaa aat ata gac att gtt tta aaa	827
Leu Asp Glu Glu Asn Ser Tyr Glu Glu Asn Ile Asp Ile Val Leu Lys	
245 250 255	
ggc cat ttc acg cgc tac cct tat tgc aag ggt tct aag gat aac att	875
Gly His Phe Thr Arg Tyr Pro Tyr Cys Lys Gly Ser Lys Asp Asn Ile	
260 265 270	
atc ggc atg gtg cat att agg gat ttg ctt tcg cgc tct att ttt acc	923
Ile Gly Met Val His Ile Arg Asp Leu Leu Ser Arg Ser Ile Phe Thr	
275 280 285	
ccc aaa atg cat gat ttc aat caa atc gtt agg aaa atg atc atc gtc	971
Pro Lys Met His Asp Phe Asn Gln Ile Val Arg Lys Met Ile Ile Val	
290 295 300 305	
ccc gaa agc gct tcc att tct caa atc ctt att aaa atg aaa gag	1019
Pro Glu Ser Ala Ser Ile Ser Gln Ile Leu Ile Lys Met Lys Lys Glu	
310 315 320	
caa atc cat acc gct ttg gtg att gat gaa tac ggc ggc aca gcc ggg	1067
Gln Ile His Thr Ala Leu Val Ile Asp Glu Tyr Gly Gly Thr Ala Gly	
325 330 335	

ttg ctc act atg gaa gac atc att gaa gag atc atg ggc gag att agc	1115
Leu Leu Thr Met Glu Asp Ile Ile Glu Glu Ile Met Gly Glu Ile Ser	
340 345 350	
gac gaa tac gac tta aaa caa gag ggc ata aac aag ctt gaa gag ggc	1163
Asp Glu Tyr Asp Leu Lys Gln Glu Gly Ile Asn Lys Leu Glu Glu Gly	
355 360 365	
gtg ttt gaa tta gag ggc atg ctg gat tta gag agc gta gaa gaa gcg	1211
Val Phe Glu Leu Glu Gly Met Leu Asp Leu Glu Ser Val Glu Glu Ala	
370 375 380 385	
ctt cac att gaa ttt gat aaa gaa tgc gag cag gta acg ctt ggg ggc	1259
Leu His Ile Glu Phe Asp Lys Glu Cys Glu Gln Val Thr Leu Gly Gly	
390 395 400	
tat gtt ttt agc ttg tta gag cgc atg cct atg gag gga gat aca atc	1307
Tyr Val Phe Ser Leu Leu Glu Arg Met Pro Met Glu Gly Asp Thr Ile	
405 410 415	
gtt tcg cat ggg tat tct ttt gaa gtc tta agc gtg gat ggg gct agg	1355
Val Ser His Gly Tyr Ser Phe Glu Val Leu Ser Val Asp Gly Ala Arg	
420 425 430	
ata aaa cgc tta aaa gcg gtt aaa caa gat cag gga gaa aat gaa gca	1403
Ile Lys Arg Leu Lys Ala Val Lys Gln Asp Gln Gly Glu Asn Glu Ala	
435 440 445	

tgaaaaaaac aaccctcttt gtattgggct tattatttaa 1443

<210> 372

<211> 449

<212> PRT

<213> Helicobacter pylori

<400> 372

Met Gly Arg Asn Gln Gly Ala Tyr Leu Asp Pro Ser Glu Ser Ile Leu	
1 5 10 15	
Met Leu Met Val Ala Phe Leu Leu Val Leu Leu Asn Ala Phe Phe Val	
20 25 30	
Leu Ser Glu Phe Ala Leu Val Lys Val Arg Lys Thr Arg Leu Glu Glu	
35 40 45	
Leu Val Lys Ile Gly Asn Ser Asn Ala Lys Leu Ala Leu Lys Met Ser	
50 55 60	
Gln Arg Leu Asp Thr Tyr Leu Ser Ala Thr Gln Leu Gly Ile Thr Leu	
65 70 75 80	
Ser Ser Leu Ala Leu Gly Trp Val Gly Glu Pro Ala Ile Ala Lys Leu	
85 90 95	
Leu Ala Ala Leu Phe Glu Ser Met Asp Leu Arg Glu Asn Pro Ile Phe	
100 105 110	
Ile His Ser Met Ser Val Val Ile Ala Phe Leu Ser Ile Thr Phe Leu	
115 120 125	
His Val Val Leu Gly Glu Ile Val Pro Lys Ser Leu Ala Ile Ala Lys	
130 135 140	
Ser Glu Lys Ala Thr Leu Phe Ala Ala Arg Pro Leu His Val Phe Trp	
145 150 155 160	
Val Val Phe Tyr Pro Val Val Arg Leu Phe Asp Val Ile Ala His Phe	
165 170 175	

Phe	Leu	Lys	Lys	Met	Gly	Ile	Asn	Pro	Lys	Glu	His	Asp	Gly	Thr	His
			180					185					190		
Ser	Glu	Glu	Glu	Leu	Lys	Ile	Ile	Val	Gly	Glu	Ser	Leu	Arg	Glu	Gly
		195					200					205			
Ile	Ile	Asp	Ser	Val	Glu	Gly	Glu	Ile	Ile	Lys	Asn	Ala	Val	Asp	Phe
	210					215					220				
Ser	Asp	Thr	Ser	Ala	Lys	Glu	Ile	Met	Thr	Pro	Arg	Lys	Asp	Met	Val
225					230					235					240
Cys	Leu	Asp	Glu	Glu	Asn	Ser	Tyr	Glu	Glu	Asn	Ile	Asp	Ile	Val	Leu
			245						250					255	
Lys	Gly	His	Phe	Thr	Arg	Tyr	Pro	Tyr	Cys	Lys	Gly	Ser	Lys	Asp	Asn
			260					265					270		
Ile	Ile	Gly	Met	Val	His	Ile	Arg	Asp	Leu	Leu	Ser	Arg	Ser	Ile	Phe
	275						280					285			
Thr	Pro	Lys	Met	His	Asp	Phe	Asn	Gln	Ile	Val	Arg	Lys	Met	Ile	Ile
	290					295					300				
Val	Pro	Glu	Ser	Ala	Ser	Ile	Ser	Gln	Ile	Leu	Ile	Lys	Met	Lys	Lys
305					310					315					320
Glu	Gln	Ile	His	Thr	Ala	Leu	Val	Ile	Asp	Glu	Tyr	Gly	Gly	Thr	Ala
				325					330					335	
Gly	Leu	Leu	Thr	Met	Glu	Asp	Ile	Ile	Glu	Glu	Ile	Met	Gly	Glu	Ile
			340					345					350		
Ser	Asp	Glu	Tyr	Asp	Leu	Lys	Gln	Glu	Gly	Ile	Asn	Lys	Leu	Glu	Glu
	355						360					365			
Gly	Val	Phe	Glu	Leu	Glu	Gly	Met	Leu	Asp	Leu	Glu	Ser	Val	Glu	Glu
	370					375					380				
Ala	Leu	His	Ile	Glu	Phe	Asp	Lys	Glu	Cys	Glu	Gln	Val	Thr	Leu	Gly
385					390					395					400
Gly	Tyr	Val	Phe	Ser	Leu	Leu	Glu	Arg	Met	Pro	Met	Glu	Gly	Asp	Thr
				405					410					415	
Ile	Val	Ser	His	Gly	Tyr	Ser	Phe	Glu	Val	Leu	Ser	Val	Asp	Gly	Ala
			420					425					430		
Arg	Ile	Lys	Arg	Leu	Lys	Ala	Val	Lys	Gln	Asp	Gln	Gly	Glu	Asn	Glu
		435					440					445			
Ala															

<210> 373
 <211> 394
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (47)...(367)

<400> 373															
agaaaccggc	acggttacca	accaagcggc	aacaatcttt	tttaaa	atg	gag	cgt								55
						Met	Glu	Arg							
						1									
ttg	atc	act	tct	tct	tta	tac	act	ttt	tta	agc	gac	ttt	ttt	tct	ttc
Leu	Ile	Thr	Ser	Ser	Leu	Tyr	Thr	Phe	Leu	Ser	Asp	Phe	Phe	Ser	Phe
	5						10				15				103
ttt	ttc	aat	tcc	aaa	gcg	atg	gcg	gtg	ttc	ttg	ctt	ttt	ttt	aag	ctc
Phe	Phe	Asn	Ser	Lys	Ala	Met	Ala	Val	Phe	Leu	Leu	Phe	Phe	Lys	Leu
	20				25					30					35

tct agc atg agc gat ttt tct ttc aaa ttg gct tta tca aag cgc tct	199
Ser Ser Met Ser Asp Phe Ser Phe Lys Leu Ala Leu Ser Lys Arg Ser	
40 45 50	
aaa aag cct tca att tct tct aaa tct tcc cca aag tgc gcg gct aca	247
Lys Lys Pro Ser Ile Ser Ser Lys Ser Ser Pro Lys Cys Ala Ala Thr	
55 60 65	
atg ttg tct ctg att cta gca aaa cgc ctt ctt gat tgc tct ctt aag	295
Met Leu Ser Leu Ile Leu Ala Lys Arg Leu Leu Asp Cys Ser Leu Lys	
70 75 80	
cgc tcc ctt aaa aag ccc acc cca aac acc gcg ccc acc aca ata tgc	343
Arg Ser Leu Lys Lys Pro Thr Pro Asn Thr Ala Pro Thr Thr Ile Cys	
85 90 95	
gta gag ctt acg ggc aag cct aat tgagaggcta aaagcacggt gatgact	394
Val Glu Leu Thr Gly Lys Pro Asn	
100 105	

<210> 374
 <211> 107
 <212> PRT
 <213> Helicobacter pylori

<400> 374															
Met Glu Arg Leu Ile Thr Ser Ser Leu Tyr Thr Phe Leu Ser Asp Phe															
1 5 10 15															
Phe Ser Phe Phe Phe Asn Ser Lys Ala Met Ala Val Phe Leu Leu Phe															
20 25 30															
Phe Lys Leu Ser Ser Met Ser Asp Phe Ser Phe Lys Leu Ala Leu Ser															
35 40 45															
Lys Arg Ser Lys Lys Pro Ser Ile Ser Ser Lys Ser Ser Pro Lys Cys															
50 55 60															
Ala Ala Thr Met Leu Ser Leu Ile Leu Ala Lys Arg Leu Leu Asp Cys															
65 70 75 80															
Ser Leu Lys Arg Ser Leu Lys Lys Pro Thr Pro Asn Thr Ala Pro Thr															
85 90 95															
Thr Ile Cys Val Glu Leu Thr Gly Lys Pro Asn															
100 105															

<210> 375
 <211> 342
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (16)...(321)

<400> 375															
tcaaattctt cataa atg att ttt tct ttt aaa agg act tct ttt tgc gtg	51														
Met Ile Phe Ser Phe Lys Arg Thr Ser Phe Cys Val															
1 5 10															
agc gtg ccg gtt ttg tct ata aag att ttt ttc act tta gcc aga gtt	99														

Ser	Val	Pro	Val	Leu	Ser	Ile	Lys	Ile	Phe	Phe	Thr	Leu	Ala	Arg	Val	
		15					20					25				
tct	aaa	aac	aac	gct	tct	tta	aac	acg	atc	aaa	ggg	ttt	tta	aac	acc	147
Ser	Lys	Asn	Asn	Ala	Ser	Leu	Asn	Thr	Ile	Lys	Gly	Phe	Leu	Asn	Thr	
	30					35				40						
cct	atc	act	aac	gca	atg	ggc	gta	gcc	aga	gcg	aac	gcg	caa	ggg	cag	195
Pro	Ile	Thr	Asn	Ala	Met	Gly	Val	Ala	Arg	Ala	Asn	Ala	Gln	Gly	Gln	
	45				50				55						60	
ctg	atg	act	agc	acg	cta	ata	cac	acc	att	aag	gct	ttt	tca	aaa	tta	243
Leu	Met	Thr	Ser	Thr	Leu	Ile	His	Thr	Ile	Lys	Ala	Phe	Ser	Lys	Leu	
				65				70						75		
ccc	ccc	aaa	cca	aat	tgc	cat	aac	aaa	aag	ctt	aca	aag	gct	aaa	aac	291
Pro	Pro	Lys	Pro	Asn	Cys	His	Asn	Lys	Lys	Leu	Thr	Lys	Ala	Lys	Asn	
			80					85					.90			
aac	acc	gct	tta	gaa	aaa	ata	tcc	gca	att	tgattcgcgc	tactctcaat					341
Asn	Thr	Ala	Leu	Glu	Lys	Ile	Ser	Ala	Ile							
		95					100									
t																342

<210> 376
 <211> 102
 <212> PRT
 <213> Helicobacter pylori

Met	Ile	Phe	Ser	Phe	Lys	Arg	Thr	Ser	Phe	Cys	Val	Ser	Val	Pro	Val	
1				5					10					15		
Leu	Ser	Ile	Lys	Ile	Phe	Phe	Thr	Leu	Ala	Arg	Val	Ser	Lys	Asn	Asn	
			20					25					30			
Ala	Ser	Leu	Asn	Thr	Ile	Lys	Gly	Phe	Leu	Asn	Thr	Pro	Ile	Thr	Asn	
	35					40					45					
Ala	Met	Gly	Val	Ala	Arg	Ala	Asn	Ala	Gln	Gly	Gln	Leu	Met	Thr	Ser	
	50				55				60							
Thr	Leu	Ile	His	Thr	Ile	Lys	Ala	Phe	Ser	Lys	Leu	Pro	Pro	Lys	Pro	
	65				70				75					80		
Asn	Cys	His	Asn	Lys	Lys	Leu	Thr	Lys	Ala	Lys	Asn	Asn	Thr	Ala	Leu	
			85					90						95		
Glu	Lys	Ile	Ser	Ala	Ile											
			100													

<210> 377
 <211> 1108
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (31)...(1062)

aggctttttg	ctcttgccctt	ttttcccatc	atg	aga	ctt	tat	gag	agt	tta	tta	54
			Met	Arg	Leu	Tyr	Glu	Ser	Leu	Leu	

1										5						
gaa atg tgc ttg aat aag gca tgg gag cat caa acc cta gcc tta gaa	102															
Glu Met Cys Leu Asn Lys Ala Trp Glu His Gln Thr Leu Ala Leu Glu																
10 15 20																
aac cca agc gta gct tgc atg gtg ttg gat aaa aac cat gag atc ttg	150															
Asn Pro Ser Val Ala Cys Met Val Leu Asp Lys Asn His Glu Ile Leu																
25 30 35 40																
agt tta gaa acc cac aaa aaa gcc aaa acc ccg cat gca gaa gtc tta	198															
Ser Leu Glu Thr His Lys Lys Ala Lys Thr Pro His Ala Glu Val Leu																
45 50 55																
gcc gcc caa tca gcg cta aag att tta cgc ccc agt ttg aaa aac gat	246															
Ala Ala Gln Ser Ala Leu Lys Ile Leu Arg Pro Ser Leu Lys Asn Asp																
60 65 70																
tta gaa aag tta gaa gac cct aaa act tta agc gat ttt tta aaa acg	294															
Leu Glu Lys Leu Glu Asp Pro Lys Thr Leu Ser Asp Phe Leu Lys Thr																
75 80 85																
cac cac gat aac gct ttt aca gac tgc gtt ttt tta atc acc tta gag	342															
His His Asp Asn Ala Phe Thr Asp Cys Val Phe Leu Ile Thr Leu Glu																
90 95 100																
cca tgc aat tct tat ggc aaa acc ccg gct tgt agc gaa ttg tta gaa	390															
Pro Cys Asn Ser Tyr Gly Lys Thr Pro Ala Cys Ser Glu Leu Leu Glu																
105 110 115 120																
att tta aag cct aaa aga gtg gtc att gcc aca gaa gaa aac gaa gct	438															
Ile Leu Lys Pro Lys Arg Val Val Ile Ala Thr Glu Glu Asn Glu Ala																
125 130 135																
aaa aaa ggg ggt tta gca agg cta caa aag gct cgt att gaa aca ata	486															
Lys Lys Gly Gly Leu Ala Arg Leu Gln Lys Ala Arg Ile Glu Thr Ile																
140 145 150																
att tgc cac aat tta gaa aac aaa gct aaa gac ttg ctc ttg cct ttt	534															
Ile Cys His Asn Leu Glu Asn Lys Ala Lys Asp Leu Leu Leu Pro Phe																
155 160 165																
agg gta atg gaa caa aag ggg cgt ttt aat ttg ttc aaa ctc gct tta	582															
Arg Val Met Glu Gln Lys Gly Arg Phe Asn Leu Phe Lys Leu Ala Leu																
170 175 180																
aga atg aat ggg gat tac cat cat ggc aag atc acc ggg caa aaa agc	630															
Arg Met Asn Gly Asp Tyr His His Gly Lys Ile Thr Gly Gln Lys Ser																
185 190 195 200																
gtt att ttc acg cac aac cag cga gca ata tgc gac acg ctt att gtt	678															
Val Ile Phe Thr His Asn Gln Arg Ala Ile Cys Asp Thr Leu Ile Val																
205 210 215																
tct ggg aaa acc ata aga acg gac aac ccc tta ttg gac gct cgc ttt	726															
Ser Gly Lys Thr Ile Arg Thr Asp Asn Pro Leu Leu Asp Ala Arg Phe																
220 225 230																
tgc gac agc ttt tat caa aat aaa aac ccc aat atc gct att tta tcc	774															

Cys	Asp	Ser	Phe	Tyr	Gln	Asn	Lys	Asn	Pro	Asn	Ile	Ala	Ile	Leu	Ser		
		235					240					245					
aag	cgc	tca	att	gac	cct	aat	tca	aaa	gtt	ttt	tct	gcg	cct	aat	cgt	822	
Lys	Arg	Ser	Ile	Asp	Pro	Asn	Ser	Lys	Val	Phe	Ser	Ala	Pro	Asn	Arg		
	250					255					260						
tta	gtt	aac	act	ttc	cat	gac	ccc	aaa	gat	tta	ccc	cta	gag	aag	ggg	870	
Leu	Val	Asn	Thr	Phe	His	Asp	Pro	Lys	Asp	Leu	Pro	Leu	Glu	Lys	Gly		
265					270					275					280		
ttt	aat	ttc	att	gaa	ggg	ggg	tgg	gaa	ttg	ttt	gag	agc	ttg	agg	gat	918	
Phe	Asn	Phe	Ile	Glu	Gly	Gly	Trp	Glu	Leu	Phe	Glu	Ser	Leu	Arg	Asp		
				285				290						295			
aaa	ata	gac	gcg	ttg	ctt	ttg	cat	tcg	cat	gcg	tct	atg	att	ggc	gaa	966	
Lys	Ile	Asp	Ala	Leu	Leu	Leu	His	Ser	His	Ala	Ser	Met	Ile	Gly	Glu		
			300					305					310				
gcg	ttt	aag	gca	ctc	gct	cta	aaa	acc	cct	ttt	aaa	gga	cgg	ttg	ttg	1014	
Ala	Phe	Lys	Ala	Leu	Ala	Leu	Lys	Thr	Pro	Phe	Lys	Gly	Arg	Leu	Leu		
		315					320					325					
cat	gcg	caa	atc	tta	gaa	aat	gaa	gcc	ctt	tta	tgg	ata	gaa	aac	tct	1062	
His	Ala	Gln	Ile	Leu	Glu	Asn	Glu	Ala	Leu	Leu	Trp	Ile	Glu	Asn	Ser		
	330					335					340						
taagattata ccagcctttg aacgcttatt cttacaacag cgattc																1108	

<210> 378

<211> 344

<212> PRT

<213> Helicobacter pylori

<400> 378

Met	Arg	Leu	Tyr	Glu	Ser	Leu	Leu	Glu	Met	Cys	Leu	Asn	Lys	Ala	Trp		
1				5				10						15			
Glu	His	Gln	Thr	Leu	Ala	Leu	Glu	Asn	Pro	Ser	Val	Ala	Cys	Met	Val		
		20						25					30				
Leu	Asp	Lys	Asn	His	Glu	Ile	Leu	Ser	Leu	Glu	Thr	His	Lys	Lys	Ala		
		35				40						45					
Lys	Thr	Pro	His	Ala	Glu	Val	Leu	Ala	Ala	Gln	Ser	Ala	Leu	Lys	Ile		
	50					55					60						
Leu	Arg	Pro	Ser	Leu	Lys	Asn	Asp	Leu	Glu	Lys	Leu	Glu	Asp	Pro	Lys		
65					70					75				80			
Thr	Leu	Ser	Asp	Phe	Leu	Lys	Thr	His	His	Asp	Asn	Ala	Phe	Thr	Asp		
				85				90						95			
Cys	Val	Phe	Leu	Ile	Thr	Leu	Glu	Pro	Cys	Asn	Ser	Tyr	Gly	Lys	Thr		
			100					105					110				
Pro	Ala	Cys	Ser	Glu	Leu	Leu	Glu	Ile	Leu	Lys	Pro	Lys	Arg	Val	Val		
		115					120					125					
Ile	Ala	Thr	Glu	Glu	Asn	Glu	Ala	Lys	Lys	Gly	Gly	Leu	Ala	Arg	Leu		
	130					135					140						
Gln	Lys	Ala	Arg	Ile	Glu	Thr	Ile	Ile	Cys	His	Asn	Leu	Glu	Asn	Lys		
145					150					155					160		
Ala	Lys	Asp	Leu	Leu	Leu	Pro	Phe	Arg	Val	Met	Glu	Gln	Lys	Gly	Arg		
			165					170						175			
Phe	Asn	Leu	Phe	Lys	Leu	Ala	Leu	Arg	Met	Asn	Gly	Asp	Tyr	His	His		
		180						185					190				

Gly Lys Ile Thr Gly Gln Lys Ser Val Ile Phe Thr His Asn Gln Arg
 195 200 205
 Ala Ile Cys Asp Thr Leu Ile Val Ser Gly Lys Thr Ile Arg Thr Asp
 210 215 220
 Asn Pro Leu Leu Asp Ala Arg Phe Cys Asp Ser Phe Tyr Gln Asn Lys
 225 230 235 240
 Asn Pro Asn Ile Ala Ile Leu Ser Lys Arg Ser Ile Asp Pro Asn Ser
 245 250 255
 Lys Val Phe Ser Ala Pro Asn Arg Leu Val Asn Thr Phe His Asp Pro
 260 265 270
 Lys Asp Leu Pro Leu Glu Lys Gly Phe Asn Phe Ile Glu Gly Gly Trp
 275 280 285
 Glu Leu Phe Glu Ser Leu Arg Asp Lys Ile Asp Ala Leu Leu Leu His
 290 295 300
 Ser His Ala Ser Met Ile Gly Glu Ala Phe Lys Ala Leu Ala Leu Lys
 305 310 315 320
 Thr Pro Phe Lys Gly Arg Leu Leu His Ala Gln Ile Leu Glu Asn Glu
 325 330 335
 Ala Leu Leu Trp Ile Glu Asn Ser
 340

<210> 379
 <211> 823
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (14)...(799)

<400> 379
 acgatttttaa aaa atg gct aga agt ttc aag cat tct caa tat cct aaa 49
 Met Ala Arg Ser Phe Lys His Ser Gln Tyr Pro Lys
 1 5 10

 att ttt aag cca cta tac cct aac aac tta acg ctt tca ctt aaa aag 97
 Ile Phe Lys Pro Leu Tyr Pro Asn Asn Leu Thr Leu Ser Leu Lys Lys
 15 20 25

 caa cat gtt ata atg atc gct att tta ttt gaa agg gta ttt atg gaa 145
 Gln His Val Ile Met Ile Ala Ile Leu Phe Glu Arg Val Phe Met Glu
 30 35 40

 agc gtt tta aat ttc cta acc aat atc aat gtg att ttc acc ctt ttg 193
 Ser Val Leu Asn Phe Leu Thr Asn Ile Asn Val Ile Phe Thr Leu Leu
 45 50 55 60

 ggc tat ttg att ggg ggg att cct ttt ggc tat gcg tta atg aaa atc 241
 Gly Tyr Leu Ile Gly Gly Ile Pro Phe Gly Tyr Ala Leu Met Lys Ile
 65 70 75

 ttt tac ggc atg gat att act aaa atc gga tcg ggg ggc att ggc gca 289
 Phe Tyr Gly Met Asp Ile Thr Lys Ile Gly Ser Gly Gly Ile Gly Ala
 80 85 90

 acg aat gtc ttg cgt gct tta caa agt aag ggc gtg agt aac gct aaa 337
 Thr Asn Val Leu Arg Ala Leu Gln Ser Lys Gly Val Ser Asn Ala Lys
 95 100 105

caa atg gcc cta tta gtt tta atc ttg gat ctc ttc aaa ggc atg ttt	385
Gln Met Ala Leu Leu Val Leu Ile Leu Asp Leu Phe Lys Gly Met Phe	
110 115 120	
gca gta ttt ttg agc aaa ttg ttt ggg ttg gat tat agt ttg caa tgg	433
Ala Val Phe Leu Ser Lys Leu Phe Gly Leu Asp Tyr Ser Leu Gln Trp	
125 130 135 140	
atg gtc gct atc gct agc att tta ggg cat tgc tat tcg cct ttt ttg	481
Met Val Ala Ile Ala Ser Ile Leu Gly His Cys Tyr Ser Pro Phe Leu	
145 150 155	
aat ttc aat gga ggt aag ggc gtt tct acg atc atg ggc tct gtg gtg	529
Asn Phe Asn Gly Gly Lys Gly Val Ser Thr Ile Met Gly Ser Val Val	
160 165 170	
ttg ctc atc cct att gaa agt ctc atc ggc tta acg gtg tgg ttt ttt	577
Leu Leu Ile Pro Ile Glu Ser Leu Ile Gly Leu Thr Val Trp Phe Phe	
175 180 185	
gtg ggt aag gtg ctt aaa atc tct tca ctc gct agc att cta ggg gta	625
Val Gly Lys Val Leu Lys Ile Ser Ser Leu Ala Ser Ile Leu Gly Val	
190 195 200	
ggc aca gcg act gtt ctt atc ttt ttt gtg cct tat atg cat atc cca	673
Gly Thr Ala Thr Val Leu Ile Phe Phe Val Pro Tyr Met His Ile Pro	
205 210 215 220	
gac agc gtc aat atc ctt aaa gaa gtc ggc acg caa acg ccg atg gtg	721
Asp Ser Val Asn Ile Leu Lys Glu Val Gly Thr Gln Thr Pro Met Val	
225 230 235	
ctt att ttt att ttc acc ctt atc aag cat gcg ggt aat att ttt aat	769
Leu Ile Phe Ile Phe Thr Leu Ile Lys His Ala Gly Asn Ile Phe Asn	
240 245 250	
tta ttg gcc ggc aag gaa aag aaa gtc tta tgaaaaactaa acaaggcggtt	819
Leu Leu Ala Gly Lys Glu Lys Lys Val Leu	
255 260	

cata 823

<210> 380

<211> 262

<212> PRT

<213> Helicobacter pylori

<400> 380

Met Ala Arg Ser Phe Lys His Ser Gln Tyr Pro Lys Ile Phe Lys Pro	
1 5 10 15	
Leu Tyr Pro Asn Asn Leu Thr Leu Ser Leu Lys Lys Gln His Val Ile	
20 25 30	
Met Ile Ala Ile Leu Phe Glu Arg Val Phe Met Glu Ser Val Leu Asn	
35 40 45	
Phe Leu Thr Asn Ile Asn Val Ile Phe Thr Leu Leu Gly Tyr Leu Ile	
50 55 60	
Gly Gly Ile Pro Phe Gly Tyr Ala Leu Met Lys Ile Phe Tyr Gly Met	
65 70 75 80	

gaa ctt tat tta aaa atc agc aag tta gag att tct ccc aat tct caa 342
 Glu Leu Tyr Leu Lys Ile Ser Lys Leu Glu Ile Ser Pro Asn Ser Gln
 90 95 100

gtg gga gcg agc gtg aaa atc cgc tat gaa agc aat ctt tagcctcttt 391
 Val Gly Ala Ser Val Lys Ile Arg Tyr Glu Ser Asn Leu
 105 110 115

ttccttctta ttg 404

<210> 382

<211> 117

<212> PRT

<213> Helicobacter pylori

<400> 382

Met Lys Thr Lys Gln Gly Val His Ile His Asn Leu Val Phe Glu Ala
 1 5 10 15
 Ile Leu Gly Ile Leu Glu Phe Glu Arg Leu Lys Pro Gln Lys Ile Ser
 20 25 30
 Val Asn Leu Asp Leu Phe Tyr Thr Gln Leu Pro Asn Lys Val Tyr Leu
 35 40 45
 Asp Tyr Met Glu Ile Gln Glu Leu Ile Gln Lys Met Met Gln Glu Asn
 50 55 60
 Gln Tyr Leu Leu Ile Glu Asp Ala Leu Lys Asp Leu Ser His Ala Leu
 65 70 75 80
 Lys Thr Arg Tyr Lys Glu Ile Thr Glu Leu Tyr Leu Lys Ile Ser Lys
 85 90 95
 Leu Glu Ile Ser Pro Asn Ser Gln Val Gly Ala Ser Val Lys Ile Arg
 100 105 110
 Tyr Glu Ser Asn Leu
 115

<210> 383

<211> 1227

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (52)...(1209)

<400> 383

taaaataacg cttatttttaa actctcaaaa aaggaatcaa acgcactcat c atg gct 57
 Met Ala
 1

aaa gaa acg ctt gaa ata acc ccg gat ctt ttg aaa aac cct tat caa 105
 Lys Glu Thr Leu Glu Ile Thr Pro Asp Leu Leu Lys Asn Pro Tyr Gln
 5 10 15

aaa atc atc aat gcg agc gcg agc gtt ttt gat gaa aag cat ggg cga 153
 Lys Ile Ile Asn Ala Ser Ala Ser Val Phe Asp Glu Lys His Gly Arg
 20 25 30

tcg ttt ttt agc acg caa ttt tat gaa aaa att gaa cct tat tta aaa 201
 Ser Phe Phe Ser Thr Gln Phe Tyr Glu Lys Ile Glu Pro Tyr Leu Lys

35	40	45	50	
gaa gtt tta acc cat ccc att gat tta gaa tgc gat cta aac acc gct	249			
Glu Val Leu Thr His Pro Ile Asp Leu Glu Cys Asp Leu Asn Thr Ala				
55 60 65				
aaa aaa aag aac cgc tta acc cct tta aaa cag ctt ttt aaa gcg tgt	297			
Lys Lys Lys Asn Arg Leu Thr Pro Leu Lys Gln Leu Phe Lys Ala Cys				
70 75 80				
ttt aac acc gaa gaa att ttg att gtg aat aat aac acc agc gcg att	345			
Phe Asn Thr Glu Glu Ile Leu Ile Val Asn Asn Asn Thr Ser Ala Ile				
85 90 95				
ttc ctc atc gct aac gct tta gcg caa gaa aaa gaa atc att gtt tct	393			
Phe Leu Ile Ala Asn Ala Leu Ala Gln Glu Lys Glu Ile Ile Val Ser				
100 105 110				
tat ggc gaa tta gtg ggg ggg gat ttt aac ctt aaa gat att tta tta	441			
Tyr Gly Glu Leu Val Gly Gly Asp Phe Asn Leu Lys Asp Ile Leu Leu				
115 120 125 130				
aat agt ggg gct agg ctg cat tta gtg ggg aat att aat cgc gct tat	489			
Asn Ser Gly Ala Arg Leu His Leu Val Gly Asn Ile Asn Arg Ala Tyr				
135 140 145				
tta agg gat tac cgc tta gcc ttg aat gaa aac agc aaa ata ctc ttt	537			
Leu Arg Asp Tyr Arg Leu Ala Leu Asn Glu Asn Ser Lys Ile Leu Phe				
150 155 160				
aaa acc cac aac ccc cat ttt aaa aaa gac acg ccc ttt aaa gat tta	585			
Lys Thr His Asn Pro His Phe Lys Lys Asp Thr Pro Phe Lys Asp Leu				
165 170 175				
caa act ctt gct aaa gag cat gat ctc att gat tat tac aat tta ggg	633			
Gln Thr Leu Ala Lys Glu His Asp Leu Ile Asp Tyr Tyr Asn Leu Gly				
180 185 190				
gat gtg gat ttg tca aac aga gtg gct ttg gaa gaa att tta gcc cta	681			
Asp Val Asp Leu Ser Asn Arg Val Ala Leu Glu Glu Ile Leu Ala Leu				
195 200 205 210				
aaa cca tcg ctt tta agc ttt agc gcg gat aaa ttc ttt aac agt gcg	729			
Lys Pro Ser Leu Leu Ser Phe Ser Ala Asp Lys Phe Phe Asn Ser Ala				
215 220 225				
caa gcg ggc att att atg ggg caa aaa gaa cgg gtt gaa gcg tta aaa	777			
Gln Ala Gly Ile Ile Met Gly Gln Lys Glu Arg Val Glu Ala Leu Lys				
230 235 240				
aac cac ccc ctt tat aga gtt tta agg gtg ggt aaa atc acg ctc acc	825			
Asn His Pro Leu Tyr Arg Val Leu Arg Val Gly Lys Ile Thr Leu Thr				
245 250 255				
ttg ctt ttt tgc agc cta aaa gca tgg ata aat cat caa gaa gac att	873			
Leu Leu Phe Cys Ser Leu Lys Ala Trp Ile Asn His Gln Glu Asp Ile				
260 265 270				
aca atc cat gcg tta ttg aac caa act aaa gac gca tta ttg caa aaa	921			

Thr 275	Ile	His	Ala	Leu	Leu	Asn	Gln	Thr	Lys	Asp	Ala	Leu	Leu	Gln	Lys	290	
280										285							
gcc	ctc	aaa	ctc	tac	gct	ctt	tta	aag	cct	tta	gaa	ttg	aat	gtg	agc	969	
Ala	Leu	Lys	Leu	Tyr	Ala	Leu	Leu	Lys	Pro	Leu	Glu	Leu	Asn	Val	Ser	305	
295									300								
ata	gcc	tct	agc	ttt	tct	aaa	ata	ggg	aat	ttg	ttt	ggt	agg	gaa	tta	1017	
Ile	Ala	Ser	Ser	Phe	Ser	Lys	Ile	Gly	Asn	Leu	Phe	Gly	Arg	Glu	Leu	320	
310								315									
gaa	tcc	ttt	tgc	gtg	aaa	atc	cag	ccc	aaa	aac	acc	cgt	gct	tta	aat	1065	
Glu	Ser	Phe	Cys	Val	Lys	Ile	Gln	Pro	Lys	Asn	Thr	Arg	Ala	Leu	Asn	335	
325							330										
agt	gag	aaa	ctt	tat	tta	aag	ctt	ttc	caa	aaa	ggc	gtt	atc	gca	agg	1113	
Ser	Glu	Lys	Leu	Tyr	Leu	Lys	Leu	Phe	Gln	Lys	Gly	Val	Ile	Ala	Arg	350	
340						345											
att	tca	tgc	gaa	ttc	gtg	tgc	ttt	gaa	gtc	ttt	agc	ttg	aat	gaa	aaa	1161	
Ile	Ser	Cys	Glu	Phe	Val	Cys	Phe	Glu	Val	Phe	Ser	Leu	Asn	Glu	Lys	370	
355					360					365							
gat	ttt	gaa	aaa	atc	gct	ctg	gtt	tta	gaa	gaa	att	ctt	aat	aaa	gct	1209	
Asp	Phe	Glu	Lys	Ile	Ala	Leu	Val	Leu	Glu	Glu	Ile	Leu	Asn	Lys	Ala	385	
375									380								
taaaaattcg ctataata																1227	

<210> 384

<211> 386

<212> PRT

<213> Helicobacter pylori

<400> 384

Met	Ala	Lys	Glu	Thr	Leu	Glu	Ile	Thr	Pro	Asp	Leu	Leu	Lys	Asn	Pro
1				5					10					15	
Tyr	Gln	Lys	Ile	Ile	Asn	Ala	Ser	Ala	Ser	Val	Phe	Asp	Glu	Lys	His
			20					25					30		
Gly	Arg	Ser	Phe	Phe	Ser	Thr	Gln	Phe	Tyr	Glu	Lys	Ile	Glu	Pro	Tyr
		35					40					45			
Leu	Lys	Glu	Val	Leu	Thr	His	Pro	Ile	Asp	Leu	Glu	Cys	Asp	Leu	Asn
50					55					60					
Thr	Ala	Lys	Lys	Lys	Asn	Arg	Leu	Thr	Pro	Leu	Lys	Gln	Leu	Phe	Lys
65					70					75				80	
Ala	Cys	Phe	Asn	Thr	Glu	Glu	Ile	Leu	Ile	Val	Asn	Asn	Asn	Thr	Ser
			85						90					95	
Ala	Ile	Phe	Leu	Ile	Ala	Asn	Ala	Leu	Ala	Gln	Glu	Lys	Glu	Ile	Ile
			100					105					110		
Val	Ser	Tyr	Gly	Glu	Leu	Val	Gly	Gly	Asp	Phe	Asn	Leu	Lys	Asp	Ile
		115					120					125			
Leu	Leu	Asn	Ser	Gly	Ala	Arg	Leu	His	Leu	Val	Gly	Asn	Ile	Asn	Arg
130						135					140				
Ala	Tyr	Leu	Arg	Asp	Tyr	Arg	Leu	Ala	Leu	Asn	Glu	Asn	Ser	Lys	Ile
145				150						155				160	
Leu	Phe	Lys	Thr	His	Asn	Pro	His	Phe	Lys	Lys	Asp	Thr	Pro	Phe	Lys
				165					170					175	
Asp	Leu	Gln	Thr	Leu	Ala	Lys	Glu	His	Asp	Leu	Ile	Asp	Tyr	Tyr	Asn
			180					185					190		

Leu Gly Asp Val Asp Leu Ser Asn Arg Val Ala Leu Glu Glu Ile Leu
 195 200 205
 Ala Leu Lys Pro Ser Leu Leu Ser Phe Ser Ala Asp Lys Phe Phe Asn
 210 215 220
 Ser Ala Gln Ala Gly Ile Ile Met Gly Gln Lys Glu Arg Val Glu Ala
 225 230 235 240
 Leu Lys Asn His Pro Leu Tyr Arg Val Leu Arg Val Gly Lys Ile Thr
 245 250 255
 Leu Thr Leu Leu Phe Cys Ser Leu Lys Ala Trp Ile Asn His Gln Glu
 260 265 270
 Asp Ile Thr Ile His Ala Leu Leu Asn Gln Thr Lys Asp Ala Leu Leu
 275 280 285
 Gln Lys Ala Leu Lys Leu Tyr Ala Leu Leu Lys Pro Leu Glu Leu Asn
 290 295 300
 Val Ser Ile Ala Ser Ser Phe Ser Lys Ile Gly Asn Leu Phe Gly Arg
 305 310 315 320
 Glu Leu Glu Ser Phe Cys Val Lys Ile Gln Pro Lys Asn Thr Arg Ala
 325 330 335
 Leu Asn Ser Glu Lys Leu Tyr Leu Lys Leu Phe Gln Lys Gly Val Ile
 340 345 350
 Ala Arg Ile Ser Cys Glu Phe Val Cys Phe Glu Val Phe Ser Leu Asn
 355 360 365
 Glu Lys Asp Phe Glu Lys Ile Ala Leu Val Leu Glu Glu Ile Leu Asn
 370 375 380
 Lys Ala
 385

<210> 385
 <211> 1238
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (13)...(1197)

<400> 385
 aggaacttaa ga atg gaa aaa atc agc gat ctt ata gaa tgc att gcg tat 51
 Met Glu Lys Ile Ser Asp Leu Ile Glu Cys Ile Ala Tyr
 1 5 10

 gaa aaa aat ttg cct aaa gag atg att tca aaa gtg att caa ggc tgt 99
 Glu Lys Asn Leu Pro Lys Glu Met Ile Ser Lys Val Ile Gln Gly Cys
 15 20 25

 ttg tta aaa atg gcg caa aat gag tta gac ccc cta gca cgc tac ttg 147
 Leu Leu Lys Met Ala Gln Asn Glu Leu Asp Pro Leu Ala Arg Tyr Leu
 30 35 40 45

 gtg gtt gaa gaa aac aag cag ctc cag ctt atc cag ttg gta gaa gtt 195
 Val Val Glu Glu Asn Lys Gln Leu Gln Leu Ile Gln Leu Val Glu Val
 50 55 60

 tta gaa gat ggt gat gaa aga ttg gtt aac gac cct tct aaa tac atc 243
 Leu Glu Asp Gly Asp Glu Arg Leu Val Asn Asp Pro Ser Lys Tyr Ile
 65 70 75

 agc ctg tct aaa gcc aaa gaa atg gat cca agc gtt aag att aaa gac 291

Ser	Leu	Ser	Lys	Ala	Lys	Glu	Met	Asp	Pro	Ser	Val	Lys	Ile	Lys	Asp	
		80					85					90				
gaa	ttg	tcc	tat	agc	ttg	agt	ttg	gag	agc	atg	aaa	caa	gga	gcg	atc	339
Glu	Leu	Ser	Tyr	Ser	Leu	Ser	Leu	Glu	Ser	Met	Lys	Gln	Gly	Ala	Ile	
	95					100					105					
aac	cgc	ctt	ttt	aaa	gat	ttg	caa	tac	cag	tta	gaa	aaa	gcg	tta	gaa	387
Asn	Arg	Leu	Phe	Lys	Asp	Leu	Gln	Tyr	Gln	Leu	Glu	Lys	Ala	Leu	Glu	
110					115					120					125	
gac	agc	cac	ttt	gaa	gcg	ttt	caa	aag	cgt	ctt	aac	agc	ggt	tta	atg	435
Asp	Ser	His	Phe	Glu	Ala	Phe	Gln	Lys	Arg	Leu	Asn	Ser	Val	Leu	Met	
				130					135					140		
ggg	caa	gtg	att	tta	gtg	gat	cac	aac	caa	aac	acc	ttt	att	gag	att	483
Gly	Gln	Val	Ile	Leu	Val	Asp	His	Asn	Gln	Asn	Thr	Phe	Ile	Glu	Ile	
			145					150					155			
gag	cag	caa	ttt	cag	ggc	gtt	ctt	tcc	atg	cgc	cat	cgc	atc	aag	ggc	531
Glu	Gln	Gln	Phe	Gln	Gly	Val	Leu	Ser	Met	Arg	His	Arg	Ile	Lys	Gly	
		160					165					170				
gag	agt	ttt	aaa	gtg	ggc	gat	agc	att	aaa	gcg	gtt	tta	acg	caa	gtc	579
Glu	Ser	Phe	Lys	Val	Gly	Asp	Ser	Ile	Lys	Ala	Val	Leu	Thr	Gln	Val	
	175					180					185					
aaa	cgc	acg	aaa	aaa	ggc	tta	tta	tta	gag	ctg	agc	cgc	acc	acc	cct	627
Lys	Arg	Thr	Lys	Lys	Gly	Leu	Leu	Leu	Glu	Leu	Ser	Arg	Thr	Thr	Pro	
190					195					200					205	
aaa	atg	ctt	gaa	gct	ttg	ttg	gaa	ttg	gaa	gtc	cct	gaa	att	aaa	gac	675
Lys	Met	Leu	Glu	Ala	Leu	Leu	Glu	Leu	Glu	Val	Pro	Glu	Ile	Lys	Asp	
				210					215					220		
aaa	gaa	att	gaa	atc	atc	cat	tgt	gcg	cga	atc	cca	ggc	aac	aga	gcg	723
Lys	Glu	Ile	Glu	Ile	Ile	His	Cys	Ala	Arg	Ile	Pro	Gly	Asn	Arg	Ala	
			225					230					235			
aaa	gtg	agc	ttt	ttt	tcc	cat	aac	gct	agg	att	gac	ccc	ata	ggc	gcg	771
Lys	Val	Ser	Phe	Phe	Ser	His	Asn	Ala	Arg	Ile	Asp	Pro	Ile	Gly	Ala	
		240					245					250				
gct	gtg	ggg	gtt	aag	ggc	gtg	cgc	att	aat	gcg	atc	agt	aac	gaa	ttg	819
Ala	Val	Gly	Val	Lys	Gly	Val	Arg	Ile	Asn	Ala	Ile	Ser	Asn	Glu	Leu	
	255					260					265					
aat	aaa	gaa	aac	att	gat	tgc	ata	gaa	tat	tct	aat	gtg	cct	gaa	att	867
Asn	Lys	Glu	Asn	Ile	Asp	Cys	Ile	Glu	Tyr	Ser	Asn	Val	Pro	Glu	Ile	
270					275					280					285	
tac	atc	act	ctc	gca	ctc	gct	cca	gcc	aaa	att	tta	agc	ggt	gaa	atc	915
Tyr	Ile	Thr	Leu	Ala	Leu	Ala	Pro	Ala	Lys	Ile	Leu	Ser	Val	Glu	Ile	
				290					295					300		
aaa	aaa	atc	cct	ata	gaa	gaa	ttg	aat	gct	gaa	gaa	aaa	gaa	tcc	att	963
Lys	Lys	Ile	Pro	Ile	Glu	Glu	Leu	Asn	Ala	Glu	Glu	Lys		Ser	Ile	
			305					310					315			

caa gag cgt ttt atc gtc aat aac cat ttg caa aag gct aaa gtg cgt	1011
Gln Glu Arg Phe Ile Val Asn Asn His Leu Gln Lys Ala Lys Val Arg	
320 325 330	
tta ttg gac att gaa aaa tct aag gct atc ggt aag ggc ggg gtg aat	1059
Leu Leu Asp Ile Glu Lys Ser Lys Ala Ile Gly Lys Gly Gly Val Asn	
335 340 345	
gtg tgc tta gcg tcc atg ctt aca ggc tat cac ata gag ttt gaa acc	1107
Val Cys Leu Ala Ser Met Leu Thr Gly Tyr His Ile Glu Phe Glu Thr	
350 355 360 365	
att cct agc gtg aaa gaa aac gca gaa aat gaa agc gaa aaa gaa acg	1155
Ile Pro Ser Val Lys Glu Asn Ala Glu Asn Glu Ser Glu Lys Glu Thr	
370 375 380	
cca aaa gtg ggg gta gaa gct tta gag tct ttg ttt aag aat	1197
Pro Lys Val Gly Val Glu Ala Leu Glu Ser Leu Phe Lys Asn	
385 390 395	
taagggtatc taaaattcaa tctctaaaaa agcttttaac t	1238

<210> 386

<211> 395

<212> PRT

<213> *Helicobacter pylori*

<400> 386

Met Glu Lys Ile Ser Asp Leu Ile Glu Cys Ile Ala Tyr Glu Lys Asn	
1 5 10 15	
Leu Pro Lys Glu Met Ile Ser Lys Val Ile Gln Gly Cys Leu Leu Lys	
20 25 30	
Met Ala Gln Asn Glu Leu Asp Pro Leu Ala Arg Tyr Leu Val Val Glu	
35 40 45	
Glu Asn Lys Gln Leu Gln Leu Ile Gln Leu Val Glu Val Leu Glu Asp	
50 55 60	
Gly Asp Glu Arg Leu Val Asn Asp Pro Ser Lys Tyr Ile Ser Leu Ser	
65 70 75 80	
Lys Ala Lys Glu Met Asp Pro Ser Val Lys Ile Lys Asp Glu Leu Ser	
85 90 95	
Tyr Ser Leu Ser Leu Glu Ser Met Lys Gln Gly Ala Ile Asn Arg Leu	
100 105 110	
Phe Lys Asp Leu Gln Tyr Gln Leu Glu Lys Ala Leu Glu Asp Ser His	
115 120 125	
Phe Glu Ala Phe Gln Lys Arg Leu Asn Ser Val Leu Met Gly Gln Val	
130 135 140	
Ile Leu Val Asp His Asn Gln Asn Thr Phe Ile Glu Ile Glu Gln Gln	
145 150 155 160	
Phe Gln Gly Val Leu Ser Met Arg His Arg Ile Lys Gly Glu Ser Phe	
165 170 175	
Lys Val Gly Asp Ser Ile Lys Ala Val Leu Thr Gln Val Lys Arg Thr	
180 185 190	
Lys Lys Gly Leu Leu Leu Glu Leu Ser Arg Thr Thr Pro Lys Met Leu	
195 200 205	
Glu Ala Leu Leu Glu Leu Glu Val Pro Glu Ile Lys Asp Lys Glu Ile	
210 215 220	
Glu Ile Ile His Cys Ala Arg Ile Pro Gly Asn Arg Ala Lys Val Ser	
225 230 235 240	
Phe Phe Ser His Asn Ala Arg Ile Asp Pro Ile Gly Ala Ala Val Gly	

Val	Lys	Gly	Val	Arg	Ile	Asn	Ala	Ile	Ser	Asn	Glu	Leu	Asn	Lys	Glu
			245					250					255		
Asn	Ile	Asp	Cys	Ile	Glu	Tyr	Ser	Asn	Val	Pro	Glu	Ile	Tyr	Ile	Thr
		275					280					285			
Leu	Ala	Leu	Ala	Pro	Ala	Lys	Ile	Leu	Ser	Val	Glu	Ile	Lys	Lys	Ile
	290					295					300				
Pro	Ile	Glu	Glu	Leu	Asn	Ala	Glu	Glu	Lys	Glu	Ser	Ile	Gln	Glu	Arg
305					310					315					320
Phe	Ile	Val	Asn	Asn	His	Leu	Gln	Lys	Ala	Lys	Val	Arg	Leu	Leu	Asp
			325					330					335		
Ile	Glu	Lys	Ser	Lys	Ala	Ile	Gly	Lys	Gly	Gly	Val	Asn	Val	Cys	Leu
			340				345					350			
Ala	Ser	Met	Leu	Thr	Gly	Tyr	His	Ile	Glu	Phe	Glu	Thr	Ile	Pro	Ser
	355					360					365				
Val	Lys	Glu	Asn	Ala	Glu	Asn	Glu	Ser	Glu	Lys	Glu	Thr	Pro	Lys	Val
	370					375					380				
Gly	Val	Glu	Ala	Leu	Glu	Ser	Leu	Phe	Lys	Asn					
385					390					395					

<210> 387

<211> 3903

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (21) ... (3857)

<400> 387

aagcgatgta aggaattaac atg gat tat aaa aaa tta gat tta ccc aac aca 53
Met Asp Tyr Lys Lys Leu Asp Leu Pro Asn Thr
1 5 10

aac tac cca aat caa gag caa ctg aaa gct ttt gaa acc gct ttt gac 101
Asn Tyr Pro Asn Gln Glu Gln Leu Lys Ala Phe Glu Thr Ala Phe Asp
15 20 25

gcc ttt tta gaa acc aac caa caa gaa aat gaa aat cac caa aac gac 149
Ala Phe Leu Glu Thr Asn Gln Gln Glu Asn Glu Asn His Gln Asn Asp
30 35 40

gct ttt aat gat tta ttg aaa ggc gtt ttt aaa tac aag gtt aag ccc 197
Ala Phe Asn Asp Leu Leu Lys Gly Val Phe Lys Tyr Lys Val Lys Pro
45 50 55

acc aaa aaa ata gac agc act att ctt aat gaa aat aac gaa gtg gag 245
Thr Lys Lys Ile Asp Ser Thr Ile Leu Asn Glu Asn Asn Glu Val Glu
60 65 70 75

gtg atc att gaa ttt aaa gcc ctt aaa aac ccc aac gaa ttt att aaa 293
Val Ile Ile Glu Phe Lys Ala Leu Lys Asn Pro Asn Glu Phe Ile Lys
80 85 90

aag ggc gat ttg aat gtt aaa gcc ttt cat gaa agc ctt ttg tct tat 341
Lys Gly Asp Leu Asn Val Lys Ala Phe His Glu Ser Leu Leu Ser Tyr
95 100 105

ctc aca gaa aga aaa gag ggt aat aac aac ctt aag cat ctt atc tta	389
Leu Thr Glu Arg Lys Glu Gly Asn Asn Asn Leu Lys His Leu Ile Leu	
110 115 120	
gcc act att aaa gag ctt tat atc att gat gca aac gaa ttt gag gtt	437
Ala Thr Ile Lys Glu Leu Tyr Ile Ile Asp Ala Asn Glu Phe Glu Val	
125 130 135	
ttt aat aaa gat aaa gaa att gaa aac gcc ttt aaa aat tgc cac gat	485
Phe Asn Lys Asp Lys Glu Ile Glu Asn Ala Phe Lys Asn Cys His Asp	
140 145 150 155	
aga aag ggt aac gat aca cgc aca aaa gcg ttt tat gat gct tgc caa	533
Arg Lys Gly Asn Asp Thr Arg Thr Lys Ala Phe Tyr Asp Ala Cys Gln	
160 165 170	
aag cgc ctt aat gag ttt gat cgt tct ttg aaa tac cac tat atc ccc	581
Lys Arg Leu Asn Glu Phe Asp Arg Ser Leu Lys Tyr His Tyr Ile Pro	
175 180 185	
ctc aaa aaa gaa aat tta gcc cta atc tat caa gcc cta agc cct aat	629
Leu Lys Lys Glu Asn Leu Ala Leu Ile Tyr Gln Ala Leu Ser Pro Asn	
190 195 200	
ttt ttg ctc aaa att cca aaa tat tct gac gct aac acg ctt aac aaa	677
Phe Leu Leu Lys Ile Pro Lys Tyr Ser Asp Ala Asn Thr Leu Asn Lys	
205 210 215	
gat ttt tat gaa gaa ttg ctt tac att tta ggg tta gaa gag caa aat	725
Asp Phe Tyr Glu Glu Leu Leu Tyr Ile Leu Gly Leu Glu Glu Gln Asn	
220 225 230 235	
gac aaa ggg aaa att tta atc aag ccc agc cgc acc caa aat tcc cta	773
Asp Lys Gly Lys Ile Leu Ile Lys Pro Ser Arg Thr Gln Asn Ser Leu	
240 245 250	
agc gat gct tta aaa aag gaa tac aaa aat tta gac gat gaa gaa gtc	821
Ser Asp Ala Leu Lys Lys Glu Tyr Lys Asn Leu Asp Asp Glu Glu Val	
255 260 265	
atg gcg ttg ctc atc gct tgg aat aac cgc atc ttg ttt tta cgg ctt	869
Met Ala Leu Leu Ile Ala Trp Asn Asn Arg Ile Leu Phe Leu Arg Leu	
270 275 280	
tta gaa agc ctt tta att tct ttt aag cat ttt gaa aat cct ttc tta	917
Leu Glu Ser Leu Leu Ile Ser Phe Lys His Phe Glu Asn Pro Phe Leu	
285 290 295	
acc aca gaa aac ttt gaa aat ttc aac gat tta aac acg ctc ttt ttt	965
Thr Thr Glu Asn Phe Glu Asn Phe Asn Asp Leu Asn Thr Leu Phe Phe	
300 305 310 315	
gaa gtc cta gcc aag aaa aac agc gag cgc tta cca gaa att aaa gaa	1013
Glu Val Leu Ala Lys Lys Asn Ser Glu Arg Leu Pro Glu Ile Lys Glu	
320 325 330	
gac aag att tta gaa aaa atc cct tat ttg aat tcc agt ttg ttt gat	1061
Asp Lys Ile Leu Glu Lys Ile Pro Tyr Leu Asn Ser Ser Leu Phe Asp	
335 340 345	

aaa acg cct tta gaa tta aag ggg cat gaa atc aag ctt tta gac aat	1109
Lys Thr Pro Leu Glu Leu Lys Gly His Glu Ile Lys Leu Leu Asp Asn	
350 355 360	
aaa aag cta gaa atc tat aaa aat tcc gtt ctc aaa aaa cat aaa gat	1157
Lys Lys Leu Glu Ile Tyr Lys Asn Ser Val Leu Lys Lys His Lys Asp	
365 370 375	
tat caa aaa gaa aaa cct ttg ccc ttg cta aaa tac ctt ttt aaa ttt	1205
Tyr Gln Lys Glu Lys Pro Leu Pro Leu Leu Lys Tyr Leu Phe Lys Phe	
380 385 390 395	
ttg cgt ctt tat aaa ttc acc acc acc cct aaa gac att aaa gat aat	1253
Leu Arg Leu Tyr Lys Phe Thr Thr Thr Pro Lys Asp Ile Lys Asp Asn	
400 405 410	
acc gat acc agc gaa agc cgt ttg att aac cct agc gtt tta ggg ctt	1301
Thr Asp Thr Ser Glu Ser Arg Leu Ile Asn Pro Ser Val Leu Gly Leu	
415 420 425	
gtt ttt gaa aaa ctc aac ggc tat aaa gag ggg agc ttt tat acc cca	1349
Val Phe Glu Lys Leu Asn Gly Tyr Lys Glu Gly Ser Phe Tyr Thr Pro	
430 435 440	
agc ttt atc aca agc tac atg tgc aaa gag agc atc acg ccc atc gtg	1397
Ser Phe Ile Thr Ser Tyr Met Cys Lys Glu Ser Ile Thr Pro Ile Val	
445 450 455	
ttg gat aaa ttc aac gcc att tat cag tgg gac tgc gaa aat cta aaa	1445
Leu Asp Lys Phe Asn Ala Ile Tyr Gln Trp Asp Cys Glu Asn Leu Lys	
460 465 470 475	
gcg ttg cga gga gaa ata gac aga aat ttt tca aat gaa aaa gct aaa	1493
Ala Leu Arg Gly Glu Ile Asp Arg Asn Phe Ser Asn Glu Lys Ala Lys	
480 485 490	
gaa tac cta aac acg ctt tta acc ttg cgt att tgc gat ccg gcg gtg	1541
Glu Tyr Leu Asn Thr Leu Leu Thr Leu Arg Ile Cys Asp Pro Ala Val	
495 500 505	
ggg agc ggg cat ttc ttg gtt tca gcg ctc aat gaa atg gtg cgg gtt	1589
Gly Ser Gly His Phe Leu Val Ser Ala Leu Asn Glu Met Val Arg Val	
510 515 520	
gct tat gag cta gga ctt att gct tcc ttg tat cgc tac gat ctt aaa	1637
Ala Tyr Glu Leu Gly Leu Ile Ala Ser Leu Tyr Arg Tyr Asp Leu Lys	
525 530 535	
tta gaa aac gat gaa atc atc att cac cac acg cca acg ggt gaa atc	1685
Leu Glu Asn Asp Glu Ile Ile Ile His His Thr Pro Thr Gly Glu Ile	
540 545 550 555	
ttt aac tac ata aaa cca gat agc gaa aac gac ccc cac cac cac atc	1733
Phe Asn Tyr Ile Lys Pro Asp Ser Glu Asn Asp Pro His His His Ile	
560 565 570	
caa aaa gaa ctt ttt aat ctt aaa aaa tcc att att gaa aac tgc ctt	1781
Gln Lys Glu Leu Phe Asn Leu Lys Lys Ser Ile Ile Glu Asn Cys Leu	

575					580					585					
ttt ggc gtg gat att aac ccc aat tct tgc gaa atc acc aag ctc agg	1829														
Phe Gly Val Asp Ile Asn Pro Asn Ser Cys Glu Ile Thr Lys Leu Arg															
590 595 600															
cta tgg ata gag ctt tta aaa tac agc tat tat att ttt gaa aag ggc	1877														
Leu Trp Ile Glu Leu Leu Lys Tyr Ser Tyr Tyr Ile Phe Glu Lys Gly															
605 610 615															
aag aac act aac gcg ctt gaa acc ctc ccc aac att gat att aac att	1925														
Lys Asn Thr Asn Ala Leu Glu Thr Leu Pro Asn Ile Asp Ile Asn Ile															
620 625 630 635															
aag tgc gct aat tcg ctc att tct agg ttt gcc ctc aaa gat aaa gcc	1973														
Lys Cys Ala Asn Ser Leu Ile Ser Arg Phe Ala Leu Lys Asp Lys Ala															
640 645 650															
ttg tta aaa agc gaa aaa aat aaa aac cta gaa tac tct atc gct gaa	2021														
Leu Leu Lys Ser Glu Lys Asn Lys Asn Leu Glu Tyr Ser Ile Ala Glu															
655 660 665															
tac aaa gaa ctc gtt aaa atc tat aaa gac cct aaa atc tta gaa acc	2069														
Tyr Lys Glu Leu Val Lys Ile Tyr Lys Asp Pro Lys Ile Leu Glu Thr															
670 675 680															
cta acg cac ccc ata aaa gac tct aac gcc gtt aga aaa tac gct aaa	2117														
Leu Thr His Pro Ile Lys Asp Ser Asn Ala Val Arg Lys Tyr Ala Lys															
685 690 695															
gaa cgc ctt tat caa gaa cta aaa caa aat cct aac aaa gat ttt aaa	2165														
Glu Arg Leu Tyr Gln Glu Leu Lys Gln Asn Pro Asn Lys Asp Phe Lys															
700 705 710 715															
aag gct ctc aat gat agg ata gag aaa att aaa aaa gct ttt aaa ctc	2213														
Lys Ala Leu Asn Asp Arg Ile Glu Lys Ile Lys Lys Ala Phe Lys Leu															
720 725 730															
act tta aac ccc cct cca aaa gaa tta aaa ttt aaa aaa ttt tta aaa	2261														
Thr Leu Asn Pro Pro Lys Glu Leu Lys Phe Lys Lys Phe Leu Lys															
735 740 745															
gag cat tta gaa ctc tat ggc aag agt atc tta gaa gag gca aac tac	2309														
Glu His Leu Glu Leu Tyr Gly Lys Ser Ile Leu Glu Glu Ala Asn Tyr															
750 755 760															
aac ggc tta gaa ttg gaa gcc cta gca tta gaa aag caa atg gcg aat	2357														
Asn Gly Leu Glu Leu Glu Ala Leu Ala Leu Glu Lys Gln Met Ala Asn															
765 770 775															
ctt ttt ttt gat tat aga ccc tac ccc aaa cta gac aaa tcg gat aaa	2405														
Leu Phe Phe Asp Tyr Arg Pro Tyr Pro Lys Leu Asp Lys Ser Asp Lys															
780 785 790 795															
gta gta gga cta gaa cat ttt aac cgc tat gtc cta aca tct tat aaa	2453														
Val Val Gly Leu Glu His Phe Asn Arg Tyr Val Leu Thr Ser Tyr Lys															
800 805 810															
gat tta caa gat gaa aac gaa cgc tac gct aac gct ctt gaa tgg cgc	2501														

Asp	Leu	Gln	Asp	Glu	Asn	Glu	Arg	Tyr	Ala	Asn	Ala	Leu	Glu	Trp	Arg		
			815					820					825				
ttt	gaa	ttc	cct	gaa	gtt	tta	gat	gat	gag	ggg	gat	ttt	tca	ggc	ttt	2549	
Phe	Glu	Phe	Pro	Glu	Val	Leu	Asp	Asp	Glu	Gly	Asp	Phe	Ser	Gly	Phe		
		830					835					840					
gat	tgc	atc	att	ggg	aat	cca	cct	tat	atc	cgc	caa	gaa	cac	atc	aaa	2597	
Asp	Cys	Ile	Ile	Gly	Asn	Pro	Pro	Tyr	Ile	Arg	Gln	Glu	His	Ile	Lys		
	845					850					855						
gac	tta	aag	cct	tta	tta	gaa	aag	caa	tac	caa	gat	ttc	tat	aac	agc	2645	
Asp	Leu	Lys	Pro	Leu	Leu	Glu	Lys	Gln	Tyr	Gln	Asp	Phe	Tyr	Asn	Ser		
	860				865					870					875		
acc	gct	gac	att	tac	acc	tac	ttt	ttt	gcc	ctg	gct	ttc	cac	ctt	tta	2693	
Thr	Ala	Asp		Tyr	Thr	Tyr	Phe	Phe	Ala	Leu	Ala	Phe	His	Leu	Leu		
				880					885					890			
aaa	gaa	aag	ggg	ttt	agc	gcl	ttc	atc	act	tct	aac	aaa	tat	acg	cga	2741	
Lys	Glu	Lys	Gly	Phe	Ser	Ala	Phe	Ile	Thr	Ser	Asn	Lys	Tyr	Thr	Arg		
			895					900					905				
gcc	aaa	tac	ggc	gct	aaa	ttg	agg	gaa	tgg	ctg	ctc	aaa	aaa	acc	acc	2789	
Ala	Lys	Tyr	Gly	Ala	Lys	Leu	Arg	Glu	Trp	Leu	Leu	Lys	Lys	Thr	Thr		
		910					915					920					
atc	gtc	agc	tac	atg	gaa	cta	aac	gcc	tta	aaa	gtc	ttt	gag	agc	gct	2837	
Ile	Val	Ser	Tyr	Met	Glu	Leu	Asn	Ala	Leu	Lys	Val	Phe	Glu	Ser	Ala		
	925					930					935						
gca	gtg	gat	acc	agc	atc	att	cat	ttc	atc	aaa	caa	acg	ccc	tct	aaa	2885	
Ala	Val	Asp	Thr	Ser	Ile	Ile	His	Phe	Ile	Lys	Gln	Thr	Pro	Ser	Lys		
	940				945					950					955		
gag	agc	gaa	ttt	aaa	tat	tac	gaa	ccc	acc	cca	aac	gat	aaa	gac	gat	2933	
Glu	Ser	Glu	Phe	Lys	Tyr	Tyr	Glu	Pro	Thr	Pro	Asn	Asp	Lys	Asp	Asp		
				960				965						970			
ttg	aaa	agc	acc	cca	cac	ctt	ttg	atg	aaa	caa	aac	gtg	ctt	tca	aca	2981	
Leu	Lys	Ser	Thr	Pro	His	Leu	Leu	Met	Lys	Gln	Asn	Val	Leu	Ser	Thr		
			975					980					985				
gaa	agc	ttt	att	ttt	gcc	aac	gcc	acg	ctt	tta	gat	ttg	agg	gac	aaa	3029	
Glu	Ser	Phe	Ile	Phe	Ala	Asn	Ala	Thr	Leu	Leu	Asp	Leu	Arg	Asp	Lys		
		990					995					1000					
ata	gag	agt	gtt	ggc	acc	ccg	ctt	aaa	gac	tgg	gac	att	caa	atc	aat	3077	
Ile	Glu	Ser	Val	Gly	Thr	Pro	Leu	Lys	Asp	Trp	Asp	Ile	Gln	Ile	Asn		
	1005					1010					1015						
tat	ggg	ata	aaa	acc	ggc	gcg	aac	gaa	gcc	ttt	atc	att	ccc	act	gaa	3125	
Tyr	Gly	Ile	Lys	Thr	Gly	Ala	Asn	Glu	Ala	Phe	Ile	Ile	Pro	Thr	Glu		
	1020				1025					1030					1035		
aaa	aga	gaa	gag	atc	tta	aac	gct	tgc	aag	acg	caa	gaa	gaa	agg	gag	3173	
Lys	Arg	Glu	Glu	Ile	Leu	Asn	Ala	Cys	Lys	Thr	Gln	Glu	Glu	Arg	Glu		
				1040				1045						1050			

cgc aca gag agg ctt att aag cct att tta aga ggg aaa gac att aaa	3221
Arg Thr Glu Arg Leu Ile Lys Pro Ile Leu Arg Gly Lys Asp Ile Lys	
1055 1060 1065	
agg tat tct tat gag tgg gcg cat ttg tgg gtt atc aac acc cat aac	3269
Arg Tyr Ser Tyr Glu Trp Ala His Leu Trp Val Ile Asn Thr His Asn	
1070 1075 1080	
ggc tac act tct tct ctc aaa tcc aaa atc cct ccc att gat ata gaa	3317
Gly Tyr Thr Ser Ser Leu Lys Ser Lys Ile Pro Pro Ile Asp Ile Glu	
1085 1090 1095	
aaa tac ccc gca att aaa gcg cat tta gac gct cat tac gac act att	3365
Lys Tyr Pro Ala Ile Lys Ala His Leu Asp Ala His Tyr Asp Thr Ile	
1100 1105 1110 1115	
gca aca cga tgc gat caa gga gac acc ccc tat cac tta agg aat tgc	3413
Ala Thr Arg Cys Asp Gln Gly Asp Thr Pro Tyr His Leu Arg Asn Cys	
1120 1125 1130	
gcg tat tta gag gat ttt gaa aaa gag aaa att gtg tgg gca agt gtg	3461
Ala Tyr Leu Glu Asp Phe Glu Lys Glu Lys Ile Val Trp Ala Ser Val	
1135 1140 1145	
gga ttt gtt gaa tat tgt atg atc cca gga tta ttg ata ctt gat aca	3509
Gly Phe Val Glu Tyr Cys Met Ile Pro Gly Leu Leu Ile Leu Asp Thr	
1150 1155 1160	
aat tat ttt ttt gaa gtc agt aaa ttt ggc aat aca aaa aac tat ttg	3557
Asn Tyr Phe Phe Glu Val Ser Lys Phe Gly Asn Thr Lys Asn Tyr Leu	
1165 1170 1175	
ctt gga ctt tta aat tca aaa ttg cta act ttt tgg tta aaa gct aaa	3605
Leu Gly Leu Leu Asn Ser Lys Leu Leu Thr Phe Trp Leu Lys Ala Lys	
1180 1185 1190 1195	
aat aca cca tta ggc gat atg gga gct tat aga aat tat aag tat aat	3653
Asn Thr Pro Leu Gly Asp Met Gly Ala Tyr Arg Asn Tyr Lys Tyr Asn	
1200 1205 1210	
att atg gag tta ccg atg gta aaa ata acg gca aaa aat aaa aaa atc	3701
Ile Met Glu Leu Pro Met Val Lys Ile Thr Ala Lys Asn Lys Lys Ile	
1215 1220 1225	
gcc gat aaa atc atc gct tta gtg gat aaa atc cta caa gca aaa gaa	3749
Ala Asp Lys Ile Ile Ala Leu Val Asp Lys Ile Leu Gln Ala Lys Glu	
1230 1235 1240	
aaa gac cct aaa gcc aac acc caa aag tta gaa aaa gaa att gac gcc	3797
Lys Asp Pro Lys Ala Asn Thr Gln Lys Leu Glu Lys Glu Ile Asp Ala	
1245 1250 1255	
tta gtc tat cag ctc tac cac ctc acc gat gaa gaa att aag atc att	3845
Leu Val Tyr Gln Leu Tyr His Leu Thr Asp Glu Glu Ile Lys Ile Ile	
1260 1265 1270 1275	
gaa gag ggg cag tgaatggaaa agttatttga aaagatattg catgaaatga	3897
Glu Glu Gly Gln	

gatcaa

3903

<210> 388

<211> 1279

<212> PRT

<213> Helicobacter pylori

<400> 388

Met	Asp	Tyr	Lys	Lys	Leu	Asp	Leu	Pro	Asn	Thr	Asn	Tyr	Pro	Asn	Gln
1				5					10					15	
Glu	Gln	Leu	Lys	Ala	Phe	Glu	Thr	Ala	Phe	Asp	Ala	Phe	Leu	Glu	Thr
			20					25					30		
Asn	Gln	Gln	Glu	Asn	Glu	Asn	His	Gln	Asn	Asp	Ala	Phe	Asn	Asp	Leu
		35				40					45				
Leu	Lys	Gly	Val	Phe	Lys	Tyr	Lys	Val	Lys	Pro	Thr	Lys	Lys	Ile	Asp
50					55						60				
Ser	Thr	Ile	Leu	Asn	Glu	Asn	Asn	Glu	Val	Glu	Val	Ile	Ile	Glu	Phe
65				70						75				80	
Lys	Ala	Leu	Lys	Asn	Pro	Asn	Glu	Phe	Ile	Lys	Lys	Gly	Asp	Leu	Asn
			85						90					95	
Val	Lys	Ala	Phe	His	Glu	Ser	Leu	Leu	Ser	Tyr	Leu	Thr	Glu	Arg	Lys
		100					105						110		
Glu	Gly	Asn	Asn	Asn	Leu	Lys	His	Leu	Ile	Leu	Ala	Thr	Ile	Lys	Glu
		115					120						125		
Leu	Tyr	Ile	Ile	Asp	Ala	Asn	Glu	Phe	Glu	Val	Phe	Asn	Lys	Asp	Lys
	130					135					140				
Glu	Ile	Glu	Asn	Ala	Phe	Lys	Asn	Cys	His	Asp	Arg	Lys	Gly	Asn	Asp
145				150						155				160	
Thr	Arg	Thr	Lys	Ala	Phe	Tyr	Asp	Ala	Cys	Gln	Lys	Arg	Leu	Asn	Glu
			165						170					175	
Phe	Asp	Arg	Ser	Leu	Lys	Tyr	His	Tyr	Ile	Pro	Leu	Lys	Lys	Glu	Asn
		180						185					190		
Leu	Ala	Leu	Ile	Tyr	Gln	Ala	Leu	Ser	Pro	Asn	Phe	Leu	Leu	Lys	Ile
	195						200					205			
Pro	Lys	Tyr	Ser	Asp	Ala	Asn	Thr	Leu	Asn	Lys	Asp	Phe	Tyr	Glu	Glu
	210					215					220				
Leu	Leu	Tyr	Ile	Leu	Gly	Leu	Glu	Glu	Gln	Asn	Asp	Lys	Gly	Lys	Ile
225				230						235				240	
Leu	Ile	Lys	Pro	Ser	Arg	Thr	Gln	Asn	Ser	Leu	Ser	Asp	Ala	Leu	Lys
				245					250					255	
Lys	Glu	Tyr	Lys	Asn	Leu	Asp	Asp	Glu	Glu	Val	Met	Ala	Leu	Leu	Ile
		260						265					270		
Ala	Trp	Asn	Asn	Arg	Ile	Leu	Phe	Leu	Arg	Leu	Leu	Glu	Ser	Leu	Leu
		275					280					285			
Ile	Ser	Phe	Lys	His	Phe	Glu	Asn	Pro	Phe	Leu	Thr	Thr	Glu	Asn	Phe
	290					295					300				
Glu	Asn	Phe	Asn	Asp	Leu	Asn	Thr	Leu	Phe	Phe	Glu	Val	Leu	Ala	Lys
305					310					315				320	
Lys	Asn	Ser	Glu	Arg	Leu	Pro	Glu	Ile	Lys	Glu	Asp	Lys	Ile	Leu	Glu
			325						330					335	
Lys	Ile	Pro	Tyr	Leu	Asn	Ser	Ser	Leu	Phe	Asp	Lys	Thr	Pro	Leu	Glu
		340						345					350		
Leu	Lys	Gly	His	Glu	Ile	Lys	Leu	Leu	Asp	Asn	Lys	Lys	Leu	Glu	Ile
		355					360					365			
Tyr	Lys	Asn	Ser	Val	Leu	Lys	Lys	His	Lys	Asp	Tyr	Gln	Lys	Glu	Lys
	370					375					380				
Pro	Leu	Pro	Leu	Leu	Lys	Tyr	Leu	Phe	Lys	Phe	Leu	Arg	Leu	Tyr	Lys
385				390						395					400

Phe	Thr	Thr	Thr	Pro	Lys	Asp	Ile	Lys	Asp	Asn	Thr	Asp	Thr	Ser	Glu
				405					410					415	
Ser	Arg	Leu	Ile	Asn	Pro	Ser	Val	Leu	Gly	Leu	Val	Phe	Glu	Lys	Leu
			420					425					430		
Asn	Gly	Tyr	Lys	Glu	Gly	Ser	Phe	Tyr	Thr	Pro	Ser	Phe	Ile	Thr	Ser
		435					440					445			
Tyr	Met	Cys	Lys	Glu	Ser	Ile	Thr	Pro	Ile	Val	Leu	Asp	Lys	Phe	Asn
	450					455					460				
Ala	Ile	Tyr	Gln	Trp	Asp	Cys	Glu	Asn	Leu	Lys	Ala	Leu	Arg	Gly	Glu
465					470					475					480
Ile	Asp	Arg	Asn	Phe	Ser	Asn	Glu	Lys	Ala	Lys	Glu	Tyr	Leu	Asn	Thr
				485					490					495	
Leu	Leu	Thr	Leu	Arg	Ile	Cys	Asp	Pro	Ala	Val	Gly	Ser	Gly	His	Phe
			500					505					510		
Leu	Val	Ser	Ala	Leu	Asn	Glu	Met	Val	Arg	Val	Ala	Tyr	Glu	Leu	Gly
		515					520					525			
Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Tyr	Asp	Leu	Lys	Leu	Glu	Asn	Asp	Glu
	530					535					540				
Ile	Ile	Ile	His	His	Thr	Pro	Thr	Gly	Glu	Ile	Phe	Asn	Tyr	Ile	Lys
545					550					555					560
Pro	Asp	Ser	Glu	Asn	Asp	Pro	His	His	His	Ile	Gln	Lys	Glu	Leu	Phe
				565					570					575	
Asn	Leu	Lys	Lys	Ser	Ile	Ile	Glu	Asn	Cys	Leu	Phe	Gly	Val	Asp	Ile
			580					585					590		
Asn	Pro	Asn	Ser	Cys	Glu	Ile	Thr	Lys	Leu	Arg	Leu	Trp	Ile	Glu	Leu
		595					600					605			
Leu	Lys	Tyr	Ser	Tyr	Tyr	Ile	Phe	Glu	Lys	Gly	Lys	Asn	Thr	Asn	Ala
	610					615					620				
Leu	Glu	Thr	Leu	Pro	Asn	Ile	Asp	Ile	Asn	Ile	Lys	Cys	Ala	Asn	Ser
625					630					635					640
Leu	Ile	Ser	Arg	Phe	Ala	Leu	Lys	Asp	Lys	Ala	Leu	Leu	Lys	Ser	Glu
				645					650					655	
Lys	Asn	Lys	Asn	Leu	Glu	Tyr	Ser	Ile	Ala	Glu	Tyr	Lys	Glu	Leu	Val
			660					665					670		
Lys	Ile	Tyr	Lys	Asp	Pro	Lys	Ile	Leu	Glu	Thr	Leu	Thr	His	Pro	Ile
		675					680					685			
Lys	Asp	Ser	Asn	Ala	Val	Arg	Lys	Tyr	Ala	Lys	Glu	Arg	Leu	Tyr	Gln
	690					695					700				
Glu	Leu	Lys	Gln	Asn	Pro	Asn	Lys	Asp	Phe	Lys	Lys	Ala	Leu	Asn	Asp
705				710						715					720
Arg	Ile	Glu	Lys	Ile	Lys	Lys	Ala	Phe	Lys	Leu	Thr	Leu	Asn	Pro	Pro
				725					730					735	
Pro	Lys	Glu	Leu	Lys	Phe	Lys	Lys	Phe	Leu	Lys	Glu	His	Leu	Glu	Leu
			740					745					750		
Tyr	Gly	Lys	Ser	Ile	Leu	Glu	Glu	Ala	Asn	Tyr	Asn	Gly	Leu	Glu	Leu
		755					760					765			
Glu	Ala	Leu	Ala	Leu	Glu	Lys	Gln	Met	Ala	Asn	Leu	Phe	Phe	Asp	Tyr
	770					775					780				
Arg	Pro	Tyr	Pro	Lys	Leu	Asp	Lys	Ser	Asp	Lys	Val	Val	Gly	Leu	Glu
785				790						795					800
His	Phe	Asn	Arg	Tyr	Val	Leu	Thr	Ser	Tyr	Lys	Asp	Leu	Gln	Asp	Glu
				805					810					815	
Asn	Glu	Arg	Tyr	Ala	Asn	Ala	Leu	Glu	Trp	Arg	Phe	Glu	Phe	Pro	Glu
				820				825					830		
Val	Leu	Asp	Asp	Glu	Gly	Asp	Phe	Ser	Gly	Phe	Asp	Cys	Ile	Ile	Gly
		835					840					845			
Asn	Pro	Pro	Tyr	Ile	Arg	Gln	Glu	His	Ile	Lys	Asp	Leu	Lys	Pro	Leu
	850					855					860				
Leu	Glu	Lys	Gln	Tyr	Gln	Asp	Phe	Tyr	Asn	Ser	Thr	Ala	Asp	Ile	Tyr

865					870					875					880
Thr	Tyr	Phe	Phe	Ala	Leu	Ala	Phe	His	Leu	Leu	Lys	Glu	Lys	Gly	Phe
				885					890					895	
Ser	Ala	Phe	Ile	Thr	Ser	Asn	Lys	Tyr	Thr	Arg	Ala	Lys	Tyr	Gly	Ala
			900					905					910		
Lys	Leu	Arg	Glu	Trp	Leu	Leu	Lys	Thr	Thr	Ile	Val	Ser	Tyr	Met	
		915					920				925				
Glu	Leu	Asn	Ala	Leu	Lys	Val	Phe	Glu	Ser	Ala	Ala	Val	Asp	Thr	Ser
	930					935					940				
Ile	Ile	His	Phe	Ile	Lys	Gln	Thr	Pro	Ser	Lys	Glu	Ser	Glu	Phe	Lys
945					950				955						960
Tyr	Tyr	Glu	Pro	Thr	Pro	Asn	Asp	Lys	Asp	Asp	Leu	Lys	Ser	Thr	Pro
				965					970					975	
His	Leu	Leu	Met	Lys	Gln	Asn	Val	Leu	Ser	Thr	Glu	Ser	Phe	Ile	Phe
			980					985					990		
Ala	Asn	Ala	Thr	Leu	Leu	Asp	Leu	Arg	Asp	Lys	Ile	Glu	Ser	Val	Gly
		995					1000					1005			
Thr	Pro	Leu	Lys	Asp	Trp	Asp	Ile	Gln	Ile	Asn	Tyr	Gly	Ile	Lys	Thr
	1010					1015					1020				
Gly	Ala	Asn	Glu	Ala	Phe	Ile	Ile	Pro	Thr	Glu	Lys	Arg	Glu	Glu	Ile
1025					1030					1035				1040	
Leu	Asn	Ala	Cys	Lys	Thr	Gln	Glu	Glu	Arg	Glu	Arg	Thr	Glu	Arg	Leu
			1045						1050					1055	
Ile	Lys	Pro	Ile	Leu	Arg	Gly	Lys	Asp	Ile	Lys	Arg	Tyr	Ser	Tyr	Glu
		1060					1065					1070			
Trp	Ala	His	Leu	Trp	Val	Ile	Asn	Thr	His	Asn	Gly	Tyr	Thr	Ser	Ser
	1075					1080					1085				
Leu	Lys	Ser	Lys	Ile	Pro	Pro	Ile	Asp	Ile	Glu	Lys	Tyr	Pro	Ala	Ile
	1090				1095					1100					
Lys	Ala	His	Leu	Asp	Ala	His	Tyr	Asp	Thr	Ile	Ala	Thr	Arg	Cys	Asp
1105				1110					1115					1120	
Gln	Gly	Asp	Thr	Pro	Tyr	His	Leu	Arg	Asn	Cys	Ala	Tyr	Leu	Glu	Asp
			1125						1130					1135	
Phe	Glu	Lys	Glu	Lys	Ile	Val	Trp	Ala	Ser	Val	Gly	Phe	Val	Glu	Tyr
	1140						1145					1150			
Cys	Met	Ile	Pro	Gly	Leu	Leu	Ile	Leu	Asp	Thr	Asn	Tyr	Phe	Phe	Glu
	1155					1160					1165				
Val	Ser	Lys	Phe	Gly	Asn	Thr	Lys	Asn	Tyr	Leu	Leu	Gly	Leu	Leu	Asn
	1170				1175				1180						
Ser	Lys	Leu	Leu	Thr	Phe	Trp	Leu	Lys	Ala	Lys	Asn	Thr	Pro	Leu	Gly
1185				1190					1195					1200	
Asp	Met	Gly	Ala	Tyr	Arg	Asn	Tyr	Lys	Tyr	Asn	Ile	Met	Glu	Leu	Pro
			1205						1210				1215		
Met	Val	Lys	Ile	Thr	Ala	Lys	Asn	Lys	Lys	Ile	Ala	Asp	Lys	Ile	Ile
			1220				1225					1230			
Ala	Leu	Val	Asp	Lys	Ile	Leu	Gln	Ala	Lys	Glu	Lys	Asp	Pro	Lys	Ala
	1235					1240					1245				
Asn	Thr	Gln	Lys	Leu	Glu	Lys	Glu	Ile	Asp	Ala	Leu	Val	Tyr	Gln	Leu
	1250				1255					1260					
Tyr	His	Leu	Thr	Asp	Glu	Glu	Ile	Lys	Ile	Ile	Glu	Glu	Gly	Gln	
1265				1270					1275						

<210> 389
 <211> 1415
 <212> DNA
 <213> Helicobacter pylori

<220>

<221> CDS

<222> (28)...(1377)

<400> 389

tttaaatacat ttaaaaaaag gatagag atg caa aat aaa gaa att ggt gaa gaa 54
Met Gln Asn Lys Glu Ile Gly Glu Glu
1 5

aaa agc gtt aat gaa aaa aat gta gag gtt ttt aat cgt tat ttt ccc 102
Lys Ser Val Asn Glu Lys Asn Val Glu Val Phe Asn Arg Tyr Phe Pro
10 15 20 25

ggg tgc ttg agt ata gaa aat gat aac aag ctc acg ctg gat aca gga 150
Gly Cys Leu Ser Ile Glu Asn Asp Asn Lys Leu Thr Leu Asp Thr Gly
30 35 40

aaa tta aaa gcg tta cta ggg gat ttt agc gag ata aaa gaa gag ggc 198
Lys Leu Lys Ala Leu Leu Gly Asp Phe Ser Glu Ile Lys Glu Glu Gly
45 50 55

tat ggg ttg gat ttt gtg ggt aag aaa atc gcc tta aac caa gct ttt 246
Tyr Gly Leu Asp Phe Val Gly Lys Lys Ile Ala Leu Asn Gln Ala Phe
60 65 70

aag aaa aat cat aag att tta aag ccc tta aac gaa tcc act agc aag 294
Lys Lys Asn His Lys Ile Leu Lys Pro Leu Asn Glu Ser Thr Ser Lys
75 80 85

cac gtt ctc atc aag ggc gat aat tta gac gct ctc aaa atc tta aaa 342
His Val Leu Ile Lys Gly Asp Asn Leu Asp Ala Leu Lys Ile Leu Lys
90 95 100 105

caa agc tat agt gaa aaa atc aaa atg att tac att gac ccg cct tac 390
Gln Ser Tyr Ser Glu Lys Ile Lys Met Ile Tyr Ile Asp Pro Pro Tyr
110 115 120

aac acg aaa aac gag aat ttt atc tat ggc gat gat ttc tcg caa tcc 438
Asn Thr Lys Asn Glu Asn Phe Ile Tyr Gly Asp Asp Phe Ser Gln Ser
125 130 135

aat gaa gag gtt tta aaa aca ttg gat tat tct aaa gaa aaa ttg gat 486
Asn Glu Glu Val Leu Lys Thr Leu Asp Tyr Ser Lys Glu Lys Leu Asp
140 145 150

tac atc aag aac ctt ttt ggg tca aaa tgc cat agc ggg tgg ctt agt 534
Tyr Ile Lys Asn Leu Phe Gly Ser Lys Cys His Ser Gly Trp Leu Ser
155 160 165

ttc atg tat ccc aga ttg ttg ctc gct aaa gat ttg ctc aaa caa gac 582
Phe Met Tyr Pro Arg Leu Leu Leu Ala Lys Asp Leu Leu Lys Gln Asp
170 175 180 185

ggc gtg att ttc att tct att gac gat aac gaa tgc gct caa ctc aaa 630
Gly Val Ile Phe Ile Ser Ile Asp Asp Asn Glu Cys Ala Gln Leu Lys
190 195 200

ctt tta tgc gat gaa att ttt ggg gag ggg aat ttt gtg gcg tgt tta 678
Leu Leu Cys Asp Glu Ile Phe Gly Glu Gly Asn Phe Val Ala Cys Leu
205 210 215

aaa tgg aaa aag aaa aaa caa cca agt ttt tta tca aaa gta gcc gta	726
Lys Trp Lys Lys Lys Lys Gln Pro Ser Phe Leu Ser Lys Val Ala Val	
220 225 230	
ata tta gaa tat att tta gta tat gca aaa gat ttt agt cta att gat	774
Ile Leu Glu Tyr Ile Leu Val Tyr Ala Lys Asp Phe Ser Leu Ile Asp	
235 240 245	
aag tta ggt tta gat aat gta tct gat agc gat aaa cct atc att aat	822
Lys Leu Gly Leu Asp Asn Val Ser Asp Ser Asp Lys Pro Ile Ile Asn	
250 255 260 265	
acc tct aat aat tta tca aaa aga tat ttt aaa aaa ggt att agg gtt	870
Thr Ser Asn Asn Leu Ser Lys Arg Tyr Phe Lys Lys Gly Ile Arg Val	
270 275 280	
aaa tct gat tta aat ttt ata aag agt gga aag tat caa aat aag aca	918
Lys Ser Asp Leu Asn Phe Ile Lys Ser Gly Lys Tyr Gln Asn Lys Thr	
285 290 295	
atg acg att gaa ttt atg aat gat att ttt att gaa aat ggc aga act	966
Met Thr Ile Glu Phe Met Asn Asp Ile Phe Ile Glu Asn Gly Arg Thr	
300 305 310	
aaa aat gat ttt gaa tgt ata ggt aaa ttt aga aca gga caa gaa aat	1014
Lys Asn Asp Phe Glu Cys Ile Gly Lys Phe Arg Thr Gly Gln Glu Asn	
315 320 325	
att aat gaa ttt att gaa aaa gat tta att ttt ata aca aaa aat tta	1062
Ile Asn Glu Phe Ile Glu Lys Asp Leu Ile Phe Ile Thr Lys Asn Leu	
330 335 340 345	
ggg att aga aga gat tta tta gaa gaa gag caa tca aat aaa aaa aca	1110
Gly Ile Arg Arg Asp Leu Leu Glu Glu Glu Gln Ser Asn Lys Lys Thr	
350 355 360	
att aca gat tta tta aca gaa tgg gga caa aat caa gat gct act aat	1158
Ile Thr Asp Leu Leu Thr Glu Trp Gly Gln Asn Gln Asp Ala Thr Asn	
365 370 375	
gaa tta aat att tta ttt aat aat tct agc gat gaa agt att ttt tca	1206
Glu Leu Asn Ile Leu Phe Asn Asn Ser Ser Asp Glu Ser Ile Phe Ser	
380 385 390	
aat cct aaa cct aca aaa ctc atc aac cga ttg att gaa tta tcc acc	1254
Asn Pro Lys Pro Thr Lys Leu Ile Asn Arg Leu Ile Glu Leu Ser Thr	
395 400 405	
aac gag ggc gac atc atc tta gac ttt ttt gcc ggg agc ggg aca acc	1302
Asn Glu Gly Asp Ile Ile Leu Asp Phe Phe Ala Gly Ser Gly Thr Thr	
410 415 420 425	
gcg cat gcg gtg tta gag agt aat aag agc gat tat caa aaa tta agt	1350
Ala His Ala Val Leu Glu Ser Asn Lys Ser Asp Tyr Gln Lys Leu Ser	
430 435 440	
gag ggg ggg ggg ggt tat tta atg gtt tgaacgccgc atttaaagaa	1397
Glu Gly Gly Gly Gly Tyr Leu Met Val	

445

450

aggcgcttca ttctcgtc

1415

<210> 390

<211> 450

<212> PRT

<213> Helicobacter pylori

<400> 390

```

Met Gln Asn Lys Glu Ile Gly Glu Glu Lys Ser Val Asn Glu Lys Asn
 1          5          10          15
Val Glu Val Phe Asn Arg Tyr Phe Pro Gly Cys Leu Ser Ile Glu Asn
 20          25          30
Asp Asn Lys Leu Thr Leu Asp Thr Gly Lys Leu Lys Ala Leu Leu Gly
 35          40          45
Asp Phe Ser Glu Ile Lys Glu Glu Gly Tyr Gly Leu Asp Phe Val Gly
 50          55          60
Lys Lys Ile Ala Leu Asn Gln Ala Phe Lys Lys Asn His Lys Ile Leu
 65          70          75          80
Lys Pro Leu Asn Glu Ser Thr Ser Lys His Val Leu Ile Lys Gly Asp
 85          90          95
Asn Leu Asp Ala Leu Lys Ile Leu Lys Gln Ser Tyr Ser Glu Lys Ile
100          105          110
Lys Met Ile Tyr Ile Asp Pro Pro Tyr Asn Thr Lys Asn Glu Asn Phe
115          120          125
Ile Tyr Gly Asp Asp Phe Ser Gln Ser Asn Glu Glu Val Leu Lys Thr
130          135          140
Leu Asp Tyr Ser Lys Glu Lys Leu Asp Tyr Ile Lys Asn Leu Phe Gly
145          150          155          160
Ser Lys Cys His Ser Gly Trp Leu Ser Phe Met Tyr Pro Arg Leu Leu
165          170          175
Leu Ala Lys Asp Leu Leu Lys Gln Asp Gly Val Ile Phe Ile Ser Ile
180          185          190
Asp Asp Asn Glu Cys Ala Gln Leu Lys Leu Leu Cys Asp Glu Ile Phe
195          200          205
Gly Glu Gly Asn Phe Val Ala Cys Leu Lys Trp Lys Lys Lys Lys Gln
210          215          220
Pro Ser Phe Leu Ser Lys Val Ala Val Ile Leu Glu Tyr Ile Leu Val
225          230          235          240
Tyr Ala Lys Asp Phe Ser Leu Ile Asp Lys Leu Gly Leu Asp Asn Val
245          250          255
Ser Asp Ser Asp Lys Pro Ile Ile Asn Thr Ser Asn Asn Leu Ser Lys
260          265          270
Arg Tyr Phe Lys Lys Gly Ile Arg Val Lys Ser Asp Leu Asn Phe Ile
275          280          285
Lys Ser Gly Lys Tyr Gln Asn Lys Thr Met Thr Ile Glu Phe Met Asn
290          295          300
Asp Ile Phe Ile Glu Asn Gly Arg Thr Lys Asn Asp Phe Glu Cys Ile
305          310          315          320
Gly Lys Phe Arg Thr Gly Gln Glu Asn Ile Asn Glu Phe Ile Glu Lys
325          330          335
Asp Leu Ile Phe Ile Thr Lys Asn Leu Gly Ile Arg Arg Asp Leu Leu
340          345          350
Glu Glu Glu Gln Ser Asn Lys Lys Thr Ile Thr Asp Leu Leu Thr Glu
355          360          365
Trp Gly Gln Asn Gln Asp Ala Thr Asn Glu Leu Asn Ile Leu Phe Asn
370          375          380
Asn Ser Ser Asp Glu Ser Ile Phe Ser Asn Pro Lys Pro Thr Lys Leu

```


130		135		140		145	
ttt gat aag cgc gat ttg aat gaa ttc gct cta gtg atc act gat gaa	537						
Phe Asp Lys Arg Asp Leu Asn Glu Phe Ala Leu Val Ile Thr Asp Glu							
		150		155		160	
cag cac cga ttt ggc acc aag cag cgc tac caa tta gaa aaa atg gca	585						
Gln His Arg Phe Gly Thr Lys Gln Arg Tyr Gln Leu Glu Lys Met Ala							
		165		170		175	
agc agt aag ggt aat aaa ccc cat tct ttg caa ttt tcc gct acc ccc	633						
Ser Ser Lys Gly Asn Lys Pro His Ser Leu Gln Phe Ser Ala Thr Pro							
		180		185		190	
att cct cgc acg ctc gcc cta gcc aaa agc gcg ttt gtg aaa acg acc	681						
Ile Pro Arg Thr Leu Ala Leu Ala Lys Ser Ala Phe Val Lys Thr Thr							
		195		200		205	
atg att aga gaa atc cct tat cct aaa gag att gaa act cta gtc ttg	729						
Met Ile Arg Glu Ile Pro Tyr Pro Lys Glu Ile Glu Thr Leu Val Leu							
		210		215		220	
cat aaa aga gat ttt aaa ata gtg atg gag aaa atc agc gaa gaa atc	777						
His Lys Arg Asp Phe Lys Ile Val Met Glu Lys Ile Ser Glu Glu Ile							
		230		235		240	
gct aaa aac cat caa gtc att gtc gtc tat ccg ctg gtg aat gag agc	825						
Ala Lys Asn His Gln Val Ile Val Val Tyr Pro Leu Val Asn Glu Ser							
		245		250		255	
gaa aaa atc ccg tat tta tcg ctc agt gag ggg gcg agt ttt tgg caa	873						
Glu Lys Ile Pro Tyr Leu Ser Leu Ser Glu Gly Ala Ser Phe Trp Gln							
		260		265		270	
aaa cgc ttt aaa aag gtt tat acc act tca ggg caa gat aaa aat aaa	921						
Lys Arg Phe Lys Lys Val Tyr Thr Thr Ser Gly Gln Asp Lys Asn Lys							
		275		280		285	
gaa gaa gtg att gaa gaa ttt aga gaa tcc ggg agc att ctt tta gcg	969						
Glu Glu Val Ile Glu Glu Phe Arg Glu Ser Gly Ser Ile Leu Leu Ala							
		290		295		300	
act acg ctc att gag gtg ggc att tct tta cca cga ttg agc gtg atg	1017						
Thr Thr Leu Ile Glu Val Gly Ile Ser Leu Pro Arg Leu Ser Val Met							
		310		315		320	
gtg att tta gcg ccc gaa agg tta ggc tta gcg act tta cac cag tta	1065						
Val Ile Leu Ala Pro Glu Arg Leu Gly Leu Ala Thr Leu His Gln Leu							
		325		330		335	
agg ggg cgc gtt tct cgt aac ggc ttg aaa ggc tat tgt ttt tta tgc	1113						
Arg Gly Arg Val Ser Arg Asn Gly Leu Lys Gly Tyr Cys Phe Leu Cys							
		340		345		350	
acg atc caa gaa gaa aac gaa cga tta gaa aag ttt gct gat gaa ttg	1161						
Thr Ile Gln Glu Glu Asn Glu Arg Leu Glu Lys Phe Ala Asp Glu Leu							
		355		360		365	
gac ggc ttt aaa atc gct gaa ttg gat tta gaa tac aga aaa agc ggg	1209						

Asp	Gly	Phe	Lys	Ile	Ala	Glu	Leu	Asp	Leu	Glu	Tyr	Arg	Lys	Ser	Gly	
370					375					380					385	
gat tta ctc cag gga ggg gag cag agc ggg aat agt ttt gaa tac att 1257																
Asp	Leu	Leu	Gln	Gly	Gly	Glu	Gln	Ser	Gly	Asn	Ser	Phe	Glu	Tyr	Ile	
				390					395					400		
gac tta gcc aaa gat gaa aac att atc gct gaa gtg aaa cgg gat ttt 1305																
Asp	Leu	Ala	Lys	Asp	Glu	Asn	Ile	Ile	Ala	Glu	Val	Lys	Arg	Asp	Phe	
			405					410					415			
tta aag gcc gct agc gtt tca cgg gga aca ttt gaa aat tgaaaattaa 1354																
Leu	Lys	Ala	Ala	Ser	Val	Ser	Arg	Gly	Thr	Phe	Glu	Asn				
		420					425					430				
ggcagaattg ggtaatttaa atcatttaaaa aaaag 1389																

<210> 392

<211> 430

<212> PRT

<213> Helicobacter pylori

<400> 392

Met	Leu	Phe	Tyr	Met	Lys	Asn	Leu	Glu	Arg	Lys	Lys	Leu	Gln	Phe	Gly	
1				5					10					15		
Ala	Lys	Ile	Ala	Cys	Pro	Asn	Asn	Asn	Glu	Arg	Leu	Lys	Ala	Phe	Ile	
			20					25					30			
Ala	Ser	Leu	Pro	Phe	Lys	Leu	Thr	Arg	Asp	Gln	Gln	Asn	Ala	Ile	Lys	
		35					40					45				
Glu	Ile	Gln	Asn	Asp	Leu	Thr	Ser	Ser	Ile	Ala	Cys	Lys	Arg	Leu	Ile	
	50					55					60					
Ile	Gly	Asp	Val	Gly	Cys	Gly	Lys	Thr	Met	Val	Ile	Leu	Ala	Ser	Met	
65					70				75						80	
Val	Leu	Thr	Tyr	Pro	Asn	Lys	Thr	Leu	Leu	Met	Ala	Pro	Thr	Ser	Ile	
				85					90					95		
Leu	Ala	Lys	Gln	Leu	Tyr	Asn	Glu	Ala	Leu	Lys	Phe	Leu	Pro	Pro	Tyr	
			100					105					110			
Phe	Glu	Val	Glu	Leu	Leu	Leu	Gly	Gly	Ser	Tyr	Lys	Lys	Arg	Ser	Asn	
		115					120					125				
His	Leu	Phe	Glu	Thr	Ile	Thr	His	Val	Val	Ile	Gly	Thr	Gln	Ala	Leu	
	130					135					140					
Leu	Phe	Asp	Lys	Arg	Asp	Leu	Asn	Glu	Phe	Ala	Leu	Val	Ile	Thr	Asp	
145					150					155					160	
Glu	Gln	His	Arg	Phe	Gly	Thr	Lys	Gln	Arg	Tyr	Gln	Leu	Glu	Lys	Met	
				165					170					175		
Ala	Ser	Ser	Lys	Gly	Asn	Lys	Pro	His	Ser	Leu	Gln	Phe	Ser	Ala	Thr	
			180					185					190			
Pro	Ile	Pro	Arg	Thr	Leu	Ala	Leu	Ala	Lys	Ser	Ala	Phe	Val	Lys	Thr	
		195					200					205				
Thr	Met	Ile	Arg	Glu	Ile	Pro	Tyr	Pro	Lys	Glu	Ile	Glu	Thr	Leu	Val	
	210					215					220					
Leu	His	Lys	Arg	Asp	Phe	Lys	Ile	Val	Met	Glu	Lys	Ile	Ser	Glu	Glu	
225					230					235					240	
Ile	Ala	Lys	Asn	His	Gln	Val	Ile	Val	Val	Tyr	Pro	Leu	Val	Asn	Glu	
				245						250				255		
Ser	Glu	Lys	Ile	Pro	Tyr	Leu	Ser	Leu	Ser	Glu	Gly	Ala	Ser	Phe	Trp	
			260					265					270			
Gln	Lys	Arg	Phe	Lys	Lys	Val	Tyr	Thr	Thr	Ser	Gly	Gln	Asp	Lys	Asn	
		275					280					285				

Lys Glu Glu Val Ile Glu Glu Phe Arg Glu Ser Gly Ser Ile Leu Leu
 290 295 300
 Ala Thr Thr Leu Ile Glu Val Gly Ile Ser Leu Pro Arg Leu Ser Val
 305 310 315 320
 Met Val Ile Leu Ala Pro Glu Arg Leu Gly Leu Ala Thr Leu His Gln
 325 330 335
 Leu Arg Gly Arg Val Ser Arg Asn Gly Leu Lys Gly Tyr Cys Phe Leu
 340 345 350
 Cys Thr Ile Gln Glu Glu Asn Glu Arg Leu Glu Lys Phe Ala Asp Glu
 355 360 365
 Leu Asp Gly Phe Lys Ile Ala Glu Leu Asp Leu Glu Tyr Arg Lys Ser
 370 375 380
 Gly Asp Leu Leu Gln Gly Gly Glu Gln Ser Gly Asn Ser Phe Glu Tyr
 385 390 395 400
 Ile Asp Leu Ala Lys Asp Glu Asn Ile Ile Ala Glu Val Lys Arg Asp
 405 410 415
 Phe Leu Lys Ala Ala Ser Val Ser Arg Gly Thr Phe Glu Asn
 420 425 430

<210> 393
 <211> 1463
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (47)...(1417)

<400> 393
 tgttattcct ttttcattca ccacttattc acgctataat aacgcc atg gat acc 55
 Met Asp Thr
 1

 aac aac aat att gaa aaa gaa atc ttg gcg cta gtc aaa caa aat cct 103
 Asn Asn Asn Ile Glu Lys Glu Ile Leu Ala Leu Val Lys Gln Asn Pro
 5 10 15

 aaa gtt agt ctc ata gag tat gaa aat tac ttt agc caa ctc aaa tac 151
 Lys Val Ser Leu Ile Glu Tyr Glu Asn Tyr Phe Ser Gln Leu Lys Tyr
 20 25 30 35

 aac cct aac gca agc aag agc gat att gcc ttt ttt tat gcc ccc aac 199
 Asn Pro Asn Ala Ser Lys Ser Asp Ile Ala Phe Phe Tyr Ala Pro Asn
 40 45 50

 caa gtc tta tgc acc acg att aca gct aaa tac ggc gcg ttg ctt aaa 247
 Gln Val Leu Cys Thr Thr Ile Thr Ala Lys Tyr Gly Ala Leu Leu Lys
 55 60 65

 gaa att tta agc cag aat aaa gtc ggc atg cat tta gcc cac agc gtg 295
 Glu Ile Leu Ser Gln Asn Lys Val Gly Met His Leu Ala His Ser Val
 70 75 80

 gat gtg cgt att gaa gta gcg cct aaa atc caa att aac gcc caa tct 343
 Asp Val Arg Ile Glu Val Ala Pro Lys Ile Gln Ile Asn Ala Gln Ser
 85 90 95

 aat atc aat tac aaa gcc ata aaa acg agc gtc aaa gac tct tac act 391

Asn	Ile	Asn	Tyr	Lys	Ala	Ile	Lys	Thr	Ser	Val	Lys	Asp	Ser	Tyr	Thr	
100					105					110					115	
ttt	gaa	aat	ttt	gtc	gta	ggc	tca	tgc	aat	aac	acc	gtt	tat	gaa	atc	439
Phe	Glu	Asn	Phe	Val	Val	Gly	Ser	Cys	Asn	Asn	Thr	Val	Tyr	Glu	Ile	
				120					125					130		
gct	aaa	aaa	gtc	gcc	caa	agc	gat	acc	ccc	cct	tat	aac	ccg	gtg	ctt	487
Ala	Lys	Lys	Val	Ala	Gln	Ser	Asp	Thr	Pro	Pro	Tyr	Asn	Pro	Val	Leu	
			135					140					145			
ttt	tat	ggc	ggc	aca	ggg	tta	ggc	aaa	acg	cac	att	tta	aac	gct	atc	535
Phe	Tyr	Gly	Gly	Thr	Gly	Leu	Gly	Lys	Thr	His	Ile	Leu	Asn	Ala	Ile	
		150					155					160				
ggc	aac	cat	gcc	cta	gaa	aag	cat	aaa	aaa	gtc	gtg	tta	gtc	act	tca	583
Gly	Asn	His	Ala	Leu	Glu	Lys	His	Lys	Lys	Val	Val	Leu	Val	Thr	Ser	
	165					170					175					
gaa	gac	ttt	ttg	aca	gac	ttt	tta	aag	cat	tta	gac	aac	aaa	acc	atg	631
Glu	Asp	Phe	Leu	Thr	Asp	Phe	Leu	Lys	His	Leu	Asp	Asn	Lys	Thr	Met	
180					185					190					195	
gat	tct	ttt	aaa	gca	aaa	tac	cgc	cat	tgc	gac	ttt	ttc	ttg	tta	gat	679
Asp	Ser	Phe	Lys	Ala	Lys	Tyr	Arg	His	Cys	Asp	Phe	Phe	Leu	Leu	Asp	
				200					205					210		
gac	gct	caa	ttt	ttg	caa	gga	aaa	ccc	aag	cta	gaa	gaa	gaa	ttt	ttc	727
Asp	Ala	Gln	Phe	Leu	Gln	Gly	Lys	Pro	Lys	Leu	Glu	Glu	Glu	Phe	Phe	
			215					220					225			
cac	acc	ttt	aac	gaa	ttg	cac	gcc	aac	agc	aaa	caa	atc	gta	ttg	att	775
His	Thr	Phe	Asn	Glu	Leu	His	Ala	Asn	Ser	Lys	Gln	Ile	Val	Leu	Ile	
		230					235					240				
tca	gac	cga	tcg	cct	aaa	aac	atc	gcc	ggc	tta	gaa	gat	cgc	tta	aaa	823
Ser	Asp	Arg	Ser	Pro	Lys	Asn	Ile	Ala	Gly	Leu	Glu	Asp	Arg	Leu	Lys	
	245					250					255					
tcg	cgc	ttt	gaa	tgg	ggg	ata	acc	gct	aaa	gtc	atg	ccc	cct	gat	tta	871
Ser	Arg	Phe	Glu	Trp	Gly	Ile	Thr	Ala	Lys	Val	Met	Pro	Pro	Asp	Leu	
260					265					270					275	
gaa	acc	aaa	ctt	tcc	att	gtc	aaa	caa	aaa	tgc	cag	ctc	aat	caa	atc	919
Glu	Thr	Lys	Leu	Ser	Ile	Val	Lys	Gln	Lys	Cys	Gln	Leu	Asn	Gln	Ile	
			280						285					290		
act	ttg	cct	gaa	gag	gtg	atg	gaa	tac	atc	gcc	caa	cac	atc	agc	gac	967
Thr	Leu	Pro	Glu	Glu	Val	Met	Glu	Tyr	Ile	Ala	Gln	His	Ile	Ser	Asp	
			295					300					305			
aat	atc	cgc	caa	atg	gaa	ggc	gcg	atc	att	aaa	atc	agc	gtg	aac	gcg	1015
Asn	Ile	Arg	Gln	Met	Glu	Gly	Ala	Ile	Ile	Lys	Ile	Ser	Val	Asn	Ala	
		310					315					320				
aac	ttg	atg	aac	gct	tcc	att	gat	ttg	aac	ctc	gct	aaa	acc	gtt	tta	1063
Asn	Leu	Met	Asn	Ala	Ser	Ile	Asp	Leu	Asn	Leu	Ala	Lys	Thr	Val	Leu	
	325					330					335					

gaa gat ttg caa aaa gat cat gct gaa ggt tca agc ttg gaa aat atc	1111
Glu Asp Leu Gln Lys Asp His Ala Glu Gly Ser Ser Leu Glu Asn Ile	
340 345 350 355	

cta ctc gct gtc gcg caa agc ctg aat ctc aaa tcc agc gaa atc aaa	1159
Leu Leu Ala Val Ala Gln Ser Leu Asn Leu Lys Ser Ser Glu Ile Lys	
360 365 370	

gtc tct tcg cgc caa aaa aat gtc gct ttg gcg agg aaa tta gtc gtg	1207
Val Ser Ser Arg Gln Lys Asn Val Ala Leu Ala Arg Lys Leu Val Val	
375 380 385	

tat ttc gcc agg ctt tat acc cct aac ccc acg ctc tcg ctc gct caa	1255
Tyr Phe Ala Arg Leu Tyr Thr Pro Asn Pro Thr Leu Ser Leu Ala Gln	
390 395 400	

ttt ttg gat tta aag gat cat tca agc att tct aaa atg tat tct ggc	1303
Phe Leu Asp Leu Lys Asp His Ser Ser Ile Ser Lys Met Tyr Ser Gly	
405 410 415	

gtt aaa aaa atg ctt gaa gaa gaa aaa agc cct ttt gtc tta agc ctt	1351
Val Lys Lys Met Leu Glu Glu Glu Lys Ser Pro Phe Val Leu Ser Leu	
420 425 430 435	

aga gaa gaa atc aaa aac cgc ttg aac gaa ttg aac gac aaa aaa acc	1399
Arg Glu Glu Ile Lys Asn Arg Leu Asn Glu Leu Asn Asp Lys Lys Thr	
440 445 450	

gct ttc aat tca agt gaa tgaaaaaagg cttatgaaaa agcgtttcat	1447
Ala Phe Asn Ser Ser Glu	
455	

tcacttcttt tcaaatt	1463
--------------------	------

<210> 394
 <211> 457
 <212> PRT
 <213> Helicobacter pylori

<400> 394	
Met Asp Thr Asn Asn Asn Ile Glu Lys Glu Ile Leu Ala Leu Val Lys	
1 5 10 15	
Gln Asn Pro Lys Val Ser Leu Ile Glu Tyr Glu Asn Tyr Phe Ser Gln	
20 25 30	
Leu Lys Tyr Asn Pro Asn Ala Ser Lys Ser Asp Ile Ala Phe Phe Tyr	
35 40 45	
Ala Pro Asn Gln Val Leu Cys Thr Thr Ile Thr Ala Lys Tyr Gly Ala	
50 55 60	
Leu Leu Lys Glu Ile Leu Ser Gln Asn Lys Val Gly Met His Leu Ala	
65 70 75 80	
His Ser Val Asp Val Arg Ile Glu Val Ala Pro Lys Ile Gln Ile Asn	
85 90 95	
Ala Gln Ser Asn Ile Asn Tyr Lys Ala Ile Lys Thr Ser Val Lys Asp	
100 105 110	
Ser Tyr Thr Phe Glu Asn Phe Val Val Gly Ser Cys Asn Asn Thr Val	
115 120 125	
Tyr Glu Ile Ala Lys Lys Val Ala Gln Ser Asp Thr Pro Pro Tyr Asn	
130 135 140	
Pro Val Leu Phe Tyr Gly Gly Thr Gly Leu Gly Lys Thr His Ile Leu	

-454-

gtg cta atg aca gaa tat tgg atc cct aaa aac atc aat ttt tta tgg	147
Val Leu Met Thr Glu Tyr Trp Ile Pro Lys Asn Ile Asn Phe Leu Trp	
30 35 40	
gcg atg ggg gtg att tta tta acc ctt ttt ggc gtg ctt gtg gtc tca	195
Ala Met Gly Val Ile Leu Leu Thr Leu Phe Gly Val Leu Val Val Ser	
45 50 55	
ggg att ttc ttg ctc atg tat tac aag cct gat gcg aaa atg gcg ttt	243
Gly Ile Phe Leu Leu Met Tyr Tyr Lys Pro Asp Ala Lys Met Ala Phe	
60 65 70	
gat agc gtg aat ttc acc atc atg caa gaa gtg gct tat ggc tgg ctt	291
Asp Ser Val Asn Phe Thr Ile Met Gln Glu Val Ala Tyr Gly Trp Leu	
75 80 85	
tgg cgc cac atg cat gcc acg gca gcg agc atg att ttt gtc atc att	339
Trp Arg His Met His Ala Thr Ala Ala Ser Met Ile Phe Val Ile Ile	
90 95 100 105	
tat atc cac atg ttt gtt ggc atc tat tat ggc tct tac aaa aag ggt	387
Tyr Ile His Met Phe Val Gly Ile Tyr Tyr Gly Ser Tyr Lys Lys Gly	
110 115 120	
cgt gag atg att tgg att agc ggg atg att ttg ttt gtg gtc ttt agc	435
Arg Glu Met Ile Trp Ile Ser Gly Met Ile Leu Phe Val Val Phe Ser	
125 130 135	
gcg gaa gcc ttt agc ggg tat atg ctg cct tgg ggg cag atg agt tat	483
Ala Glu Ala Phe Ser Gly Tyr Met Leu Pro Trp Gly Gln Met Ser Tyr	
140 145 150	
tgg gcc gca gcg gtt atc acg aat tta ttt gga ggc att cct ttc att	531
Trp Ala Ala Ala Val Ile Thr Asn Leu Phe Gly Gly Ile Pro Phe Ile	
155 160 165	
ggg gct gat gtg gtg gag tgg att aga ggc aat tat gtt gtg gcg gat	579
Gly Ala Asp Val Val Glu Trp Ile Arg Gly Asn Tyr Val Val Ala Asp	
170 175 180 185	
tcc act tta acg cgc ttt ttc atg ctc cat gtg ttt tta ctg ccc att	627
Ser Thr Leu Thr Arg Phe Phe Met Leu His Val Phe Leu Leu Pro Ile	
190 195 200	
gcg atc att cta ctt gtt ggg gtg cat ttt tat tct tta cgc atc ccg	675
Ala Ile Ile Leu Leu Val Gly Val His Phe Tyr Ser Leu Arg Ile Pro	
205 210 215	
cat gtc aat aac caa gaa ggc gaa gag att gac ttt gaa tta gaa gag	723
His Val Asn Asn Gln Glu Gly Glu Glu Ile Asp Phe Glu Leu Glu Glu	
220 225 230	
aag aaa ttc att gaa ggc aag aaa aaa gaa tcc aaa gtc att cct ttt	771
Lys Lys Phe Ile Glu Gly Lys Lys Lys Glu Ser Lys Val Ile Pro Phe	
235 240 245	
tgg ccg gtg ttc ttg tct aaa gat att ttt gtg gtt tgc gcg ttc atg	819
Trp Pro Val Phe Leu Ser Lys Asp Ile Phe Val Val Cys Ala Phe Met	
250 255 260 265	

gtc ttt ttc ttt tac ttg gtg tgt tac cac tat gat ttt gcg atg gat	867
Val Phe Phe Phe Tyr Leu Val Cys Tyr His Tyr Asp Phe Ala Met Asp	
270 275 280	
cct atc aac ttt gaa agg gct aac agc ctt aaa acg ccg cct cac att	915
Pro Ile Asn Phe Glu Arg Ala Asn Ser Leu Lys Thr Pro Pro His Ile	
285 290 295	
tac cct gaa tgg tat ttc tta tgg agc tat gaa gtc tta aga ggc ttt	963
Tyr Pro Glu Trp Tyr Phe Leu Trp Ser Tyr Glu Val Leu Arg Gly Phe	
300 305 310	
ttc ttt agc gct gat tta ggg cta atg gcc ttt ggc gtg gcg caa gtg	1011
Phe Phe Ser Ala Asp Leu Gly Leu Met Ala Phe Gly Val Ala Gln Val	
315 320 325	
att ttc ttt ttg cta ccc ttc ttg gat cga agt cca gtg gtc gct cct	1059
Ile Phe Phe Leu Leu Pro Phe Leu Asp Arg Ser Pro Val Val Ala Pro	
330 335 340 345	
gcg cac aaa cgg ccg gcg ttt atg gtg tgg ttt tgg ctt gta atc att	1107
Ala His Lys Arg Pro Ala Phe Met Val Trp Phe Trp Leu Val Ile Ile	
350 355 360	
gat atg att gtt tta acg atc tat ggt aaa ttg cct ccg ctt ggg att	1155
Asp Met Ile Val Leu Thr Ile Tyr Gly Lys Leu Pro Pro Leu Gly Ile	
365 370 375	
ggg aaa tac att ggc tta gcg ggt tca atc act ttt ttg gcc ctt ttc	1203
Gly Lys Tyr Ile Gly Leu Ala Gly Ser Ile Thr Phe Leu Ala Leu Phe	
380 385 390	
ttt gtg gta ttg ccc atc atc act atc gct gag agc aag aaa caa ggg	1251
Phe Val Val Leu Pro Ile Ile Thr Ile Ala Glu Ser Lys Lys Gln Gly	
395 400 405	
ggg gtt aga tgaaagagtt taagattcta atcatcctca ttgtggtggt	1300
Gly Val Arg	
410	
aggcgtgatt tattatgggg ttga	1324
<210> 396	
<211> 412	
<212> PRT	
<213> Helicobacter pylori	
<400> 396	
Met Ala Glu Ile Lys Lys Ala Lys Asn Leu Gly Glu Trp Leu Asp Met	
1 5 10 15	
Arg Leu Gly Thr Asn Lys Leu Val Lys Val Leu Met Thr Glu Tyr Trp	
20 25 30	
Ile Pro Lys Asn Ile Asn Phe Leu Trp Ala Met Gly Val Ile Leu Leu	
35 40 45	
Thr Leu Phe Gly Val Leu Val Val Ser Gly Ile Phe Leu Leu Met Tyr	
50 55 60	
Tyr Lys Pro Asp Ala Lys Met Ala Phe Asp Ser Val Asn Phe Thr Ile	
65 70 75 80	

Met	Gln	Glu	Val	Ala	Tyr	Gly	Trp	Leu	Trp	Arg	His	Met	His	Ala	Thr	
				85					90					95		
Ala	Ala	Ser	Met	Ile	Phe	Val	Ile	Ile	Tyr	Ile	His	Met	Phe	Val	Gly	
			100					105					110			
Ile	Tyr	Tyr	Gly	Ser	Tyr	Lys	Lys	Gly	Arg	Glu	Met	Ile	Trp	Ile	Ser	
		115					120					125				
Gly	Met	Ile	Leu	Phe	Val	Val	Phe	Ser	Ala	Glu	Ala	Phe	Ser	Gly	Tyr	
	130					135					140					
Met	Leu	Pro	Trp	Gly	Gln	Met	Ser	Tyr	Trp	Ala	Ala	Ala	Val	Ile	Thr	
145					150					155					160	
Asn	Leu	Phe	Gly	Gly	Ile	Pro	Phe	Ile	Gly	Ala	Asp	Val	Val	Glu	Trp	
			165						170					175		
Ile	Arg	Gly	Asn	Tyr	Val	Val	Ala	Asp	Ser	Thr	Leu	Thr	Arg	Phe	Phe	
			180					185					190			
Met	Leu	His	Val	Phe	Leu	Leu	Pro	Ile	Ala	Ile	Ile	Leu	Leu	Val	Gly	
		195					200					205				
Val	His	Phe	Tyr	Ser	Leu	Arg	Ile	Pro	His	Val	Asn	Asn	Gln	Glu	Gly	
	210					215					220					
Glu	Glu	Ile	Asp	Phe	Glu	Leu	Glu	Glu	Lys	Lys	Phe	Ile	Glu	Gly	Lys	
225					230					235					240	
Lys	Lys	Glu	Ser	Lys	Val	Ile	Pro	Phe	Trp	Pro	Val	Phe	Leu	Ser	Lys	
			245						250					255		
Asp	Ile	Phe	Val	Val	Cys	Ala	Phe	Met	Val	Phe	Phe	Phe	Tyr	Leu	Val	
		260						265					270			
Cys	Tyr	His	Tyr	Asp	Phe	Ala	Met	Asp	Pro	Ile	Asn	Phe	Glu	Arg	Ala	
		275					280					285				
Asn	Ser	Leu	Lys	Thr	Pro	Pro	His	Ile	Tyr	Pro	Glu	Trp	Tyr	Phe	Leu	
	290					295					300					
Trp	Ser	Tyr	Glu	Val	Leu	Arg	Gly	Phe	Phe	Phe	Ser	Ala	Asp	Leu	Gly	
305					310					315					320	
Leu	Met	Ala	Phe	Gly	Val	Ala	Gln	Val	Ile	Phe	Phe	Leu	Leu	Pro	Phe	
			325						330					335		
Leu	Asp	Arg	Ser	Pro	Val	Val	Ala	Pro	Ala	His	Lys	Arg	Pro	Ala	Phe	
			340					345					350			
Met	Val	Trp	Phe	Trp	Leu	Val	Ile	Ile	Asp	Met	Ile	Val	Leu	Thr	Ile	
		355					360					365				
Tyr	Gly	Lys	Leu	Pro	Pro	Leu	Gly	Ile	Gly	Lys	Tyr	Ile	Gly	Leu	Ala	
	370					375					380					
Gly	Ser	Ile	Thr	Phe	Leu	Ala	Leu	Phe	Phe	Val	Val	Leu	Pro	Ile	Ile	
385					390					395					400	
Thr	Ile	Ala	Glu	Ser	Lys	Lys	Gln	Gly	Gly	Val	Arg					
			405						410							

<210> 397

<211> 462

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (22)...(429)

<400> 397

caataaagaa	aggagcatca	g	atg	gca	atc	ttt	gat	aac	aat	aat	aaa	tcg	51
		Met	Ala	Ile	Phe	Asp	Asn	Asn	Asn	Lys	Ser		
		1				5					10		

gct	aat	gca	aaa	aca	gga	cca	gcg	act	atc	atc	gct	caa	ggc	aca	aaa	99
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----

Ala	Asn	Ala	Lys	Thr	Gly	Pro	Ala	Thr	Ile	Ile	Ala	Gln	Gly	Thr	Lys		
				15					20					25			
ata	aag	ggg	gag	ctt	cat	tta	gat	tac	cat	ttg	cac	gta	gat	ggc	gaa	147	
Ile	Lys	Gly	Glu	Leu	His	Leu	Asp	Tyr	His	Leu	His	Val	Asp	Gly	Glu		
			30					35					40				
tta	gaa	ggg	gtg	gtg	cat	tct	aaa	agc	acg	gtg	gtg	atc	ggg	caa	acc	195	
Leu	Glu	Gly	Val	Val	His	Ser	Lys	Ser	Thr	Val	Val	Ile	Gly	Gln	Thr		
			45				50					55					
ggc	tcg	gta	gtg	ggt	gag	att	ttt	act	aat	aaa	tta	gtg	gtc	agt	ggc	243	
Gly	Ser	Val	Val	Gly	Glu	Ile	Phe	Thr	Asn	Lys	Leu	Val	Val	Ser	Gly		
			60			65					70						
aag	ttc	act	ggc	acg	gtg	gag	gcg	gaa	gtg	gta	gaa	atc	atg	cct	tta	291	
Lys	Phe	Thr	Gly	Thr	Val	Glu	Ala	Glu	Val	Val	Glu	Ile	Met	Pro	Leu		
	75				80				85						90		
ggg	cac	ctt	gat	ggc	aaa	atc	tct	agc	caa	gag	ctt	gtg	gtg	gaa	aga	339	
Gly	His	Leu	Asp	Gly	Lys	Ile	Ser	Ser	Gln	Glu	Leu	Val	Val	Glu	Arg		
				95					100					105			
aag	ggg	att	ttg	att	ggg	gaa	act	cgc	cct	aag	aat	att	caa	ggg	ggg	387	
Lys	Gly	Ile	Leu	Ile	Gly	Glu	Thr	Arg	Pro	Lys	Asn	Ile	Gln	Gly	Gly		
			110					115					120				
gcg	ttg	tta	atc	aat	gag	caa	gaa	aag	aaa	att	gaa	aat	aaa			429	
Ala	Leu	Leu	Ile	Asn	Glu	Gln	Glu	Lys	Lys	Ile	Glu	Asn	Lys				
			125				130					135					
tagggaatga	tc	caatccag	cctttataga	gcc												462	

<210> 398

<211> 136

<212> PRT

<213> Helicobacter pylori

<400> 398

Met	Ala	Ile	Phe	Asp	Asn	Asn	Asn	Lys	Ser	Ala	Asn	Ala	Lys	Thr	Gly		
1				5				10						15			
Pro	Ala	Thr	Ile	Ile	Ala	Gln	Gly	Thr	Lys	Ile	Lys	Gly	Glu	Leu	His		
			20					25					30				
Leu	Asp	Tyr	His	Leu	His	Val	Asp	Gly	Glu	Leu	Glu	Gly	Val	Val	His		
		35					40					45					
Ser	Lys	Ser	Thr	Val	Val	Ile	Gly	Gln	Thr	Gly	Ser	Val	Val	Gly	Glu		
		50				55					60						
Ile	Phe	Thr	Asn	Lys	Leu	Val	Val	Ser	Gly	Lys	Phe	Thr	Gly	Thr	Val		
				70						75				80			
Glu	Ala	Glu	Val	Val	Glu	Ile	Met	Pro	Leu	Gly	His	Leu	Asp	Gly	Lys		
				85				90						95			
Ile	Ser	Ser	Gln	Glu	Leu	Val	Val	Glu	Arg	Lys	Gly	Ile	Leu	Ile	Gly		
			100					105					110				
Glu	Thr	Arg	Pro	Lys	Asn	Ile	Gln	Gly	Gly	Ala	Leu	Leu	Ile	Asn	Glu		
		115					120					125					
Gln	Glu	Lys	Lys	Ile	Glu	Asn	Lys										
		130				135											

<210> 399
 <211> 391
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (13)...(348)

<400> 399
 taaggagttt ct atg gat tgg ggt cgg gtc gtt cat gtg ctg ttc agc ctt 51
 Met Asp Trp Gly Arg Val Val His Val Leu Phe Ser Leu
 1 5 10

att tct tta acc acc att gca ggg ttt ttg tat gag cct aat acg gtg 99
 Ile Ser Leu Thr Thr Ile Ala Gly Phe Leu Tyr Glu Pro Asn Thr Val
 15 20 25

gtg ttg ttt gta gcg tta gct tta aac ctt att tct gtt acg ctt aaa 147
 Val Leu Phe Val Ala Leu Ala Leu Asn Leu Ile Ser Val Thr Leu Lys
 30 35 40 45

att ggg gtg atc aag cgt ttc gct tca gag cta ttg gcc agc tct tta 195
 Ile Gly Val Ile Lys Arg Phe Ala Ser Glu Leu Leu Ala Ser Ser Leu
 50 55 60

gcc acc gta ttg cat ctc ata ccg gca ttt gtg ttt tta cag att tta 243
 Ala Thr Val Leu His Leu Ile Pro Ala Phe Val Phe Leu Gln Ile Leu
 65 70 75

aat aat ttg gtt acc gct tac atg ctc atg atc ggg gcg ttg att agc 291
 Asn Asn Leu Val Thr Ala Tyr Met Leu Met Ile Gly Ala Leu Ile Ser
 80 85 90

aac gct ttc agt ctc atc ttt ttg ttg att gaa agc gtt gta acg agc 339
 Asn Ala Phe Ser Leu Ile Phe Leu Leu Ile Glu Ser Val Val Thr Ser
 95 100 105

gaa acg gat taaggggtag tgatggattt tatcaatata gaaaaaaaaat 388
 Glu Thr Asp
 110

ggc 391

<210> 400
 <211> 112
 <212> PRT
 <213> Helicobacter pylori

<400> 400
 Met Asp Trp Gly Arg Val Val His Val Leu Phe Ser Leu Ile Ser Leu
 1 5 10 15
 Thr Thr Ile Ala Gly Phe Leu Tyr Glu Pro Asn Thr Val Val Leu Phe
 20 25 30
 Val Ala Leu Ala Leu Asn Leu Ile Ser Val Thr Leu Lys Ile Gly Val
 35 40 45
 Ile Lys Arg Phe Ala Ser Glu Leu Leu Ala Ser Ser Leu Ala Thr Val
 50 55 60
 Leu His Leu Ile Pro Ala Phe Val Phe Leu Gln Ile Leu Asn Asn Leu

<400> 401															
gaataaaaaga gcttaggagg tttt atg gaa tta ttc aaa cga act aga atc															51
Met Glu Leu Phe Lys Arg Thr Arg Ile															
1 5															
tta agc ttc atg cgt tat tcc aat tat ggg gtg atc gtt tca gca att															99
Leu Ser Phe Met Arg Tyr Ser Asn Tyr Gly Val Ile Val Ser Ala Ile															
10 15 20 25															
tta gcg ctt cta gcg ttg ggg ctt ttg ttt ttc aaa ggg ttt tct tta															147
Leu Ala Leu Leu Ala Leu Gly Leu Leu Phe Phe Lys Gly Phe Ser Leu															
30 35 40															
ggg att gat ttt gcg ggg ggg agt ttg gtg caa gtg cgc tac act caa															195
Gly Ile Asp Phe Ala Gly Gly Ser Leu Val Gln Val Arg Tyr Thr Gln															
45 50 55															
aac gcc ccc att aaa gaa gtg cgc gat ctg ttt gaa aaa gaa gct cgc															243
Asn Ala Pro Ile Lys Glu Val Arg Asp Leu Phe Glu Lys Glu Ala Arg															
60 65 70															
ttc aaa ggc gtg caa gtg agc gaa ttt ggc tct aaa gaa gaa att tta															291
Phe Lys Gly Val Gln Val Ser Glu Phe Gly Ser Lys Glu Glu Ile Leu															
75 80 85															
atc aaa ttc cct ttt gta gaa acg gct gaa aat gaa gat ctg aac gct															339
Ile Lys Phe Pro Phe Val Glu Thr Ala Glu Asn Glu Asp Leu Asn Ala															
90 95 100 105															
atc gtg gcc aac att cta aaa ccc agc ggc gat ttt gaa atc cgt aaa															387
Ile Val Ala Asn Ile Leu Lys Pro Ser Gly Asp Phe Glu Ile Arg Lys															
110 115 120															
ttt gac acc gtg ggc cct aga gtg ggg agc gaa ttg aaa gag aaa ggc															435
Phe Asp Thr Val Gly Pro Arg Val Gly Ser Glu Leu Lys Glu Lys Gly															
125 130 135															
att ttg tcg ctg att tta gca tta ata gcg atc atg gtt tat gtg agt															483
Ile Leu Ser Leu Ile Leu Ala Leu Ile Ala Ile Met Val Tyr Val Ser															
140 145 150															
ttc cgc tat gaa tgg cgt ttt gct tta gcg agc gtc att gcg ctt gtg															531
Phe Arg Tyr Glu Trp Arg Phe Ala Leu Ala Ser Val Ile Ala Leu Val															

155	160	165	
cat gat gtg att tta gtg gca agc tcg gtg att gtt ttt aag att gat			579
His Asp Val Ile Leu Val Ala Ser Ser Val Ile Val Phe Lys Ile Asp			
170	175	180	185
atg aat ttg gaa gtg att gcg gcc ttg ctc acc ttg att ggg tat tcc			627
Met Asn Leu Glu Val Ile Ala Ala Leu Leu Thr Leu Ile Gly Tyr Ser			
	190	195	200
att aat gat acg atc att att ttt gac agg atc aga gaa gag atg cty			675
Ile Asn Asp Thr Ile Ile Ile Phe Asp Arg Ile Arg Glu Glu Met Xaa			
	205	210	215
tct caa aaa acc aaa aac gcc act caa gcc att gat gaa gcc att tct			723
Ser Gln Lys Thr Lys Asn Ala Thr Gln Ala Ile Asp Glu Ala Ile Ser			
	220	225	230
agc acg ctc acg cgc acg ctt tta act tct tta acc gtg ttt ttt gtg			771
Ser Thr Leu Thr Arg Thr Leu Leu Thr Ser Leu Thr Val Phe Phe Val			
	235	240	245
gtg ttg att ttg tgc gtg ttt ggg agt aag atc atc att ggc ttt tca			819
Val Leu Ile Leu Cys Val Phe Gly Ser Lys Ile Ile Ile Gly Phe Ser			
	250	255	260
ttg ccc atg tta ata ggc acg att gta ggg act tat agc tct att ttc			867
Leu Pro Met Leu Ile Gly Thr Ile Val Gly Thr Tyr Ser Ser Ile Phe			
	270	275	280
atc gcc cct aaa gtg gcg tta ttg tta ggc ttt gat atg gat aaa tat			915
Ile Ala Pro Lys Val Ala Leu Leu Leu Gly Phe Asp Met Asp Lys Tyr			
	285	290	295
tat gag aat gag act aga aaa att aaa aaa gct caa gag aaa gaa aaa			963
Tyr Glu Asn Glu Thr Arg Lys Ile Lys Lys Ala Gln Glu Lys Glu Lys			
	300	305	310
atg cgc cgt ttg tat gag agc ggt caa gtt taaggagttt ctatggattg			1013
Met Arg Arg Leu Tyr Glu Ser Gly Gln Val			
	315	320	
gggtcgggtc gttcatgtgc tg			1035
<210> 402			
<211> 323			
<212> PRT			
<213> Helicobacter pylori			
<220>			
<221> VARIANT			
<222> 217			
<223> Xaa = Any Amino Acid			
<400> 402			
Met Glu Leu Phe Lys Arg Thr Arg Ile Leu Ser Phe Met Arg Tyr Ser			
1	5	10	15
Asn Tyr Gly Val Ile Val Ser Ala Ile Leu Ala Leu Leu Ala Leu Gly			
	20	25	30

Ile	Ala	Ser	Leu	Cys	Ser	Leu	Val	Lys	Ala	Arg	Leu	Glu	Ile	Asn	Ile		
		20					25					30					
gac	atg	gta	aag	cca	atc	cct	gct	aaa	agc	cca	gcc	cct	aaa	ata	tgc	202	
Asp	Met	Val	Lys	Pro	Ile	Pro	Ala	Lys	Ser	Pro	Ala	Pro	Lys	Ile	Cys		
	35					40					45						
cac	cag	ctg	atg	cct	tta	ggg	cgt	gcg	gtg	att	tta	agc	ttt	tcg	ctt	250	
His	Gln	Leu	Met	Pro	Leu	Gly	Arg	Ala	Val	Ile	Leu	Ser	Phe	Ser	Leu		
	50				55					60					65		
ata	aaa	gtg	att	aag	aaa	atc	cct	aaa	ggg	ttg	ccc	aag	caa	agc	cct	298	
Ile	Lys	Val	Ile	Lys	Lys	Ile	Pro	Lys	Gly	Leu	Pro	Lys	Gln	Ser	Pro		
				70					75					80			
aaa	ata	acc	cct	aaa	agc	acc	tta	tcc	act	tct	aaa	ttg	atg	cta	gaa	346	
Lys	Ile	Thr	Pro	Lys	Ser	Thr	Leu	Ser	Thr	Ser	Lys	Leu	Met	Leu	Glu		
			85					90					95				
tca	acg	ctc	acc	cca	gcg	ttt	gca	aac	gcg	aat	aag	ggc	atg	atg	aaa	394	
Ser	Thr	Leu	Thr	Pro	Ala	Phe	Ala	Asn	Ala	Asn	Lys	Gly	Met	Met	Lys		
		100					105					110					
tac	ccg	cta	atg	ggg	gct	aga	aaa	tgc	tcc	aat	ctt	tct	aag	ggg	ctt	442	
Tyr	Pro	Leu	Met	Gly	Ala	Arg	Lys	Cys	Ser	Asn	Leu	Ser	Lys	Gly	Leu		
	115					120					125						
tgt	aag	gcg	ctc	gct	ttt	tct	tca	ata	gaa	tgc	aag	att	tct	tgc	tgc	490	
Cys	Lys	Ala	Leu	Ala	Phe	Ser	Ser	Ile	Glu	Cys	Lys	Ile	Ser	Cys	Cys		
	130				135					140					145		
tct	tta	ctc	aaa	agc	gct	cct	gaa	ctc	gtt	tct	gcg	tat	cgt	ttg	cct	538	
Ser	Leu	Leu	Lys	Ser	Ala	Pro	Glu	Leu	Val	Ser	Ala	Tyr	Arg	Leu	Pro		
				150					155					160			
agt	tcc	aaa	agc	tct	aca	ttt	tta	gaa	tct	tta	ggg	atc	ttc	acc	ggg	586	
Ser	Ser	Lys	Ser	Ser	Thr	Phe	Leu	Glu	Ser	Leu	Gly	Ile	Phe	Thr	Gly		
		165						170					175				
atc	ata	aaa	gct	aga	atc	act	gca	gca	atc	gtc	gca	tgg	ata	ccg	ctt	634	
Ile	Ile	Lys	Ala	Arg	Ile	Thr	Ala	Ala	Ile	Val	Ala	Trp	Ile	Pro	Leu		
		180					185					190					
tgatgcacgc	aaaaccaaag	caacaccct	aaaagc													670	

<210> 404

<211> 193

<212> PRT

<213> *Helicobacter pylori*

<400> 404

Met	Ile	Pro	Glu	Ile	Lys	Asp	Pro	Ser	Lys	Ile	Ala	Ile	Phe	Ala	Thr		
1				5					10					15			
Ser	Ile	Ala	Ser	Leu	Cys	Ser	Leu	Val	Lys	Ala	Arg	Leu	Glu	Ile	Asn		
		20						25					30				
Ile	Asp	Met	Val	Lys	Pro	Ile	Pro	Ala	Lys	Ser	Pro	Ala	Pro	Lys	Ile		
	35					40					45						
Cys	His	Gln	Leu	Met	Pro	Leu	Gly	Arg	Ala	Val	Ile	Leu	Ser	Phe	Ser		
	50					55					60						

Leu	Ser	Ser	Phe	Lys	Lys	Ala	Ser	Phe	Pro	Val	Ile	Ala	Ala	Ile	Gly	
		110					115					120				
ggc	atg	ata	gcc	cca	gga	ttg	att	tat	ttt	ttt	ctt	aac	gct	aac	acg	435
Gly	Met	Ile	Ala	Pro	Gly	Leu	Ile	Tyr	Phe	Phe	Leu	Asn	Ala	Asn	Thr	
	125					130					135					
cct	tcc	cag	cat	ggt	ttt	ggg	atc	cct	atg	gcg	acg	gat	att	gcg	ttc	483
Pro	Ser	Gln	His	Gly	Phe	Gly	Ile	Pro	Met	Ala	Thr	Asp	Ile	Ala	Phe	
140				145						150					155	
gct	tta	ggc	gtg	atc	atg	ctt	tta	ggc	aag	agg	gtg	cca	acc	gct	tta	531
Ala	Leu	Gly	Val	Ile	Met	Leu	Leu	Gly	Lys	Arg	Val	Pro	Thr	Ala	Leu	
				160					165					170		
aag	gtt	ttt	tta	atc	act	cta	gcg	gtg	gct	gat	gac	ttg	ggg	gct	att	579
Lys	Val	Phe	Leu	Ile	Thr	Leu	Ala	Val	Ala	Asp	Asp	Leu	Gly	Ala	Ile	
			175					180					185			
gtg	gtg	atc	gcg	ctc	ttt	tat	acc	acg	aat	tta	aaa	ttc	gca	tgg	ctt	627
Val	Val	Ile	Ala	Leu	Phe	Tyr	Thr	Thr	Asn	Leu	Lys	Phe	Ala	Trp	Leu	
			190				195					200				
tta	ggg	gct	tta	ggg	gtg	gtt	ctt	gtt	tta	gcc	gta	tta	aac	cgc	ctg	675
Leu	Gly	Ala	Leu	Gly	Val	Val	Leu	Val	Leu	Ala	Val	Leu	Asn	Arg	Leu	
	205					210					215					
aat	atg	cgc	tcg	ctc	atc	cct	tac	ttg	ctt	tta	ggg	gtg	ttg	ctt	tgg	723
Asn	Met	Arg	Ser	Leu	Ile	Pro	Tyr	Leu	Leu	Leu	Gly	Val	Leu	Leu	Trp	
220					225					230					235	
ttt	tgc	gtg	cat	caa	agc	ggt	atc	cat	gcg	acg	att	gct	gca	gtg	att	771
Phe	Cys	Val	His	Gln	Ser	Gly	Ile	His	Ala	Thr	Ile	Ala	Ala	Val	Ile	
				240					245					250		
cta	gct	ttt	atg	ata	ccg	gtg	aag	atc	cct	aaa	gat	tct	aaa	aat	gta	819
Leu	Ala	Phe	Met	Ile	Pro	Val	Lys	Ile	Pro	Lys	Asp	Ser	Lys	Asn	Val	
			255					260					265			
gag	ctt	ttg	gaa	cta	ggc	aaa	cga	tac	gca	gaa	acg	agt	tca	gga	gcg	867
Glu	Leu	Leu	Glu	Leu	Gly	Lys	Arg	Tyr	Ala	Glu	Thr	Ser	Ser	Gly	Ala	
	270					275						280				
ctt	ttg	agt	aaa	gag	cag	caa	gaa	atc	ttg	cat	tct	att	gaa	gaa	aaa	915
Leu	Leu	Ser	Lys	Glu	Gln	Gln	Glu	Ile	Leu	His	Ser	Ile	Glu	Glu	Lys	
	285					290					295					
gcg	agc	gcc	tta	caa	agc	ccc	tta	gaa	aga	ttg	gag	cat	ttt	cta	gcc	963
Ala	Ser	Ala	Leu	Gln	Ser	Pro	Leu	Glu	Arg	Leu	Glu	His	Phe	Leu	Ala	
300					305					310					315	
ccc	att	agc	ggg	tat	ttc	atc	atg	ccc	tta	ttc	gcg	ttt	gca	aac	gct	1011
Pro	Ile	Ser	Gly	Tyr	Phe	Ile	Met	Pro	Leu	Phe	Ala	Phe	Ala	Asn	Ala	
				320					325					330		
ggg	gtg	agc	gtt	gat	tct	agc	atc	aat	tta	gaa	gtg	gat	aag	gtg	ctt	1059
Gly	Val	Ser	Val	Asp	Ser	Ser	Ile	Asn	Leu	Glu	Val	Asp	Lys	Val	Leu	
			335					340					345			

tta ggg gtt att tta ggg ctt tgc ttg ggc aaa cct tta ggg att ttc	1107
Leu Gly Val Ile Leu Gly Leu Cys Leu Gly Lys Pro Leu Gly Ile Phe	
350 355 360	
tta atc act ttt ata agc gaa aag ctt aaa atc acc gca cgc cct aaa	1155
Leu Ile Thr Phe Ile Ser Glu Lys Leu Lys Ile Thr Ala Arg Pro Lys	
365 370 375	
ggc atc agc tgg tgg cat att tta ggg gct ggg ctt tta gca ggg att	1203
Gly Ile Ser Trp Trp His Ile Leu Gly Ala Gly Leu Leu Ala Gly Ile	
380 385 390 395	
ggc ttt acc atg tct atg ttt att tct aat ctg gcc ttc acg agc gag	1251
Gly Phe Thr Met Ser Met Phe Ile Ser Asn Leu Ala Phe Thr Ser Glu	
400 405 410	
cat aaa gac gct atg gaa gtg gca aaa att gcg att tta ctc gga tct	1299
His Lys Asp Ala Met Glu Val Ala Lys Ile Ala Ile Leu Leu Gly Ser	
415 420 425	
ttg att tct ggg atc ata ggg gct ttg tat tta ttt gcg cta gac aaa	1347
Leu Ile Ser Gly Ile Ile Gly Ala Leu Tyr Leu Phe Ala Leu Asp Lys	
430 435 440	
aga gcg gct tta aag aaa tagctaaaaa tgctataatt tgagattaa	1395
Arg Ala Ala Leu Lys Lys	
445	

acatctttta aggaaattaa atgggacaaa tt	1427
-------------------------------------	------

<210> 406

<211> 449

<212> PRT

<213> Helicobacter pylori

<400> 406

Met Gly Leu Lys Leu Lys Ile Leu Arg Leu Ser Met Asn Leu Lys Lys	
1 5 10 15	
Thr Glu Asn Ala Leu Ser Leu Thr Leu Lys Asn Phe Ile Lys Ser Glu	
20 25 30	
Ser Phe Gly Gly Ile Phe Leu Phe Leu Asn Ala Val Leu Ala Met Val	
35 40 45	
Val Ala Asn Ser Phe Leu Lys Glu Ser Tyr Phe Ala Leu Trp His Thr	
50 55 60	
Pro Phe Gly Phe Gln Ile Gly Asp Phe Phe Ile Gly Phe Ser Leu His	
65 70 75 80	
Asn Trp Ile Asp Asp Val Leu Met Ala Leu Phe Phe Leu Met Ile Gly	
85 90 95	
Leu Glu Ile Lys Arg Glu Leu Leu Phe Gly Glu Leu Ser Ser Phe Lys	
100 105 110	
Lys Ala Ser Phe Pro Val Ile Ala Ala Ile Gly Gly Met Ile Ala Pro	
115 120 125	
Gly Leu Ile Tyr Phe Phe Leu Asn Ala Asn Thr Pro Ser Gln His Gly	
130 135 140	
Phe Gly Ile Pro Met Ala Thr Asp Ile Ala Phe Ala Leu Gly Val Ile	
145 150 155 160	
Met Leu Leu Gly Lys Arg Val Pro Thr Ala Leu Lys Val Phe Leu Ile	
165 170 175	
Thr Leu Ala Val Ala Asp Asp Leu Gly Ala Ile Val Val Ile Ala Leu	

			180				185				190				
Phe	Tyr	Thr	Thr	Asn	Leu	Lys	Phe	Ala	Trp	Leu	Leu	Gly	Ala	Leu	Gly
		195					200					205			
Val	Val	Leu	Val	Leu	Ala	Val	Leu	Asn	Arg	Leu	Asn	Met	Arg	Ser	Leu
	210					215					220				
Ile	Pro	Tyr	Leu	Leu	Leu	Gly	Val	Leu	Leu	Trp	Phe	Cys	Val	His	Gln
225					230					235					240
Ser	Gly	Ile	His	Ala	Thr	Ile	Ala	Ala	Val	Ile	Leu	Ala	Phe	Met	Ile
			245						250					255	
Pro	Val	Lys	Ile	Pro	Lys	Asp	Ser	Lys	Asn	Val	Glu	Leu	Leu	Glu	Leu
			260					265					270		
Gly	Lys	Arg	Tyr	Ala	Glu	Thr	Ser	Ser	Gly	Ala	Leu	Leu	Ser	Lys	Glu
		275					280					285			
Gln	Gln	Glu	Ile	Leu	His	Ser	Ile	Glu	Glu	Lys	Ala	Ser	Ala	Leu	Gln
	290					295					300				
Ser	Pro	Leu	Glu	Arg	Leu	Glu	His	Phe	Leu	Ala	Pro	Ile	Ser	Gly	Tyr
305					310					315					320
Phe	Ile	Met	Pro	Leu	Phe	Ala	Phe	Ala	Asn	Ala	Gly	Val	Ser	Val	Asp
				325					330					335	
Ser	Ser	Ile	Asn	Leu	Glu	Val	Asp	Lys	Val	Leu	Leu	Gly	Val	Ile	Leu
			340					345					350		
Gly	Leu	Cys	Leu	Gly	Lys	Pro	Leu	Gly	Ile	Phe	Leu	Ile	Thr	Phe	Ile
		355					360					365			
Ser	Glu	Lys	Leu	Lys	Ile	Thr	Ala	Arg	Pro	Lys	Gly	Ile	Ser	Trp	Trp
	370					375					380				
His	Ile	Leu	Gly	Ala	Gly	Leu	Leu	Ala	Gly	Ile	Gly	Phe	Thr	Met	Ser
385					390					395					400
Met	Phe	Ile	Ser	Asn	Leu	Ala	Phe	Thr	Ser	Glu	His	Lys	Asp	Ala	Met
				405					410					415	
Glu	Val	Ala	Lys	Ile	Ala	Ile	Leu	Leu	Gly	Ser	Leu	Ile	Ser	Gly	Ile
		420					425					430			
Ile	Gly	Ala	Leu	Tyr	Leu	Phe	Ala	Leu	Asp	Lys	Arg	Ala	Ala	Leu	Lys
		435					440					445			

Lys

<210> 407
 <211> 1903
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (13)...(1857)

<400> 407
 aagtaagtgc tt atg gat aat agg aat att gat cct tac ttc aac cca gag 51
 Met Asp Asn Arg Asn Ile Asp Pro Tyr Phe Asn Pro Glu
 1 5 10

caa ttt tta gaa acc caa aaa tac aaa ggc acg gtt aca gca tta atc 99
 Gln Phe Leu Glu Thr Gln Lys Tyr Lys Gly Thr Val Thr Ala Leu Ile
 15 20 25

ttt tta ttg ctt ttt ttt att ttt tta atg gtg gct ttt aaa aaa gct 147
 Phe Leu Leu Leu Phe Phe Ile Phe Leu Met Val Ala Phe Lys Lys Ala
 30 35 40 45

ttt ttt gcc caa gcc aac atg cct aat cta gtg atg agc aaa caa gac	195
Phe Phe Ala Gln Ala Asn Met Pro Asn Leu Val Met Ser Lys Gln Asp	
50 55 60	
act gcg gct agg ggg act atc tat agt caa gac aac tac agc cta gcc	243
Thr Ala Ala Arg Gly Thr Ile Tyr Ser Gln Asp Asn Tyr Ser Leu Ala	
65 70 75	
act tca caa acc ctt ttc aaa ctg ggc ttt gat aca agg ttt tta aac	291
Thr Ser Gln Thr Leu Phe Lys Leu Gly Phe Asp Thr Arg Phe Leu Asn	
80 85 90	
ccg gat aaa gaa gat ttt ttc att gat ttc ctt tct att tat agc aat	339
Pro Asp Lys Glu Asp Phe Phe Ile Asp Phe Leu Ser Ile Tyr Ser Asn	
95 100 105	
atc cct aaa aag tcc tta aaa gac gcc atc aat aca aaa ggc tat atc	387
Ile Pro Lys Lys Ser Leu Lys Asp Ala Ile Asn Thr Lys Gly Tyr Ile	
110 115 120 125	
att cta gcc tat gat ctc acg ccc aat atg gct gct aat att aga gac	435
Ile Leu Ala Tyr Asp Leu Thr Pro Asn Met Ala Ala Asn Ile Arg Asp	
130 135 140	
tta aat aag aaa ttt tta gcc ttt ggg gtt ttt caa aat ttc aaa gac	483
Leu Asn Lys Lys Phe Leu Ala Phe Gly Val Phe Gln Asn Phe Lys Asp	
145 150 155	
gcg cac gat aag gtg tgg caa aag caa ggg cta aac att gaa gtg agc	531
Ala His Asp Lys Val Trp Gln Lys Gln Gly Leu Asn Ile Glu Val Ser	
160 165 170	
ggc gtt tct agg cat tac cct tat caa aat agc cta gag cca atc att	579
Gly Val Ser Arg His Tyr Pro Tyr Gln Asn Ser Leu Glu Pro Ile Ile	
175 180 185	
ggc tat gtg caa aaa caa gaa gaa gac aag ctc act tta act acc ggt	627
Gly Tyr Val Gln Lys Gln Glu Glu Asp Lys Leu Thr Leu Thr Thr Gly	
190 195 200 205	
aaa aaa ggc gtt gaa aaa tct caa gat cac ttg ctt aaa gcc caa caa	675
Lys Lys Gly Val Glu Lys Ser Gln Asp His Leu Leu Lys Ala Gln Gln	
210 215 220	
aat ggc ata aga aca ggc aaa aga gac gtg agt ttt aac ttt atc caa	723
Asn Gly Ile Arg Thr Gly Lys Arg Asp Val Ser Phe Asn Phe Ile Gln	
225 230 235	
aac cac tct tat aca gag gtt gaa cgc ctt gat ggc tat gag gtg tat	771
Asn His Ser Tyr Thr Glu Val Glu Arg Leu Asp Gly Tyr Glu Val Tyr	
240 245 250	
ttg agc gtt cct tta aaa ctc caa aga gaa att gaa acc cta ttg gat	819
Leu Ser Val Pro Leu Lys Leu Gln Arg Glu Ile Glu Thr Leu Leu Asp	
255 260 265	
aaa act aaa gac aaa ctc aag gct aaa gaa atc cta gtg ggt atc att	867
Lys Thr Lys Asp Lys Leu Lys Ala Lys Glu Ile Leu Val Gly Ile Ile	
270 275 280 285	

aac cct aaa agc ggg gaa att tta tcg cta gct tca agc aag cgc ttc	915
Asn Pro Lys Ser Gly Glu Ile Leu Ser Leu Ala Ser Ser Lys Arg Phe	
290 295 300	
aat cct aat gcg att aaa acc agc gat tat gaa agc ttg aat ttg agc	963
Asn Pro Asn Ala Ile Lys Thr Ser Asp Tyr Glu Ser Leu Asn Leu Ser	
305 310 315	
gtt gct gaa aag gtt ttt gag cca ggc agc acg atc aaa ccc att gtt	1011
Val Ala Glu Lys Val Phe Glu Pro Gly Ser Thr Ile Lys Pro Ile Val	
320 325 330	
tat tcc ttg ctg tta gac aag aat ttg atc aac ccc aaa gaa cgc att	1059
Tyr Ser Leu Leu Leu Asp Lys Asn Leu Ile Asn Pro Lys Glu Arg Ile	
335 340 345	
gat tta aac cat ggc tat tac caa tta gga aaa tac acc att aaa gac	1107
Asp Leu Asn His Gly Tyr Tyr Gln Leu Gly Lys Tyr Thr Ile Lys Asp	
350 355 360 365	
gac ttt atc ccc agt aaa aaa gcc gtt gtg gaa gac att ttg atc caa	1155
Asp Phe Ile Pro Ser Lys Lys Ala Val Val Glu Asp Ile Leu Ile Gln	
370 375 380	
tct agc aat gtg ggc atg ata aaa atc agt aaa aac tta aac cca aag	1203
Ser Ser Asn Val Gly Met Ile Lys Ile Ser Lys Asn Leu Asn Pro Lys	
385 390 395	
gat ttc tat aat ggg ctt tta ggc tat gga ttt tct caa aaa acc ggc	1251
Asp Phe Tyr Asn Gly Leu Leu Gly Tyr Gly Phe Ser Gln Lys Thr Gly	
400 405 410	
att gat tta tct cta gaa gcc aca gga aag atc cct cct ttg tcc gct	1299
Ile Asp Leu Ser Leu Glu Ala Thr Gly Lys Ile Pro Pro Leu Ser Ala	
415 420 425	
ttc aag cgt gaa gtg tta aag ggg agc gtt tct tat ggc tat ggg ctg	1347
Phe Lys Arg Glu Val Leu Lys Gly Ser Val Ser Tyr Gly Tyr Gly Leu	
430 435 440 445	
aac gcg act ttt ttg cag ctt tta agg gct tat gcg gtg ttt tct aat	1395
Asn Ala Thr Phe Leu Gln Leu Leu Arg Ala Tyr Ala Val Phe Ser Asn	
450 455 460	
gaa ggc aaa ttg act acc ccc tat tta gtg caa cga gaa acc gcc cct	1443
Glu Gly Lys Leu Thr Thr Pro Tyr Leu Val Gln Arg Glu Thr Ala Pro	
465 470 475	
aat ggc gat att tac atc cct agc ccc aaa ccc acc ttt caa gtc att	1491
Asn Gly Asp Ile Tyr Ile Pro Ser Pro Lys Pro Thr Phe Gln Val Ile	
480 485 490	
agc cca aaa agc gct agg aaa atg aaa gaa acc tta atc aaa gta gtg	1539
Ser Pro Lys Ser Ala Arg Lys Met Lys Glu Thr Leu Ile Lys Val Val	
495 500 505	
cgt tat ggc aca ggc aaa aac gct caa ttt gaa ggg cta tac ata ggg	1587
Arg Tyr Gly Thr Gly Lys Asn Ala Gln Phe Glu Gly Leu Tyr Ile Gly	

510	515	520	525	
ggc aaa acc ggc acg gct agg gtc gct	aaa aac ggg agt tat agc gcg	1635		
Gly Lys Thr Gly Thr Ala Arg Val Ala	Lys Asn Gly Ser Tyr Ser Ala			
530	535	540		
cag tcc tac aac agc tct ttt ttt ggg ttt	gct gaa gat gaa agg cag	1683		
Gln Ser Tyr Asn Ser Ser Phe Phe	Gly Phe Ala Glu Asp Glu Arg Gln			
545	550	555		
gtt ttt act atc ggc gtg gtt atc tta ggt	tcg cat ggc aag gaa gaa	1731		
Val Phe Thr Ile Gly Val Val Ile Leu	Gly Ser His Gly Lys Glu Glu			
560	565	570		
tat tac gcc agc aag att gca gcc ccc att	ttt aaa gaa atc acc gaa	1779		
Tyr Tyr Ala Ser Lys Ile Ala Ala Pro	Ile Phe Lys Glu Ile Thr Glu			
575	580	585		
att tta gtg cgt tac aat tat cta tcg ccc	tct att gcg att caa aac	1827		
Ile Leu Val Arg Tyr Asn Tyr Leu Ser	Pro Ser Ile Ala Ile Gln Asn			
590	595	600	605	
gcg ctc gag aaa aac cgc ttt aag ata	aaa taaaaggctc ttttcaaccc	1877		
Ala Leu Glu Lys Asn Arg Phe Lys Ile	Lys			
610	615			
aaactccaaa aaaggagtct taagtt		1903		
<210> 408				
<211> 615				
<212> PRT				
<213> Helicobacter pylori				
<400> 408				
Met Asp Asn Arg Asn Ile Asp Pro Tyr	Phe Asn Pro Glu Gln Phe Leu			
1 5 10 15				
Glu Thr Gln Lys Tyr Lys Gly Thr Val	Thr Ala Leu Ile Phe Leu Leu			
20 25 30				
Leu Phe Phe Ile Phe Leu Met Val Ala	Phe Lys Lys Ala Phe Phe Ala			
35 40 45				
Gln Ala Asn Met Pro Asn Leu Val Met	Ser Lys Gln Asp Thr Ala Ala			
50 55 60				
Arg Gly Thr Ile Tyr Ser Gln Asp Asn	Tyr Ser Leu Ala Thr Ser Gln			
65 70 75 80				
Thr Leu Phe Lys Leu Gly Phe Asp Thr	Arg Phe Leu Asn Pro Asp Lys			
85 90 95				
Glu Asp Phe Phe Ile Asp Phe Leu Ser	Ile Tyr Ser Asn Ile Pro Lys			
100 105 110				
Lys Ser Leu Lys Asp Ala Ile Asn Thr	Lys Gly Tyr Ile Ile Leu Ala			
115 120 125				
Tyr Asp Leu Thr Pro Asn Met Ala Ala	Asn Ile Arg Asp Leu Asn Lys			
130 135 140				
Lys Phe Leu Ala Phe Gly Val Phe Gln	Asn Phe Lys Asp Ala His Asp			
145 150 155 160				
Lys Val Trp Gln Lys Gln Gly Leu Asn	Ile Glu Val Ser Gly Val Ser			
165 170 175				
Arg His Tyr Pro Tyr Gln Asn Ser Leu	Glu Pro Ile Ile Gly Tyr Val			
180 185 190				
Gln Lys Gln Glu Glu Asp Lys Leu Thr	Leu Thr Thr Gly Lys Lys Gly			

		195					200				205				
Val	Glu	Lys	Ser	Gln	Asp	His	Leu	Leu	Lys	Ala	Gln	Gln	Asn	Gly	Ile
	210					215					220				
Arg	Thr	Gly	Lys	Arg	Asp	Val	Ser	Phe	Asn	Phe	Ile	Gln	Asn	His	Ser
225					230					235					240
Tyr	Thr	Glu	Val	Glu	Arg	Leu	Asp	Gly	Tyr	Glu	Val	Tyr	Leu	Ser	Val
				245					250					255	
Pro	Leu	Lys	Leu	Gln	Arg	Glu	Ile	Glu	Thr	Leu	Leu	Asp	Lys	Thr	Lys
			260					265					270		
Asp	Lys	Leu	Lys	Ala	Lys	Glu	Ile	Leu	Val	Gly	Ile	Ile	Asn	Pro	Lys
		275				280						285			
Ser	Gly	Glu	Ile	Leu	Ser	Leu	Ala	Ser	Ser	Lys	Arg	Phe	Asn	Pro	Asn
	290					295					300				
Ala	Ile	Lys	Thr	Ser	Asp	Tyr	Glu	Ser	Leu	Asn	Leu	Ser	Val	Ala	Glu
305					310					315					320
Lys	Val	Phe	Glu	Pro	Gly	Ser	Thr	Ile	Lys	Pro	Ile	Val	Tyr	Ser	Leu
				325					330					335	
Leu	Leu	Asp	Lys	Asn	Leu	Ile	Asn	Pro	Lys	Glu	Arg	Ile	Asp	Leu	Asn
			340					345					350		
His	Gly	Tyr	Tyr	Gln	Leu	Gly	Lys	Tyr	Thr	Ile	Lys	Asp	Asp	Phe	Ile
	355					360						365			
Pro	Ser	Lys	Lys	Ala	Val	Val	Glu	Asp	Ile	Leu	Ile	Gln	Ser	Ser	Asn
	370					375						380			
Val	Gly	Met	Ile	Lys	Ile	Ser	Lys	Asn	Leu	Asn	Pro	Lys	Asp	Phe	Tyr
385					390					395					400
Asn	Gly	Leu	Leu	Gly	Tyr	Gly	Phe	Ser	Gln	Lys	Thr	Gly	Ile	Asp	Leu
				405					410					415	
Ser	Leu	Glu	Ala	Thr	Gly	Lys	Ile	Pro	Pro	Leu	Ser	Ala	Phe	Lys	Arg
			420					425					430		
Glu	Val	Leu	Lys	Gly	Ser	Val	Ser	Tyr	Gly	Tyr	Gly	Leu	Asn	Ala	Thr
	435						440					445			
Phe	Leu	Gln	Leu	Leu	Arg	Ala	Tyr	Ala	Val	Phe	Ser	Asn	Glu	Gly	Lys
	450					455					460				
Leu	Thr	Thr	Pro	Tyr	Leu	Val	Gln	Arg	Glu	Thr	Ala	Pro	Asn	Gly	Asp
465					470					475					480
Ile	Tyr	Ile	Pro	Ser	Pro	Lys	Pro	Thr	Phe	Gln	Val	Ile	Ser	Pro	Lys
				485					490					495	
Ser	Ala	Arg	Lys	Met	Lys	Glu	Thr	Leu	Ile	Lys	Val	Val	Arg	Tyr	Gly
			500					505					510		
Thr	Gly	Lys	Asn	Ala	Gln	Phe	Glu	Gly	Leu	Tyr	Ile	Gly	Gly	Lys	Thr
	515						520					525			
Gly	Thr	Ala	Arg	Val	Ala	Lys	Asn	Gly	Ser	Tyr	Ser	Ala	Gln	Ser	Tyr
	530					535					540				
Asn	Ser	Ser	Phe	Phe	Gly	Phe	Ala	Glu	Asp	Glu	Arg	Gln	Val	Phe	Thr
545					550					555					560
Ile	Gly	Val	Val	Ile	Leu	Gly	Ser	His	Gly	Lys	Glu	Glu	Tyr	Tyr	Ala
				565					570					575	
Ser	Lys	Ile	Ala	Ala	Pro	Ile	Phe	Lys	Glu	Ile	Thr	Glu	Ile	Leu	Val
			580					585					590		
Arg	Tyr	Asn	Tyr	Leu	Ser	Pro	Ser	Ile	Ala	Ile	Gln	Asn	Ala	Leu	Glu
		595					600						605		
Lys	Asn	Arg	Phe	Lys	Ile	Lys									
	610					615									

<210> 409
 <211> 719
 <212> DNA
 <213> *Helicobacter pylori*

<220>

<221> CDS

<222> (19)...(678)

<400> 409

tagcctagtc tttatcgc	atg cta ttt aat ggg cta tgc tta ttt gaa cag	51
	Met Leu Phe Asn Gly Leu Cys Leu Phe Glu Gln	
	1 5 10	
gca agt ttg tgc ttt aga aaa gcg agc gtt tca atg aaa aag ctc aaa	99	
Ala Ser Leu Cys Phe Arg Lys Ala Ser Val Ser Met Lys Lys Leu Lys		
	15 20 25	
ggg ctt ttt ttg atc ctg ctc tta tgg gtc tat cct tta agg agt gag	147	
Gly Leu Phe Leu Ile Leu Leu Leu Trp Val Tyr Pro Leu Arg Ser Glu		
	30 35 40	
cca atc aat gag gga gca tac att tta gaa gag att ggc gat gtg ctt	195	
Pro Ile Asn Glu Gly Ala Tyr Ile Leu Glu Glu Ile Gly Asp Val Leu		
	45 50 55	
agg ttt ttg cct att ttt gta ggc acg gtc agt ttg gcg atg cgc gat	243	
Arg Phe Leu Pro Ile Phe Val Gly Thr Val Ser Leu Ala Met Arg Asp		
	60 65 70 75	
tat aga ggg tta ggg gaa tta gcg gtc ggc aca ttg gtt act caa ggc	291	
Tyr Arg Gly Leu Gly Glu Leu Ala Val Gly Thr Leu Val Thr Gln Gly		
	80 85 90	
gtg att tat ggc ctt aaa gga gct ttt agc aac gcc cat aaa gat ggg	339	
Val Ile Tyr Gly Leu Lys Gly Ala Phe Ser Asn Ala His Lys Asp Gly		
	95 100 105	
gct aga gtg gaa ttt gct aaa cgc ccg tgc tgt aat tct tgg aga ggc	387	
Ala Arg Val Glu Phe Ala Lys Arg Pro Cys Cys Asn Ser Trp Arg Gly		
	110 115 120	
atg cca agc ggg cat gct ggg ggg gtg ttt agc gcg gct ggg ttt gtg	435	
Met Pro Ser Gly His Ala Gly Gly Val Phe Ser Ala Ala Gly Phe Val		
	125 130 135	
tat tac cgc tat ggg tgg aag ccg gct ctt cct gtg atc gct ctt gca	483	
Tyr Tyr Arg Tyr Gly Trp Lys Pro Ala Leu Pro Val Ile Ala Leu Ala		
	140 145 150 155	
atc ctc act gac gct agc aga gtg gtg gca aga caa cac acg atc ttg	531	
Ile Leu Thr Asp Ala Ser Arg Val Val Ala Arg Gln His Thr Ile Leu		
	160 165 170	
caa gtt acg atc ggc agc ctt atc gca tgg ggg ttt gct tat tta ttc	579	
Gln Val Thr Ile Gly Ser Leu Ile Ala Trp Gly Phe Ala Tyr Leu Phe		
	175 180 185	
act tca cgc tac aaa ccc aag caa tgg atg ctc tat cct gaa att tct	627	
Thr Ser Arg Tyr Lys Pro Lys Gln Trp Met Leu Tyr Pro Glu Ile Ser		
	190 195 200	
agc gat ttt aag ggc agt agc cgc tat ggg gtg agc ttt tct tat caa	675	
Ser Asp Phe Lys Gly Ser Ser Arg Tyr Gly Val Ser Phe Ser Tyr Gln		

205

210

215

tgg taaagggata aagtgcataaa aaaattatta ttcattgcac t
 Trp
 220

719

<210> 410

<211> 220

<212> PRT

<213> Helicobacter pylori

<400> 410

Met	Leu	Phe	Asn	Gly	Leu	Cys	Leu	Phe	Glu	Gln	Ala	Ser	Leu	Cys	Phe
1			5						10					15	
Arg	Lys	Ala	Ser	Val	Ser	Met	Lys	Lys	Leu	Lys	Gly	Leu	Phe	Leu	Ile
			20				25						30		
Leu	Leu	Leu	Trp	Val	Tyr	Pro	Leu	Arg	Ser	Glu	Pro	Ile	Asn	Glu	Gly
		35				40						45			
Ala	Tyr	Ile	Leu	Glu	Glu	Ile	Gly	Asp	Val	Leu	Arg	Phe	Leu	Pro	Ile
	50					55					60				
Phe	Val	Gly	Thr	Val	Ser	Leu	Ala	Met	Arg	Asp	Tyr	Arg	Gly	Leu	Gly
65					70					75				80	
Glu	Leu	Ala	Val	Gly	Thr	Leu	Val	Thr	Gln	Gly	Val	Ile	Tyr	Gly	Leu
			85						90					95	
Lys	Gly	Ala	Phe	Ser	Asn	Ala	His	Lys	Asp	Gly	Ala	Arg	Val	Glu	Phe
			100					105					110		
Ala	Lys	Arg	Pro	Cys	Cys	Asn	Ser	Trp	Arg	Gly	Met	Pro	Ser	Gly	His
		115				120						125			
Ala	Gly	Gly	Val	Phe	Ser	Ala	Ala	Gly	Phe	Val	Tyr	Tyr	Arg	Tyr	Gly
	130					135					140				
Trp	Lys	Pro	Ala	Leu	Pro	Val	Ile	Ala	Leu	Ala	Ile	Leu	Thr	Asp	Ala
145					150					155					160
Ser	Arg	Val	Val	Ala	Arg	Gln	His	Thr	Ile	Leu	Gln	Val	Thr	Ile	Gly
			165						170					175	
Ser	Leu	Ile	Ala	Trp	Gly	Phe	Ala	Tyr	Leu	Phe	Thr	Ser	Arg	Tyr	Lys
			180					185					190		
Pro	Lys	Gln	Trp	Met	Leu	Tyr	Pro	Glu	Ile	Ser	Ser	Asp	Phe	Lys	Gly
		195				200						205			
Ser	Ser	Arg	Tyr	Gly	Val	Ser	Phe	Ser	Tyr	Gln	Trp				
	210					215					220				

<210> 411

<211> 1087

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (34)...(1053)

<400> 411

ttcaagcaaa aacaccaccc aaatataaag ata atg att tta agc att gaa agt 54
 Met Ile Leu Ser Ile Glu Ser
 1 5

tct tgc gat gac agc tct tta gcc ctt aca aga ata gag gac gct caa 102
 Ser Cys Asp Asp Ser Ser Leu Ala Leu Thr Arg Ile Glu Asp Ala Gln

10					15					20						
ctc	atc	gct	cat	ttt	aaa	atc	tct	caa	gaa	aag	cac	cat	agt	tct	tat	150
Leu	Ile	Ala	His	Phe	Lys	Ile	Ser	Gln	Glu	Lys	His	His	Ser	Ser	Tyr	
25					30					35						
ggg	ggc	gtt	gtg	cct	gag	ctt	gca	tca	cgt	ttg	cat	gct	gag	aat	ttg	198
Gly	Gly	Val	Val	Pro	Glu	Leu	Ala	Ser	Arg	Leu	His	Ala	Glu	Asn	Leu	
40					45					50					55	
ccg	ctt	tta	tta	gaa	cgc	att	aaa	ata	agc	ttg	aat	aag	gat	ttt	tcc	246
Pro	Leu	Leu	Leu	Glu	Arg	Ile	Lys	Ile	Ser	Leu	Asn	Lys	Asp	Phe	Ser	
60					65					70						
aaa	att	aaa	gcc	atc	gct	atc	act	aat	cag	cca	ggg	ttg	agc	gtt	act	294
Lys	Ile	Lys	Ala	Ile	Ala	Ile	Thr	Asn	Gln	Pro	Gly	Leu	Ser	Val	Thr	
75					80					85						
tta	ata	gaa	ggg	ttg	atg	atg	gca	aaa	gcc	ttg	agc	ttg	tct	ttg	aat	342
Leu	Ile	Glu	Gly	Leu	Met	Met	Ala	Lys	Ala	Leu	Ser	Leu	Ser	Leu	Asn	
90					95					100						
ttg	ccc	ttg	att	tta	gaa	gat	cat	ttg	aga	ggg	cat	gtg	tat	tcg	ctc	390
Leu	Pro	Leu	Ile	Leu	Glu	Asp	His	Leu	Arg	Gly	His	Val	Tyr	Ser	Leu	
105					110					115						
ttt	atc	aat	gaa	aaa	caa	acc	tgc	atg	cct	tta	agc	gtg	ctc	tta	gtc	438
Phe	Ile	Asn	Glu	Lys	Gln	Thr	Cys	Met	Pro	Leu	Ser	Val	Leu	Leu	Val	
120					125					130					135	
tct	ggg	ggg	cat	tct	ttg	att	tta	gag	gct	aga	gat	tat	gag	aat	att	486
Ser	Gly	Gly	His	Ser	Leu	Ile	Leu	Glu	Ala	Arg	Asp	Tyr	Glu	Asn	Ile	
140					145					150						
aaa	atc	gtt	gcc	acg	agt	tta	gac	gat	agc	ttt	ggg	gag	agt	ttt	gat	534
Lys	Ile	Val	Ala	Thr	Ser	Leu	Asp	Asp	Ser	Phe	Gly	Glu	Ser	Phe	Asp	
155					160					165						
aag	gtt	tcc	aaa	atg	ctt	gat	tta	ggc	tat	cca	gga	ggc	cct	ata	gtg	582
Lys	Val	Ser	Lys	Met	Leu	Asp	Leu	Gly	Tyr	Pro	Gly	Gly	Pro	Ile	Val	
170					175					180						
gaa	aaa	tta	gcc	ctt	gat	tat	agg	cac	cca	aac	gag	cct	tta	atg	ttc	630
Glu	Lys	Leu	Ala	Leu	Asp	Tyr	Arg	His	Pro	Asn	Glu	Pro	Leu	Met	Phe	
185					190					195						
cct	atc	cct	tta	aaa	aac	agc	ccg	aat	ctg	gct	ttt	agt	ttt	tca	ggg	678
Pro	Ile	Pro	Leu	Lys	Asn	Ser	Pro	Asn	Leu	Ala	Phe	Ser	Phe	Ser	Gly	
200					205					210					215	
tta	aaa	aat	gcg	gtg	cgt	ttg	gag	gtt	gaa	aaa	aac	gcc	ccc	aac	ttg	726
Leu	Lys	Asn	Ala	Val	Arg	Leu	Glu	Val	Glu	Lys	Asn	Ala	Pro	Asn	Leu	
220					225					230						
aat	gaa	gcg	atc	aaa	caa	aag	att	ggc	tat	cat	ttt	caa	agt	gca	gcg	774
Asn	Glu	Ala	Ile	Lys	Gln	Lys	Ile	Gly	Tyr	His	Phe	Gln	Ser	Ala	Ala	
235					240					245						
att	gag	cat	tta	atc	cag	cag	act	aaa	cgc	tat	ttt	aaa	atc	aaa	cgc	822

Ile	Glu	His	Leu	Ile	Gln	Gln	Thr	Lys	Arg	Tyr	Phe	Lys	Ile	Lys	Arg		
		250					255					260					
cct	aaa	att	ttt	ggc	att	gtg	ggg	gga	gcg	agc	caa	aat	ttg	gct	tta	870	
Pro	Lys	Ile	Phe	Gly	Ile	Val	Gly	Gly	Ala	Ser	Gln	Asn	Leu	Ala	Leu		
	265					270					275						
aga	aag	gcg	ttt	gaa	aat	ttg	tgc	gat	gcg	ttt	gat	tgc	aag	ctt	gtt	918	
Arg	Lys	Ala	Phe	Glu	Asn	Leu	Cys	Asp	Ala	Phe	Asp	Cys	Lys	Leu	Val		
280					285					290					295		
tta	gcc	cct	tta	gaa	ttt	tgc	agc	gac	aat	gcc	gcc	atg	ata	ggg	cga	966	
Leu	Ala	Pro	Leu	Glu	Phe	Cys	Ser	Asp	Asn	Ala	Ala	Met	Ile	Gly	Arg		
				300					305					310			
tcc	agc	cta	gaa	gct	tat	caa	aaa	aag	cgc	ttt	gtc	cct	tta	gaa	aag	1014	
Ser	Ser	Leu	Glu	Ala	Tyr	Gln	Lys	Lys	Arg	Phe	Val	Pro	Leu	Glu	Lys		
			315					320					325				
gct	aac	att	tcg	cca	aga	acg	ctg	tta	aaa	agt	ttt	gag	tgaatggata			1063	
Ala	Asn	Ile	Ser	Pro	Arg	Thr	Leu	Leu	Lys	Ser	Phe	Glu					
		330					335					340					
caaaaagaaa gcgcatgata aaac																1087	

<210> 412
 <211> 340
 <212> PRT
 <213> Helicobacter pylori

<400> 412

Met	Ile	Leu	Ser	Ile	Glu	Ser	Ser	Cys	Asp	Asp	Ser	Ser	Leu	Ala	Leu		
1				5					10					15			
Thr	Arg	Ile	Glu	Asp	Ala	Gln	Leu	Ile	Ala	His	Phe	Lys	Ile	Ser	Gln		
			20					25					30				
Glu	Lys	His	His	Ser	Ser	Tyr	Gly	Gly	Val	Val	Pro	Glu	Leu	Ala	Ser		
		35					40					45					
Arg	Leu	His	Ala	Glu	Asn	Leu	Pro	Leu	Leu	Leu	Glu	Arg	Ile	Lys	Ile		
	50				55						60						
Ser	Leu	Asn	Lys	Asp	Phe	Ser	Lys	Ile	Lys	Ala	Ile	Ala	Ile	Thr	Asn		
65				70					75						80		
Gln	Pro	Gly	Leu	Ser	Val	Thr	Leu	Ile	Glu	Gly	Leu	Met	Met	Ala	Lys		
			85					90						95			
Ala	Leu	Ser	Leu	Ser	Leu	Asn	Leu	Pro	Leu	Ile	Leu	Glu	Asp	His	Leu		
			100					105					110				
Arg	Gly	His	Val	Tyr	Ser	Leu	Phe	Ile	Asn	Glu	Lys	Gln	Thr	Cys	Met		
		115					120					125					
Pro	Leu	Ser	Val	Leu	Leu	Val	Ser	Gly	Gly	His	Ser	Leu	Ile	Leu	Glu		
	130					135					140						
Ala	Arg	Asp	Tyr	Glu	Asn	Ile	Lys	Ile	Val	Ala	Thr	Ser	Leu	Asp	Asp		
145					150				155						160		
Ser	Phe	Gly	Glu	Ser	Phe	Asp	Lys	Val	Ser	Lys	Met	Leu	Asp	Leu	Gly		
			165					170						175			
Tyr	Pro	Gly	Gly	Pro	Ile	Val	Glu	Lys	Leu	Ala	Leu	Asp	Tyr	Arg	His		
			180					185					190				
Pro	Asn	Glu	Pro	Leu	Met	Phe	Pro	Ile	Pro	Leu	Lys	Asn	Ser	Pro	Asn		
	195						200					205					
Leu	Ala	Phe	Ser	Phe	Ser	Gly	Leu	Lys	Asn	Ala	Val	Arg	Leu	Glu	Val		
	210					215					220						

act tta acg ctg ttt aaa gcg ggt ggc tct cat tct tat gcg ttg gct 438
 Thr Leu Thr Leu Phe Lys Ala Gly Gly Ser His Ser Tyr Ala Leu Ala
 120 125 130 135

gta tct gtt gca gat gca atg gta aga caa act cta ggg cat gtt atg 486
 Val Ser Val Ala Asp Ala Met Val Arg Gln Thr Leu Gly His Val Met
 140 145 150

tgg tgg gta aag tagcacttaa aaaaactttg ggcgttttgg ctggccctat 538
 Trp Trp Val Lys
 155

tggttggt 547

<210> 414
 <211> 155
 <212> PRT
 <213> Helicobacter pylori

<400> 414
 Met Asn Glu Asp Leu Thr Asn Ser Thr Glu Tyr Lys Arg Tyr Gly His
 1 5 10 15
 Asp Tyr Ala Lys Tyr Pro Arg Arg Ile Ala Glu Glu Leu Gln His Tyr
 20 25 30
 Gly Gly Asn Ser Phe Ala Asn Phe Phe Arg Asp Glu Gly Val Leu Tyr
 35 40 45
 Lys Glu Ile Leu Cys Asp Ala Cys Asp His Leu Lys Val Asn Tyr Asn
 50 55 60
 Glu Glu Ser Ala Thr Ser Leu Ile Glu Gln Asn Met Leu Ser Lys Leu
 65 70 75 80
 Leu Lys Asp Ser Leu Glu Lys Met Ser Arg Arg Glu Ile Lys Glu Leu
 85 90 95
 Cys Asn Glu Leu Gly Met Thr Asn Ile Asp Lys Val Ile Gly Glu Asn
 100 105 110
 Lys Gln Val Leu Ile Ala Ser Thr Leu Thr Leu Phe Lys Ala Gly Gly
 115 120 125
 Ser His Ser Tyr Ala Leu Ala Val Ser Val Ala Asp Ala Met Val Arg
 130 135 140
 Gln Thr Leu Gly His Val Met Trp Trp Val Lys
 145 150 155

<210> 415
 <211> 523
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (19)...(486)

<400> 415
 ttatttttaa ggaatttc atg caa atc ata gaa ggg aaa ttg caa tta caa 51
 Met Gln Ile Ile Glu Gly Lys Leu Gln Leu Gln
 1 5 10

ggg aat gaa aga gtc gct att tta aca tcg cgc ttc aat cat atc atc 99
 Gly Asn Glu Arg Val Ala Ile Leu Thr Ser Arg Phe Asn His Ile Ile

15					20					25						
aca	gac	aga	ttg	caa	gaa	ggg	gcg	atg	gac	tgc	ttt	aaa	agg	cat	ggg	147
Thr	Asp	Arg	Leu	Gln	Glu	Gly	Ala	Met	Asp	Cys	Phe	Lys	Arg	His	Gly	
		30					35					40				
ggc	gat	gag	gat	ctt	tta	gac	atc	gtg	ctg	gtg	cct	ggg	gct	tat	gaa	195
Gly	Asp	Glu	Asp	Leu	Leu	Asp	Ile	Val	Leu	Val	Pro	Gly	Ala	Tyr	Glu	
	45					50					55					
ttg	cct	ttt	att	tta	gac	aaa	tta	tta	gag	agc	gaa	aaa	tac	gat	ggc	243
Leu	Pro	Phe	Ile	Leu	Asp	Lys	Leu	Leu	Glu	Ser	Glu	Lys	Tyr	Asp	Gly	
	60				65				70						75	
gtg	tgc	gtt	ttg	gga	gcg	atc	att	aga	ggg	ggg	act	ccg	cat	ttt	gat	291
Val	Cys	Val	Leu	Gly	Ala	Ile	Ile	Arg	Gly	Gly	Thr	Pro	His	Phe	Asp	
				80					85					90		
tat	gtg	agc	gcg	gaa	gcg	act	aag	ggt	att	gcc	cat	gcg	atg	ctt	aaa	339
Tyr	Val	Ser	Ala	Glu	Ala	Thr	Lys	Gly	Ile	Ala	His	Ala	Met	Leu	Lys	
			95					100					105			
tac	agc	atg	ccg	gta	agc	ttt	ggc	gtg	ctg	acc	acg	gac	aat	att	gaa	387
Tyr	Ser	Met	Pro	Val	Ser	Phe	Gly	Val	Leu	Thr	Thr	Asp	Asn	Ile	Glu	
		110					115					120				
caa	gcg	att	gaa	aga	gcg	ggc	agt	aaa	gcc	ggc	aat	aag	ggc	ttt	gaa	435
Gln	Ala	Ile	Glu	Arg	Ala	Gly	Ser	Lys	Ala	Gly	Asn	Lys	Gly	Phe	Glu	
	125					130					135					
gcg	atg	agc	acc	ctc	att	gaa	ttg	ttg	agc	ttg	tgc	caa	act	ctc	aag	483
Ala	Met	Ser	Thr	Leu	Ile	Glu	Leu	Leu	Ser	Leu	Cys	Gln	Thr	Leu	Lys	
	140				145				150						155	
ggt	taaaatggcg	acacgaactc	aagccagggg	ggctgtg												523
Gly																

<210> 416

<211> 156

<212> PRT

<213> Helicobacter pylori

<400> 416

Met	Gln	Ile	Ile	Glu	Gly	Lys	Leu	Gln	Leu	Gln	Gly	Asn	Glu	Arg	Val
1				5				10						15	
Ala	Ile	Leu	Thr	Ser	Arg	Phe	Asn	His	Ile	Ile	Thr	Asp	Arg	Leu	Gln
		20					25					30			
Glu	Gly	Ala	Met	Asp	Cys	Phe	Lys	Arg	His	Gly	Gly	Asp	Glu	Asp	Leu
	35					40					45				
Leu	Asp	Ile	Val	Leu	Val	Pro	Gly	Ala	Tyr	Glu	Leu	Pro	Phe	Ile	Leu
	50				55					60					
Asp	Lys	Leu	Leu	Glu	Ser	Glu	Lys	Tyr	Asp	Gly	Val	Cys	Val	Leu	Gly
65				70				75						80	
Ala	Ile	Ile	Arg	Gly	Gly	Thr	Pro	His	Phe	Asp	Tyr	Val	Ser	Ala	Glu
		85					90						95		
Ala	Thr	Lys	Gly	Ile	Ala	His	Ala	Met	Leu	Lys	Tyr	Ser	Met	Pro	Val
		100					105						110		

Ser	Phe	Gly	Val	Leu	Thr	Thr	Asp	Asn	Ile	Glu	Gln	Ala	Ile	Glu	Arg
		115					120					125			
Ala	Gly	Ser	Lys	Ala	Gly	Asn	Lys	Gly	Phe	Glu	Ala	Met	Ser	Thr	Leu
	130					135					140				
Ile	Glu	Leu	Leu	Ser	Leu	Cys	Gln	Thr	Leu	Lys	Gly				
145					150					155					

<210> 417
 <211> 1724
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (19)...(1656)

<400> 417																	
tattattaag	gatacaaa	atg	gca	aaa	gaa	atc	aaa	ttt	tca	gat	agc	gcg			51		
		Met	Ala	Lys	Glu	Ile	Lys	Phe	Ser	Asp	Ser	Ala					
		1				5					10						
aga aac ctt tta ttt gaa ggc gtg aga caa ctc cat gac gct gtt aaa															99		
Arg	Asn	Leu		Phe	Glu	Gly	Val	Arg	Gln	Leu	His	Asp	Ala	Val	Lys		
		15					20					25					
gta acc atg ggg cca aga ggc agg aac gtg ttg atc caa aaa agc tat															147		
Val	Thr	Met	Gly	Pro	Arg	Gly	Arg	Asn	Val	Leu	Ile	Gln	Lys	Ser	Tyr		
		30				35						40					
ggc gct cca agc atc act aaa gat ggc gtg agc gtg gct aaa gag att															195		
Gly	Ala	Pro	Ser	Ile	Thr	Lys	Asp	Gly	Val	Ser	Val	Ala	Lys	Glu	Ile		
	45					50				55							
gaa tta agt tgc ccg gta gct aac atg ggc gct caa ctc gtt aaa gaa															243		
Glu	Leu	Ser	Cys	Pro	Val	Ala	Asn	Met	Gly	Ala	Gln	Leu	Val	Lys	Glu		
	60				65				70					75			
gta gcg agc aaa acc gct gat gct gcc ggc gat ggc acg acc aca gcg															291		
Val	Ala	Ser	Lys	Thr	Ala	Asp	Ala	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala		
				80					85					90			
acc gtg ctg gct tat agc att ttt aaa gaa ggt ttg agg aac atc acg															339		
Thr	Val	Leu	Ala	Tyr	Ser	Ile	Phe	Lys	Glu	Gly	Leu	Arg	Asn	Ile	Thr		
		95					100						105				
gct ggg gct aac cct att gaa gtg aaa cga ggc atg gat aaa gcc gct															387		
Ala	Gly		Ala	Asn	Pro	Ile	Glu	Val	Lys	Arg	Gly	Met	Asp	Lys	Ala	Ala	
		110					115					120					
gaa gcc att att aat gag ctt aaa aaa gcg agc aaa aaa gtg ggc ggt															435		
Glu	Ala	Ile	Ile	Asn	Glu	Leu	Lys	Lys	Ala	Ser	Lys	Lys	Val	Gly	Gly		
	125				130						135						
aaa gaa gaa atc acc caa gtg gcg acc att tct gca aac tcc gat cac															483		
Lys	Glu	Glu	Ile	Thr	Gln	Val	Ala	Thr	Ile	Ser	Ala	Asn	Ser	Asp	His		
140					145				150						155		
aat atc ggg aaa ctc atc gct gac gct atg gaa aaa gtg ggt aaa gac															531		

Asn	Ile	Gly	Lys	Leu	Ile	Ala	Asp	Ala	Met	Glu	Lys	Val	Gly	Lys	Asp	
				160					165					170		
ggc	gtg	atc	acc	gtt	gaa	gaa	gct	aag	ggc	att	gaa	gat	gaa	cta	gat	579
Gly	Val	Ile	Thr	Val	Glu	Glu	Ala	Lys	Gly	Ile	Glu	Asp	Glu	Leu	Asp	
			175					180					185			
gtt	gta	gaa	ggc	atg	caa	ttt	gat	aga	ggc	tac	ctc	tcc	cct	tat	ttt	627
Val	Val	Glu	Gly	Met	Gln	Phe	Asp	Arg	Gly	Tyr	Leu	Ser	Pro	Tyr	Phe	
		190					195					200				
gta	aca	aac	gct	gag	aaa	atg	acc	gct	caa	ttg	gat	aac	gct	tac	atc	675
Val	Thr	Asn	Ala	Glu	Lys	Met	Thr	Ala	Gln	Leu	Asp	Asn	Ala	Tyr	Ile	
	205					210					215					
ctt	tta	acg	gat	aaa	aaa	atc	tct	agc	atg	aaa	gac	att	ctc	ccg	cta	723
Leu	Leu	Thr	Asp	Lys	Lys	Ile	Ser	Ser	Met	Lys	Asp	Ile	Leu	Pro	Leu	
220					225					230					235	
cta	gaa	aaa	acc	atg	aaa	gag	ggc	aaa	ccg	ctt	tta	atc	atc	gct	gaa	771
Leu	Glu	Lys	Thr	Met	Lys	Glu	Gly	Lys	Pro	Leu	Leu	Ile	Ile	Ala	Glu	
				240					245					250		
gac	att	gag	ggc	gaa	gct	tta	acg	act	cta	gtg	gtg	aat	aaa	tta	aga	819
Asp	Ile	Glu	Gly	Glu	Ala	Leu	Thr	Thr	Leu	Val	Val	Asn	Lys	Leu	Arg	
			255					260					265			
ggc	gtg	ttg	aat	atc	gca	gcg	gtt	aaa	gct	cca	ggc	ttt	ggg	gac	aga	867
Gly	Val	Leu	Asn	Ile	Ala	Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	
		270					275					280				
aga	aaa	gaa	atg	ctc	aaa	gac	atc	gct	att	tta	acc	ggc	ggg	caa	gtt	915
Arg	Lys	Glu	Met	Leu	Lys	Asp	Ile	Ala	Ile	Leu	Thr	Gly	Gly	Gln	Val	
	285					290					295					
att	agc	gaa	gaa	ttg	ggc	ttg	agt	cta	gaa	aac	gct	gaa	gtg	gag	ttt	963
Ile	Ser	Glu	Glu	Leu	Gly	Leu	Ser	Leu	Glu	Asn	Ala	Glu	Val	Glu	Phe	
300					305					310					315	
tta	ggc	aaa	gcc	gga	agg	att	gtg	att	gac	aaa	gac	aac	acc	acg	atc	1011
Leu	Gly	Lys	Ala	Gly	Arg	Ile	Val	Ile	Asp	Lys	Asp	Asn	Thr	Thr	Ile	
				320					325					330		
gta	gat	ggc	aaa	ggc	cat	agc	cat	gat	gtc	aaa	gac	aga	gtc	gcg	caa	1059
Val	Asp	Gly	Lys	Gly	His	Ser	His	Asp	Val	Lys	Asp	Arg	Val	Ala	Gln	
			335					340					345			
atc	aaa	acc	caa	att	gca	agc	acg	aca	agc	gat	tat	gac	aaa	gaa	aaa	1107
Ile	Lys	Thr	Gln	Ile	Ala	Ser	Thr	Thr	Ser	Asp	Tyr	Asp	Lys	Glu	Lys	
		350					355					360				
ttg	caa	gaa	agg	ttg	gct	aaa	ctc	tct	ggc	ggg	gtg	gct	gtg	att	aaa	1155
Leu	Gln	Glu	Arg	Leu	Ala	Lys	Leu	Ser	Gly	Gly	Val	Ala	Val	Ile	Lys	
	365					370					375					
gtg	ggc	gct	gcg	agt	gaa	gtg	gaa	atg	aaa	gag	aaa	aaa	gac	cgg	gtt	1203
Val	Gly	Ala	Ala	Ser	Glu	Val	Glu	Met	Lys	Glu	Lys	Lys	Asp	Arg	Val	
380					385					390					395	

gat gat gcg ttg agc gcg act aaa gcg gct gtt gaa gaa ggt att gtg 1251
Asp Asp Ala Leu Ser Ala Thr Lys Ala Ala Val Glu Glu Gly Ile Val
400 405 410

att ggc ggc ggt gcg gct ctc att cgc gcg gct caa aaa gtg cat ttg 1299
Ile Gly Gly Gly Ala Ala Leu Ile Arg Ala Ala Gln Lys Val His Leu
415 420 425

aat ttg cac gat gat gaa aaa gtg ggc tat gaa atc atc atg cgc gcc 1347
Asn Leu His Asp Asp Glu Lys Val Gly Tyr Glu Ile Ile Met Arg Ala
430 435 440

att aaa gcc cca tta gct caa atc gct atc aat gcc ggt tat gat ggc 1395
Ile Lys Ala Pro Leu Ala Gln Ile Ala Ile Asn Ala Gly Tyr Asp Gly
445 450 455

ggt gtg gtc gtg aat gaa gta gaa aaa cac gaa ggg cat ttt ggt ttt 1443
Gly Val Val Val Asn Glu Val Glu Lys His Glu Gly His Phe Gly Phe
460 465 470 475

aac gct agc aat ggc aag tat gtg gat atg ttt aaa gaa ggc att att 1491
Asn Ala Ser Asn Gly Lys Tyr Val Asp Met Phe Lys Glu Gly Ile Ile
480 485 490

gac ccc tta aaa gta gaa agg atc gct tta caa aat gcg gtt tcg gtt 1539
Asp Pro Leu Lys Val Glu Arg Ile Ala Leu Gln Asn Ala Val Ser Val
495 500 505

tca agc ctg ctt tta acc aca gaa gcc acc gtg cat gaa atc aaa gaa 1587
Ser Ser Leu Leu Leu Thr Thr Glu Ala Thr Val His Glu Ile Lys Glu
510 515 520

gaa aaa gcg gcc cca gca atg cct gat atg ggt ggc atg ggc ggt atg 1635
Glu Lys Ala Ala Pro Ala Met Pro Asp Met Gly Gly Met Gly Gly Met
525 530 535

gga ggc atg ggt ggc atg atg taagccccct tgcttttttag tatcatctgc 1686
Gly Gly Met Gly Gly Met Met
540 545

ttttaaaatc ccctaaaatc ccccctttct aaaatctc 1724

<210> 418

<211> 546

<212> PRT

<213> *Helicobacter pylori*

<400> 418

Met Ala Lys Glu Ile Lys Phe Ser Asp Ser Ala Arg Asn Leu Leu Phe
1 5 10 15
Glu Gly Val Arg Gln Leu His Asp Ala Val Lys Val Thr Met Gly Pro
20 25 30
Arg Gly Arg Asn Val Leu Ile Gln Lys Ser Tyr Gly Ala Pro Ser Ile
35 40 45
Thr Lys Asp Gly Val Ser Val Ala Lys Glu Ile Glu Leu Ser Cys Pro
50 55 60
Val Ala Asn Met Gly Ala Gln Leu Val Lys Glu Val Ala Ser Lys Thr
65 70 75 80
Ala Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Tyr

				85				90					95			
Ser	Ile	Phe	Lys	Glu	Gly	Leu	Arg	Asn	Ile	Thr	Ala	Gly	Ala	Asn	Pro	
			100					105					110			
Ile	Glu	Val	Lys	Arg	Gly	Met	Asp	Lys	Ala	Ala	Glu	Ala	Ile	Ile	Asn	
		115					120					125				
Glu	Leu	Lys	Lys	Ala	Ser	Lys	Lys	Val	Gly	Gly	Lys	Glu	Glu	Ile	Thr	
	130					135					140					
Gln	Val	Ala	Thr	Ile	Ser	Ala	Asn	Ser	Asp	His	Asn	Ile	Gly	Lys	Leu	
	145				150					155					160	
Ile	Ala	Asp	Ala	Met	Glu	Lys	Val	Gly	Lys	Asp	Gly	Val	Ile	Thr	Val	
			165						170					175		
Glu	Glu	Ala	Lys	Gly	Ile	Glu	Asp	Glu	Leu	Asp	Val	Val	Glu	Gly	Met	
		180						185					190			
Gln	Phe	Asp	Arg	Gly	Tyr	Leu	Ser	Pro	Tyr	Phe	Val	Thr	Asn	Ala	Glu	
	195						200					205				
Lys	Met	Thr	Ala	Gln	Leu	Asp	Asn	Ala	Tyr	Ile	Leu	Leu	Thr	Asp	Lys	
	210					215					220					
Lys	Ile	Ser	Ser	Met	Lys	Asp	Ile	Leu	Pro	Leu	Leu	Glu	Lys	Thr	Met	
	225				230					235					240	
Lys	Glu	Gly	Lys	Pro	Leu	Leu	Ile	Ile	Ala	Glu	Asp	Ile	Glu	Gly	Glu	
			245						250					255		
Ala	Leu	Thr	Thr	Leu	Val	Val	Asn	Lys	Leu	Arg	Gly	Val	Leu	Asn	Ile	
		260						265					270			
Ala	Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	Arg	Lys	Glu	Met	Leu	
	275						280					285				
Lys	Asp	Ile	Ala	Ile	Leu	Thr	Gly	Gly	Gln	Val	Ile	Ser	Glu	Glu	Leu	
	290					295					300					
Gly	Leu	Ser	Leu	Glu	Asn	Ala	Glu	Val	Glu	Phe	Leu	Gly	Lys	Ala	Gly	
	305				310					315					320	
Arg	Ile	Val	Ile	Asp	Lys	Asp	Asn	Thr	Thr	Ile	Val	Asp	Gly	Lys	Gly	
			325						330					335		
His	Ser	His	Asp	Val	Lys	Asp	Arg	Val	Ala	Gln	Ile	Lys	Thr	Gln	Ile	
			340					345					350			
Ala	Ser	Thr	Thr	Ser	Asp	Tyr	Asp	Lys	Glu	Lys	Leu	Gln	Glu	Arg	Leu	
	355						360					365				
Ala	Lys	Leu	Ser	Gly	Gly	Val	Ala	Val	Ile	Lys	Val	Gly	Ala	Ala	Ser	
	370					375					380					
Glu	Val	Glu	Met	Lys	Glu	Lys	Lys	Asp	Arg	Val	Asp	Asp	Ala	Leu	Ser	
	385				390					395				400		
Ala	Thr	Lys	Ala	Ala	Val	Glu	Glu	Gly	Ile	Val	Ile	Gly	Gly	Gly	Ala	
			405						410					415		
Ala	Leu	Ile	Arg	Ala	Ala	Gln	Lys	Val	His	Leu	Asn	Leu	His	Asp	Asp	
			420					425					430			
Glu	Lys	Val	Gly	Tyr	Glu	Ile	Ile	Met	Arg	Ala	Ile	Lys	Ala	Pro	Leu	
	435						440					445				
Ala	Gln	Ile	Ala	Ile	Asn	Ala	Gly	Tyr	Asp	Gly	Gly	Val	Val	Val	Asn	
	450					455					460					
Glu	Val	Glu	Lys	His	Glu	Gly	His	Phe	Gly	Phe	Asn	Ala	Ser	Asn	Gly	
	465				470					475				480		
Lys	Tyr	Val	Asp	Met	Phe	Lys	Glu	Gly	Ile	Ile	Asp	Pro	Leu	Lys	Val	
			485						490					495		
Glu	Arg	Ile	Ala	Leu	Gln	Asn	Ala	Val	Ser	Val	Ser	Ser	Leu	Leu	Leu	
			500					505					510			
Thr	Thr	Glu	Ala	Thr	Val	His	Glu	Ile	Lys	Glu	Glu	Lys	Ala	Ala	Pro	
		515					520					525				
Ala	Met	Pro	Asp	Met	Gly	Gly	Met	Gly	Gly	Met	Gly	Gly	Met	Gly	Gly	
	530					535					540					
Met	Met															
	545															

<210> 419
 <211> 881
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (14)...(838)

<400> 419
 ctaggagggtt tgc atg caa gag ttt tta ggt ttt ggt gtg gtg ggg aat 49
 Met Gln Glu Phe Leu Gly Phe Gly Val Val Gly Asn
 1 5 10

ttt gca ggg cat ttg gag caa gca gga gag agt cat agt ttt att aac 97
 Phe Ala Gly His Leu Glu Gln Ala Gly Glu Ser His Ser Phe Ile Asn
 15 20 25

atg aaa agc gaa gaa aag gac gcc cct aag ggg cta ttc cct ttt tat 145
 Met Lys Ser Glu Glu Lys Asp Ala Pro Lys Gly Leu Phe Pro Phe Tyr
 30 35 40

atc ccc tat gaa aat tgt tat ttg ggg cgt tgt tgc att gat aac cat 193
 Ile Pro Tyr Glu Asn Cys Tyr Leu Gly Arg Cys Cys Ile Asp Asn His
 45 50 55 60

aag att att ttg cct agt gat cta gat tta agg gtg caa gca gag cca 241
 Lys Ile Ile Leu Pro Ser Asp Leu Asp Leu Arg Val Gln Ala Glu Pro
 65 70 75

gaa atc gct tta gaa tgc gat gtt aaa tac gat gaa aaa cat ttg gtt 289
 Glu Ile Ala Leu Glu Cys Asp Val Lys Tyr Asp Glu Lys His Leu Val
 80 85 90

gca aag ctc gtg cct aat ttt ttc atg gcg ttt aat gac gct tct gtg 337
 Ala Lys Leu Val Pro Asn Phe Phe Met Ala Phe Asn Asp Ala Ser Val
 95 100 105

cgc aat tta gac gcc gca aaa ctc tcc caa aaa aag aat ttt tca ccg 385
 Arg Asn Leu Asp Ala Ala Lys Leu Ser Gln Lys Lys Asn Phe Ser Pro
 110 115 120

gct tct aaa ggt ata ggg cag aaa ttg ccc att gac agg ttt gtt tat 433
 Ala Ser Lys Gly Ile Gly Gln Lys Leu Pro Ile Asp Arg Phe Val Tyr
 125 130 135 140

ggg ggg gtg tgt aac aat ttc tct atc gcg tct ttt ttg aaa tac aat 481
 Gly Gly Val Cys Asn Asn Phe Ser Ile Ala Ser Phe Leu Lys Tyr Asn
 145 150 155

aat gtt tgg cac att tat ggg gaa aac agc aaa ttg ctc aaa tac gag 529
 Asn Val Trp His Ile Tyr Gly Glu Asn Ser Lys Leu Leu Lys Tyr Glu
 160 165 170

ttt ttt tat caa aag ctt tta gat tgg att aaa gac caa tta aac cac 577
 Phe Phe Tyr Gln Lys Leu Leu Asp Trp Ile Lys Asp Gln Leu Asn His
 175 180 185

caa caa gat ggc gac tct tta gag gct cta aga cct ttt tta gag cgc	625
Gln Gln Asp Gly Asp Ser Leu Glu Ala Leu Arg Pro Phe Leu Glu Arg	
190 195 200	
cat aat ttc ccc act aaa atg att ttt gca ata ggg gct acc cct tat	673
His Asn Phe Pro Thr Lys Met Ile Phe Ala Ile Gly Ala Thr Pro Tyr	
205 210 215 220	
atg cct ttt gcg caa gag cat ttt ttg caa aaa ggc gat gag gtg gtg	721
Met Pro Phe Ala Gln Glu His Phe Leu Gln Lys Gly Asp Glu Val Val	
225 230 235	
atc gtt gct tac aac cat tta caa tac agt ttt gaa aag att caa aac	769
Ile Val Ala Tyr Asn His Leu Gln Tyr Ser Phe Glu Lys Ile Gln Asn	
240 245 250	
ctc tta gaa gag gac gcc cta caa gcc aaa gaa cac gct aat ctt tct	817
Leu Leu Glu Glu Asp Ala Leu Gln Ala Lys Glu His Ala Asn Leu Ser	
255 260 265	
tat gtc tat caa atc gta gaa tagtaaggct tttacactct ttggctttgc	868
Tyr Val Tyr Gln Ile Val Glu	
270 275	
ttttttaccc ttt	881

<210> 420

<211> 275

<212> PRT

<213> Helicobacter pylori

<400> 420

Met Gln Glu Phe Leu Gly Phe Gly Val Val Gly Asn Phe Ala Gly His	
1 5 10 15	
Leu Glu Gln Ala Gly Glu Ser His Ser Phe Ile Asn Met Lys Ser Glu	
20 25 30	
Glu Lys Asp Ala Pro Lys Gly Leu Phe Pro Phe Tyr Ile Pro Tyr Glu	
35 40 45	
Asn Cys Tyr Leu Gly Arg Cys Cys Ile Asp Asn His Lys Ile Ile Leu	
50 55 60	
Pro Ser Asp Leu Asp Leu Arg Val Gln Ala Glu Pro Glu Ile Ala Leu	
65 70 75 80	
Glu Cys Asp Val Lys Tyr Asp Glu Lys His Leu Val Ala Lys Leu Val	
85 90 95	
Pro Asn Phe Phe Met Ala Phe Asn Asp Ala Ser Val Arg Asn Leu Asp	
100 105 110	
Ala Ala Lys Leu Ser Gln Lys Lys Asn Phe Ser Pro Ala Ser Lys Gly	
115 120 125	
Ile Gly Gln Lys Leu Pro Ile Asp Arg Phe Val Tyr Gly Gly Val Cys	
130 135 140	
Asn Asn Phe Ser Ile Ala Ser Phe Leu Lys Tyr Asn Asn Val Trp His	
145 150 155 160	
Ile Tyr Gly Glu Asn Ser Lys Leu Leu Lys Tyr Glu Phe Phe Tyr Gln	
165 170 175	
Lys Leu Leu Asp Trp Ile Lys Asp Gln Leu Asn His Gln Gln Asp Gly	
180 185 190	
Asp Ser Leu Glu Ala Leu Arg Pro Phe Leu Glu Arg His Asn Phe Pro	
195 200 205	
Thr Lys Met Ile Phe Ala Ile Gly Ala Thr Pro Tyr Met Pro Phe Ala	

			20					25					30			
Phe	Ala	Pro	Phe	Ile	Leu	Leu	Pro	Trp	Ile	Asp	Leu	Leu	Ser	Ala	Phe	
		35					40					45				
Leu	Leu	Tyr	Leu	Gly	Phe	Leu	Ala	Leu	Phe	Ser	Val	Leu	Glu	Phe	Phe	
	50					55					60					
Asp	Glu	Asp	Ile	Ala	Asp	Ile	Ile	Val	Ala	Lys	Ser	Lys	Ile	Lys	Thr	
65					70					75					80	
Lys	Thr	Lys	Cys	Tyr	Arg	Ala										
				85												

<210> 423
 <211> 1044
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (15)...(977)

<400> 423																
attaagggga	agtc	atg	gct	gat	agt	tta	gcg	ggc	att	gat	caa	ggt	acg			50
		Met	Ala	Asp	Ser	Leu	Ala	Gly	Ile	Asp	Gln	Val	Thr			
		1				5					10					
agt	ttg	cat	aaa	aat	aac	gag	tta	caa	ttg	ttg	tgt	ttc	agg	ctg	ggt	98
Ser	Leu	His	Lys	Asn	Asn	Glu	Leu	Gln	Leu	Leu	Cys	Phe	Arg	Leu	Gly	
		15				20						25				
aaa	aac	aag	gat	ttg	tat	gcg	gtc	aat	gtt	ttt	aag	atc	cgt	gaa	gtg	146
Lys	Asn	Lys	Asp	Leu	Tyr	Ala	Val	Asn	Val	Phe	Lys	Ile	Arg	Glu	Val	
	30					35					40					
gtg	aaa	tac	cat	ggc	aat	ctc	acc	atc	att	agc	cac	gaa	aac	aat	tcg	194
Val	Lys	Tyr	His	Gly	Asn	Leu	Thr	Ile	Ile	Ser	His	Glu	Asn	Asn	Ser	
	45				50					55					60	
ctc	gtt	gag	ggg	cta	atc	att	ata	aga	gaa	ctc	acc	att	ccc	ttg	att	242
Leu	Val	Glu	Gly	Leu	Ile	Ile	Ile	Arg	Glu	Leu	Thr	Ile	Pro	Leu	Ile	
				65					70					75		
gat	atg	aaa	aaa	tgg	ttt	tat	tat	gac	agc	caa	aac	aaa	aac	aag	gat	290
Asp	Met	Lys	Lys	Trp	Phe	Tyr	Tyr	Asp	Ser	Gln	Asn	Lys	Asn	Lys	Asp	
			80					85					90			
tta	cgc	cct	tat	agg	ata	gaa	aaa	gaa	aaa	ggc	gaa	gat	gat	att	gtt	338
Leu	Arg	Pro	Tyr	Arg	Ile	Glu	Lys	Glu	Lys	Gly	Glu	Asp	Asp	Ile	Val	
		95					100					105				
atg	att	tgt	gag	ttt	tct	cgc	tgg	act	ata	ggg	gtt	agg	atc	tat	gaa	386
Met	Ile	Cys	Glu	Phe	Ser	Arg	Trp	Thr	Ile	Gly	Val	Arg	Ile	Tyr	Glu	
	110					115					120					
gcg	gat	agg	att	ttg	agc	aag	aaa	tgg	act	gaa	atg	gag	caa	agc	gct	434
Ala	Asp	Arg	Ile	Leu	Ser	Lys	Lys	Trp	Thr	Glu	Met	Glu	Gln	Ser	Ala	
	125				130					135					140	
ggg	cta	ggg	gga	tct	gca	ggc	aat	aac	aaa	ctc	gtg	agc	cgc	acg	cgc	482
Gly	Leu	Gly	Gly	Ser	Ala	Gly	Asn	Asn	Lys	Leu	Val	Ser	Arg	Thr	Arg	

145										150					155					
tat	ttt	gat	ggg	cgc	ttg	gtg	caa	gtg	gtg	gat	att	gaa	aaa	atg	ctt	530				
Tyr	Phe	Asp	Gly	Arg	Leu	Val	Gln	Val	Val	Asp	Ile	Glu	Lys	Met	Leu					
			160					165					170							
ata	gac	gtg	ttc	cct	tgg	att	gaa	gat	gaa	aaa	cac	aac	gat	tta	gag	578				
Ile	Asp	Val	Phe	Pro	Trp	Ile	Glu	Asp	Glu	Lys	His	Asn	Asp	Leu	Glu					
		175					180					185								
acg	ctt	tct	aaa	atc	cat	tct	aac	caa	tgc	gtt	ttg	ctt	gct	gat	gac	626				
Thr	Leu	Ser	Lys	Ile	His	Ser	Asn	Gln	Cys	Val	Leu	Leu	Ala	Asp	Asp					
	190					195					200									
tcc	cca	agc	gtt	ttg	aaa	acc	atg	caa	atg	att	tta	gac	aag	ctg	ggc	674				
Ser	Pro	Ser	Val	Leu	Lys	Thr	Met	Gln	Met	Ile	Leu	Asp	Lys	Leu	Gly					
205					210					215					220					
gtc	aag	cat	ata	gat	ttt	atc	aat	ggg	aaa	acc	tta	cta	gag	cat	tta	722				
Val	Lys	His	Ile	Asp	Phe	Ile	Asn	Gly	Lys	Thr	Leu	Leu	Glu	His	Leu					
			225					230						235						
ttc	aac	ccc	aca	acc	gat	gtg	agt	aat	att	ggc	ctg	att	att	acc	gat	770				
Phe	Asn	Pro	Thr	Thr	Asp	Val	Ser	Asn	Ile	Gly	Leu	Ile	Ile	Thr	Asp					
			240					245					250							
ttg	gaa	atg	cca	gag	gcg	agc	ggg	ttt	gaa	gtg	atc	aag	cag	gtt	aaa	818				
Leu	Glu	Met	Pro	Glu	Ala	Ser	Gly	Phe	Glu	Val	Ile	Lys	Gln	Val	Lys					
	255						260					265								
aac	aat	cct	ttg	act	tca	aaa	atc	cct	atc	gtg	gtc	aat	tct	tct	atg	866				
Asn	Asn	Pro	Leu	Thr	Ser	Lys	Ile	Pro	Ile	Val	Val	Asn	Ser	Ser	Met					
	270					275					280									
agc	ggg	agt	tct	aat	gaa	gac	atg	gcc	agg	agt	ttg	aag	gcc	gat	gat	914				
Ser	Gly	Ser	Ser	Asn	Glu	Asp	Met	Ala	Arg	Ser	Leu	Lys	Ala	Asp	Asp					
285					290					295					300					
ttc	att	tcc	aag	tct	aac	ccc	aaa	gac	atc	cag	cga	gtg	gtt	aag	caa	962				
Phe	Ile	Ser	Lys	Ser	Asn	Pro	Lys	Asp	Ile	Gln	Arg	Val	Val	Lys	Gln					
				305				310						315						
ttt	ttg	gaa	tta	gca	tgaaaaaata	cagcactatc	cccacccctt	gctacgtgtt								1017				
Phe	Leu	Glu	Leu	Ala																
				320																
agagagcgaa	cgcttagaaa	aaaacgc														1044				
<210> 424																				
<211> 321																				
<212> PRT																				
<213> Helicobacter pylori																				
<400> 424																				
Met	Ala	Asp	Ser	Leu	Ala	Gly	Ile	Asp	Gln	Val	Thr	Ser	Leu	His	Lys					
1				5				10					15							
Asn	Asn	Glu	Leu	Gln	Leu	Leu	Cys	Phe	Arg	Leu	Gly	Lys	Asn	Lys	Asp					
		20					25					30								
Leu	Tyr	Ala	Val	Asn	Val	Phe	Lys	Ile	Arg	Glu	Val	Val	Lys	Tyr	His					

25	30	35	
cct aaa gtc cct aaa cag cct agc gtg cct tta atg ttt cat ttc acc			198
Pro Lys Val Pro Lys Gln Pro Ser Val Pro Leu Met Phe His Phe Thr			
40	45	50	
gag cat tat gcg cgc ttt atc cct acg att tta tct gtg gcg att ccc			246
Glu His Tyr Ala Arg Phe Ile Pro Thr Ile Leu Ser Val Ala Ile Pro			
55	60	65	70
tta atc caa aga gat gcg gta ggg ctt ttt caa gtc gct aac gct tct			294
Leu Ile Gln Arg Asp Ala Val Gly Leu Phe Gln Val Ala Asn Ala Ser			
	75	80	85
atc gct aca acc ctt ctc acg cac acc acc aaa aga gcc tta aac cat			342
Ile Ala Thr Thr Leu Leu Thr His Thr Thr Lys Arg Ala Leu Asn His			
	90	95	100
gta aca atc aac gat cag cgt ttg ggc gag cgc cct tat gga ggt aat			390
Val Thr Ile Asn Asp Gln Arg Leu Gly Glu Arg Pro Tyr Gly Gly Asn			
	105	110	115
ttc aac atg cca agc ggg cat tcg tct atg gtg ggt ttg gcg gtg gcg			438
Phe Asn Met Pro Ser Gly His Ser Ser Met Val Gly Leu Ala Val Ala			
	120	125	130
ttt tta atg cgc cgc tat tct ttt aaa aaa tac ttt tgg ctc ttg ccc			486
Phe Leu Met Arg Arg Tyr Ser Phe Lys Lys Tyr Phe Trp Leu Leu Pro			
135	140	145	150
cta gtc cct ttg acc atg ctc gct cgc att tat tta gac atg cac acc			534
Leu Val Pro Leu Thr Met Leu Ala Arg Ile Tyr Leu Asp Met His Thr			
	155	160	165
att ggc gcg gtg ctg acc ggg ctt ggc gtt gga atg ttg tgc gta asc			582
Ile Gly Ala Val Leu Thr Gly Leu Gly Val Gly Met Leu Cys Val Xaa			
	170	175	180
ttt tta caa gcc cca aaa agc ctt aat caa aag ctt tagttttctgt			628
Phe Leu Gln Ala Pro Lys Ser Leu Asn Gln Lys Leu			
	185	190	
tttta			633
<210> 426			
<211> 194			
<212> PRT			
<213> Helicobacter pylori			
<220>			
<221> VARIANT			
<222> 182			
<223> Xaa = Any Amino Acid			
<400> 426			
Met Lys Lys Phe Leu Phe Lys Gln Lys Phe Cys Glu Ser Leu Pro Lys			
1	5	10	15
Ser Phe Ser Lys Thr Leu Leu Ala Leu Ser Leu Gly Leu Ile Leu Leu			
	20	25	30

Gly	Ile	Phe	Ala	Pro	Phe	Pro	Lys	Val	Pro	Lys	Gln	Pro	Ser	Val	Pro
		35					40					45			
Leu	Met	Phe	His	Phe	Thr	Glu	His	Tyr	Ala	Arg	Phe	Ile	Pro	Thr	Ile
	50					55					60				
Leu	Ser	Val	Ala	Ile	Pro	Leu	Ile	Gln	Arg	Asp	Ala	Val	Gly	Leu	Phe
65					70					75				80	
Gln	Val	Ala	Asn	Ala	Ser	Ile	Ala	Thr	Thr	Leu	Leu	Thr	His	Thr	Thr
			85						90					95	
Lys	Arg	Ala	Leu	Asn	His	Val	Thr	Ile	Asn	Asp	Gln	Arg	Leu	Gly	Glu
			100					105					110		
Arg	Pro	Tyr	Gly	Gly	Asn	Phe	Asn	Met	Pro	Ser	Gly	His	Ser	Ser	Met
		115					120					125			
Val	Gly	Leu	Ala	Val	Ala	Phe	Leu	Met	Arg	Arg	Tyr	Ser	Phe	Lys	Lys
	130					135					140				
Tyr	Phe	Trp	Leu	Leu	Pro	Leu	Val	Pro	Leu	Thr	Met	Leu	Ala	Arg	Ile
145					150					155					160
Tyr	Leu	Asp	Met	His	Thr	Ile	Gly	Ala	Val	Leu	Thr	Gly	Leu	Gly	Val
				165					170					175	
Gly	Met	Leu	Cys	Val	Xaa	Phe	Leu	Gln	Ala	Pro	Lys	Ser	Leu	Asn	Gln
			180					185						190	
Lys	Leu														

<210> 427
 <211> 1091
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (57)...(1040)

<400> 427
 atttcccttt gttcgtttat gtttataaag aaagcaacca ggtcagtttt atcgcc atg 59
 Met
 1

atg gtt gtg gtg ctt ttt tgc gtt aat ggc gct ctt ttt ttg gcg tta 107
 Met Val Val Val Leu Phe Cys Val Asn Gly Ala Leu Phe Leu Ala Leu
 5 10 15

ggc ttg atc tct gct tct ttg atg cgt tgg agt gcg ata gtt ttt agc 155
 Gly Leu Ile Ser Ala Ser Leu Met Arg Trp Ser Ala Ile Val Phe Ser
 20 25 30

ctg ctc aat tcc gtt gct ttc tat ttc att agc gct tat aag gtg ttt 203
 Leu Leu Asn Ser Val Ala Phe Tyr Phe Ile Ser Ala Tyr Lys Val Phe
 35 40 45

tta aat aag agc atg atg ggt aat gtc tta aac acc aac acg cat gaa 251
 Leu Asn Lys Ser Met Met Gly Asn Val Leu Asn Thr Asn Thr His Glu
 50 55 60 65

gtt tta ggc ttt ttg agc gtc aaa tta ttc gtt ttt atc gtt gtt ttt 299
 Val Leu Gly Phe Leu Ser Val Lys Leu Phe Val Phe Ile Val Val Phe
 70 75 80

ggg gtg ttg cct ggc tat gtc atc tat aaa atc ccc ctt aaa aat tct 347

Gly	Val	Leu	Pro	Gly	Tyr	Val	Ile	Tyr	Lys	Ile	Pro	Leu	Lys	Asn	Ser	
			85					90					95			
tct	aaa	aaa	gcg	ccc	ttt	tta	gcg	atc	ttg	gcg	tta	gtg	ttt	atc	ttt	395
Ser	Lys	Lys	Ala	Pro	Phe	Leu	Ala	Ile	Leu	Ala	Leu	Val	Phe	Ile	Phe	
		100					105					110				
atc	gct	agc	gct	tta	gct	aac	act	aaa	aat	tgg	ctg	tgg	ttt	gac	aag	443
Ile	Ala	Ser	Ala	Leu	Ala	Asn	Thr	Lys	Asn	Trp	Leu	Trp	Phe	Asp	Lys	
	115					120					125					
cat	gcg	aaa	ttc	ata	ggg	ggc	tta	att	ttg	ccc	ttc	gct	tat	agc	gtg	491
His	Ala	Lys	Phe	Ile	Gly	Gly	Leu	Ile	Leu	Pro	Phe	Ala	Tyr	Ser	Val	
130					135					140					145	
aac	gct	ttt	aga	gtg	agc	gct	ctc	aaa	ttt	ttc	gcc	ccc	acc	atc	aag	539
Asn	Ala	Phe	Arg	Val	Ser	Ala	Leu	Lys	Phe	Phe	Ala	Pro	Thr	Ile	Lys	
				150					155					160		
cgc	ctc	cct	ctt	ttt	tca	ccc	aat	cat	tcc	cat	tcg	ttt	gtg	gtg	cta	587
Pro	Leu	Pro	Leu	Phe	Ser	Pro	Asn	His	Ser	His	Ser	Phe	Val	Val	Leu	
			165					170					175			
gtc	att	ggc	gaa	agc	gct	agg	aaa	cat	aat	tac	gcc	ctt	tat	ggc	tat	635
Val	Ile	Gly	Glu	Ser	Ala	Arg	Lys	His	Asn	Tyr	Ala	Leu	Tyr	Gly	Tyr	
		180					185					190				
caa	aaa	ccc	acc	acc	cca	aga	cta	agc	aag	cgt	tta	gcc	gat	aat	gaa	683
Gln	Lys	Pro	Thr	Thr	Pro	Arg	Leu	Ser	Lys	Arg	Leu	Ala	Asp	Asn	Glu	
	195					200					205					
ctc	act	ctt	ttc	aac	gcc	act	tct	tgc	gcc	act	tac	acg	aca	gcg	agt	731
Leu	Thr	Leu	Phe	Asn	Ala	Thr	Ser	Cys	Ala	Thr	Tyr	Thr	Thr	Ala	Ser	
210					215				220						225	
ttg	gaa	tgc	att	tta	gat	tct	tct	ttt	aaa	aac	aac	gct	tat	gaa	aat	779
Leu	Glu	Cys	Ile	Leu	Asp	Ser	Ser	Phe	Lys	Asn	Asn	Ala	Tyr	Glu	Asn	
				230				235						240		
ttg	cca	act	tac	ttg	act	aaa	gcc	ggt	atc	aaa	gtc	ttt	tgg	tat	agc	827
Leu	Pro	Thr	Tyr	Leu	Thr	Lys	Ala	Gly	Ile	Lys	Val	Phe	Trp	Tyr	Ser	
			245					250					255			
gcg	aac	gac	ggc	gaa	aag	aat	gtt	aag	gtt	aca	agc	tat	ctt	aaa	aac	875
Ala	Asn	Asp	Gly	Glu	Lys	Asn	Val	Lys	Val	Thr	Ser	Tyr	Leu	Lys	Asn	
		260					265					270				
tat	gaa	ttg	att	caa	aaa	tgc	ccc	aat	tgt	gaa	gcg	atc	gct	cct	tat	923
Tyr	Glu	Leu	Ile	Gln	Lys	Cys	Pro	Asn	Cys	Glu	Ala	Ile	Ala	Pro	Tyr	
	275					280					285					
gat	gaa	tct	tta	ctt	tat	aat	ttg	cct	gac	ctt	tta	aaa	gaa	cac	tct	971
Asp	Glu	Ser	Leu	Leu	Tyr	Asn	Leu	Pro	Asp	Leu	Leu	Lys	Glu	His	Ser	
290					295				300						305	
aat	gaa	aat	gtc	ttg	ctc	atc	tta	cac	ttg	cag	gct	cgc	atg	gcc	caa	1019
Asn	Glu	Asn	Val	Leu	Leu	Ile	Leu	His	Leu	Gln	Ala	Arg	Met	Ala	Gln	
				310					315					320		

act acg aca aca aag tgc ctt taaatttttag ggtgtttaag ccttattgct 1070
 Thr Thr Thr Thr Lys Cys Leu
 325

caagcgctga tctgtcttct t 1091

<210> 428
 <211> 328
 <212> PRT
 <213> Helicobacter pylori

<400> 428
 Met Met Val Val Val Leu Phe Cys Val Asn Gly Ala Leu Phe Leu Ala
 1 5 10 15
 Leu Gly Leu Ile Ser Ala Ser Leu Met Arg Trp Ser Ala Ile Val Phe
 20 25 30
 Ser Leu Leu Asn Ser Val Ala Phe Tyr Phe Ile Ser Ala Tyr Lys Val
 35 40 45
 Phe Leu Asn Lys Ser Met Met Gly Asn Val Leu Asn Thr Asn Thr His
 50 55 60
 Glu Val Leu Gly Phe Leu Ser Val Lys Leu Phe Val Phe Ile Val Val
 65 70 75 80
 Phe Gly Val Leu Pro Gly Tyr Val Ile Tyr Lys Ile Pro Leu Lys Asn
 85 90 95
 Ser Ser Lys Lys Ala Pro Phe Leu Ala Ile Leu Ala Leu Val Phe Ile
 100 105 110
 Phe Ile Ala Ser Ala Leu Ala Asn Thr Lys Asn Trp Leu Trp Phe Asp
 115 120 125
 Lys His Ala Lys Phe Ile Gly Gly Leu Ile Leu Pro Phe Ala Tyr Ser
 130 135 140
 Val Asn Ala Phe Arg Val Ser Ala Leu Lys Phe Phe Ala Pro Thr Ile
 145 150 155 160
 Lys Pro Leu Pro Leu Phe Ser Pro Asn His Ser His Ser Phe Val Val
 165 170 175
 Leu Val Ile Gly Glu Ser Ala Arg Lys His Asn Tyr Ala Leu Tyr Gly
 180 185 190
 Tyr Gln Lys Pro Thr Thr Pro Arg Leu Ser Lys Arg Leu Ala Asp Asn
 195 200 205
 Glu Leu Thr Leu Phe Asn Ala Thr Ser Cys Ala Thr Tyr Thr Thr Ala
 210 215 220
 Ser Leu Glu Cys Ile Leu Asp Ser Ser Phe Lys Asn Asn Ala Tyr Glu
 225 230 235 240
 Asn Leu Pro Thr Tyr Leu Thr Lys Ala Gly Ile Lys Val Phe Trp Tyr
 245 250 255
 Ser Ala Asn Asp Gly Glu Lys Asn Val Lys Val Thr Ser Tyr Leu Lys
 260 265 270
 Asn Tyr Glu Leu Ile Gln Lys Cys Pro Asn Cys Glu Ala Ile Ala Pro
 275 280 285
 Tyr Asp Glu Ser Leu Leu Tyr Asn Leu Pro Asp Leu Leu Lys Glu His
 290 295 300
 Ser Asn Glu Asn Val Leu Leu Ile Leu His Leu Gln Ala Arg Met Ala
 305 310 315 320
 Gln Thr Thr Thr Thr Lys Cys Leu
 325

<210> 429
 <211> 1879
 <212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (49)...(1827)

<400> 429

```
aagctcaaag ataaagcgct acaatctcgc ttagaaaaag gacacaaa atg cta ttg 57
                                     Met Leu Leu
                                     1

aat tac gat ttt tta gaa ttt gtt gat gag ccg aaa aga aac act tct 105
Asn Tyr Asp Phe Leu Glu Phe Val Asp Glu Pro Lys Arg Asn Thr Ser
      5                      10                      15

ttg aca gca tct att gat aaa gcg tta gcg gac agg aag tta gct aga 153
Leu Thr Ala Ser Ile Asp Lys Ala Leu Ala Asp Arg Lys Leu Ala Arg
    20                      25                      30                      35

caa aat aaa cct agc gtt agg gtg ctt ggt aag gcg atg ccc tta agc 201
Gln Asn Lys Pro Ser Val Arg Val Leu Gly Lys Ala Met Pro Leu Ser
                        40                      45                      50

aag ttt tta gat gct gtt ggc gat gaa atc tca cga ctt aaa tat gat 249
Lys Phe Leu Asp Ala Val Gly Asp Glu Ile Ser Arg Leu Lys Tyr Asp
      55                      60                      65

atg agc cac aag act att aaa ggc tct aca att gag agt tct aat ctt 297
Met Ser His Lys Thr Ile Lys Gly Ser Thr Ile Glu Ser Ser Asn Leu
      70                      75                      80

atc agc att tat aaa aag att gcg agc gga cta cct ttt ggg act atc 345
Ile Ser Ile Tyr Lys Lys Ile Ala Ser Gly Leu Pro Phe Gly Thr Ile
      85                      90                      95

tcg gcg ttt aga cct ttt aaa gac gct ttt tat aaa gac ttt acc gaa 393
Ser Ala Phe Arg Pro Phe Lys Asp Ala Phe Tyr Lys Asp Phe Thr Glu
    100                      105                      110                      115

aaa gaa caa aac gct cta atc tat gct tat aag agc gga gca gac cct 441
Lys Glu Gln Asn Ala Leu Ile Tyr Ala Tyr Lys Ser Gly Ala Asp Pro
      120                      125                      130

aaa aat gcg gac ata ata gcc aaa tat tgg tta agt caa tct gtg gat 489
Lys Asn Ala Asp Ile Ile Ala Lys Tyr Trp Leu Ser Gln Ser Val Asp
      135                      140                      145

tta gac cca tac gac cct att aaa gtt gta gat ttc ttt cac cca caa 537
Leu Asp Pro Tyr Asp Pro Ile Lys Val Val Asp Phe Phe His Pro Gln
      150                      155                      160

cct gaa aat ggt aaa gag act aca aaa ttt aag aac tac aaa gat agg 585
Pro Glu Asn Gly Lys Glu Thr Thr Lys Phe Lys Asn Tyr Lys Asp Arg
      165                      170                      175

att gag aac att tat gcg aca ctc tat aac aca ttg ggt agg ggt tat 633
Ile Glu Asn Ile Tyr Ala Thr Leu Tyr Asn Thr Leu Gly Arg Gly Tyr
    180                      185                      190                      195
```

gtg gat aaa ttt ttt aaa aaa gaa gcc aca atg agg gac ttt atg tct	681
Val Asp Lys Phe Phe Lys Lys Glu Ala Thr Met Arg Asp Phe Met Ser	
200 205 210	
agc gat aaa ttt gtt gag aga tac cgc tac act aga aaa gaa aat atg	729
Ser Asp Lys Phe Val Glu Arg Tyr Arg Tyr Thr Arg Lys Glu Asn Met	
215 220 225	
gca agg aca caa gca tta aaa gac ata atg aat att gac aga gat ttc	777
Ala Arg Thr Gln Ala Leu Lys Asp Ile Met Asn Ile Asp Arg Asp Phe	
230 235 240	
att ggt tat att gaa gtg tta ggg tat tgg aaa gac aac cct aaa gac	825
Ile Gly Tyr Ile Glu Val Leu Gly Tyr Trp Lys Asp Asn Pro Lys Asp	
245 250 255	
aat atc tta cca gac aaa gag gtt agc ttt ttt gta ttc caa aac gaa	873
Asn Ile Leu Pro Asp Lys Glu Val Ser Phe Phe Val Phe Gln Asn Glu	
260 265 270 275	
cct agt agc aca ttt gat ttg aaa aac cac tta ttg ata tgg ggt aaa	921
Pro Ser Ser Thr Phe Asp Leu Lys Asn His Leu Leu Ile Trp Gly Lys	
280 285 290	
caa ttc aga caa gta gcg att tgc tat ggc gga caa ttg att gct aat	969
Gln Phe Arg Gln Val Ala Ile Cys Tyr Gly Gly Gln Leu Ile Ala Asn	
295 300 305	
aag aat aag act tat agg ata gat ttg ata agt tgc aga cct gat aat	1017
Lys Asn Lys Thr Tyr Arg Ile Asp Leu Ile Ser Cys Arg Pro Asp Asn	
310 315 320	
ttt ggt gag gtt tgg gct aaa ttc aca ggg att aaa ttt tca gtt cct	1065
Phe Gly Glu Val Trp Ala Lys Phe Thr Gly Ile Lys Phe Ser Val Pro	
325 330 335	
agc gac tta cca caa gct ctc aca cgc ata aat gac agc gtt tat act	1113
Ser Asp Leu Pro Gln Ala Leu Thr Arg Ile Asn Asp Ser Val Tyr Thr	
340 345 350 355	
ttt ctc tct agg aat aaa gag ggt atc ggt ctt aat aaa ctc gct ctc	1161
Phe Leu Ser Arg Asn Lys Glu Gly Ile Gly Leu Asn Lys Leu Ala Leu	
360 365 370	
aat aaa gtc gtt aag aca gaa tta aaa gcg act tgt atg ccc tat gat	1209
Asn Lys Val Val Lys Thr Glu Leu Lys Ala Thr Cys Met Pro Tyr Asp	
375 380 385	
tac tct aaa ttg ggt ata gag act att ggc gag gac att aga agc aat	1257
Tyr Ser Lys Leu Gly Ile Glu Thr Ile Gly Glu Asp Ile Arg Ser Asn	
390 395 400	
att aaa gca tta cag aaa atg tct cgt ggg tat gga cac cct aaa gag	1305
Ile Lys Ala Leu Gln Lys Met Ser Arg Gly Tyr Gly His Pro Lys Glu	
405 410 415	
ttc ttt ttg gac gca atg ata aaa aaa cag gaa aat gcg att aaa cgc	1353
Phe Phe Leu Asp Ala Met Ile Lys Lys Gln Glu Asn Ala Ile Lys Arg	
420 425 430 435	

ata gaa gca cga aaa tgt gcg gta agc gat gac ttc aaa caa ggt atg	1401
Ile Glu Ala Arg Lys Cys Ala Val Ser Asp Asp Phe Lys Gln Gly Met	
440 445 450	
aaa cga aac att aaa gtt aat aac ctt gtt aaa gct atg cga caa ggc	1449
Lys Arg Asn Ile Lys Val Asn Asn Leu Val Lys Ala Met Arg Gln Gly	
455 460 465	
aaa aaa gtg agt agg aca ttg att gct aaa gtg ctt gct aac acc ata	1497
Lys Lys Val Ser Arg Thr Leu Ile Ala Lys Val Leu Ala Asn Thr Ile	
470 475 480	
gac acc gat gcg ggt tat tgc ttc att tcg ccg aca gat tta gcg aca	1545
Asp Thr Asp Ala Gly Tyr Cys Phe Ile Ser Pro Thr Asp Leu Ala Thr	
485 490 495	
caa ctt ggc aac atc agc cct aga cta tct aaa agc ata gtt acc gcc	1593
Gln Leu Gly Asn Ile Ser Pro Arg Leu Ser Lys Ser Ile Val Thr Ala	
500 505 510 515	
ata gag caa gca gag ggc gtg aga ctg aat tat gcg ttg att gac aaa	1641
Ile Glu Gln Ala Glu Gly Val Arg Leu Asn Tyr Ala Leu Ile Asp Lys	
520 525 530	
atc acc tat aac tca ctc cac aat atc tta agt ttc att ttt gat att	1689
Ile Thr Tyr Asn Ser Leu His Asn Ile Leu Ser Phe Ile Phe Asp Ile	
535 540 545	
gat aac cct tta agc gac caa gtg ttt gag aga tta gtc att gaa gtc	1737
Asp Asn Pro Leu Ser Asp Gln Val Phe Glu Arg Leu Val Ile Glu Val	
550 555 560	
cca aga gaa gca ctt aaa aat gtg aag ttg cca caa atc aaa aat gta	1785
Pro Arg Glu Ala Leu Lys Asn Val Lys Leu Pro Gln Ile Lys Asn Val	
565 570 575	
ttg act tct caa atc ttt gat ggc gct tac cac ttt aaa agt	1827
Leu Thr Ser Gln Ile Phe Asp Gly Ala Tyr His Phe Lys Ser	
580 585 590	
taaaccatgc tctttatcag cgcaactaac acgaatgccg gaaaaaccac at	1879

<210> 430

<211> 593

<212> PRT

<213> *Helicobacter pylori*

<400> 430

Met Leu Leu Asn Tyr Asp Phe Leu Glu Phe Val Asp Glu Pro Lys Arg	
1 5 10 15	
Asn Thr Ser Leu Thr Ala Ser Ile Asp Lys Ala Leu Ala Asp Arg Lys	
20 25 30	
Leu Ala Arg Gln Asn Lys Pro Ser Val Arg Val Leu Gly Lys Ala Met	
35 40 45	
Pro Leu Ser Lys Phe Leu Asp Ala Val Gly Asp Glu Ile Ser Arg Leu	
50 55 60	
Lys Tyr Asp Met Ser His Lys Thr Ile Lys Gly Ser Thr Ile Glu Ser	
65 70 75 80	

Ser	Asn	Leu	Ile	Ser	Ile	Tyr	Lys	Lys	Ile	Ala	Ser	Gly	Leu	Pro	Phe
				85					90					95	
Gly	Thr	Ile	Ser	Ala	Phe	Arg	Pro	Phe	Lys	Asp	Ala	Phe	Tyr	Lys	Asp
			100					105					110		
Phe	Thr	Glu	Lys	Glu	Gln	Asn	Ala	Leu	Ile	Tyr	Ala	Tyr	Lys	Ser	Gly
		115					120					125			
Ala	Asp	Pro	Lys	Asn	Ala	Asp	Ile	Ile	Ala	Lys	Tyr	Trp	Leu	Ser	Gln
	130					135					140				
Ser	Val	Asp	Leu	Asp	Pro	Tyr	Asp	Pro	Ile	Lys	Val	Val	Asp	Phe	Phe
145					150					155					160
His	Pro	Gln	Pro	Glu	Asn	Gly	Lys	Glu	Thr	Thr	Lys	Phe	Lys	Asn	Tyr
				165					170					175	
Lys	Asp	Arg	Ile	Glu	Asn	Ile	Tyr	Ala	Thr	Leu	Tyr	Asn	Thr	Leu	Gly
			180					185					190		
Arg	Gly	Tyr	Val	Asp	Lys	Phe	Phe	Lys	Lys	Glu	Ala	Thr	Met	Arg	Asp
		195					200						205		
Phe	Met	Ser	Ser	Asp	Lys	Phe	Val	Glu	Arg	Tyr	Arg	Tyr	Thr	Arg	Lys
	210					215					220				
Glu	Asn	Met	Ala	Arg	Thr	Gln	Ala	Leu	Lys	Asp	Ile	Met	Asn	Ile	Asp
225					230					235					240
Arg	Asp	Phe	Ile	Gly	Tyr	Ile	Glu	Val	Leu	Gly	Tyr	Trp	Lys	Asp	Asn
			245						250					255	
Pro	Lys	Asp	Asn	Ile	Leu	Pro	Asp	Lys	Glu	Val	Ser	Phe	Phe	Val	Phe
			260					265					270		
Gln	Asn	Glu	Pro	Ser	Ser	Thr	Phe	Asp	Leu	Lys	Asn	His	Leu	Leu	Ile
		275					280					285			
Trp	Gly	Lys	Gln	Phe	Arg	Gln	Val	Ala	Ile	Cys	Tyr	Gly	Gly	Gln	Leu
	290					295					300				
Ile	Ala	Asn	Lys	Asn	Lys	Thr	Tyr	Arg	Ile	Asp	Leu	Ile	Ser	Cys	Arg
305					310					315					320
Pro	Asp	Asn	Phe	Gly	Glu	Val	Trp	Ala	Lys	Phe	Thr	Gly	Ile	Lys	Phe
			325						330					335	
Ser	Val	Pro	Ser	Asp	Leu	Pro	Gln	Ala	Leu	Thr	Arg	Ile	Asn	Asp	Ser
			340					345					350		
Val	Tyr	Thr	Phe	Leu	Ser	Arg	Asn	Lys	Glu	Gly	Ile	Gly	Leu	Asn	Lys
		355					360					365			
Leu	Ala	Leu	Asn	Lys	Val	Val	Lys	Thr	Glu	Leu	Lys	Ala	Thr	Cys	Met
	370					375					380				
Pro	Tyr	Asp	Tyr	Ser	Lys	Leu	Gly	Ile	Glu	Thr	Ile	Gly	Glu	Asp	Ile
385					390					395					400
Arg	Ser	Asn	Ile	Lys	Ala	Leu	Gln	Lys	Met	Ser	Arg	Gly	Tyr	Gly	His
			405						410					415	
Pro	Lys	Glu	Phe	Phe	Leu	Asp	Ala	Met	Ile	Lys	Lys	Gln	Glu	Asn	Ala
			420					425					430		
Ile	Lys	Arg	Ile	Glu	Ala	Arg	Lys	Cys	Ala	Val	Ser	Asp	Asp	Phe	Lys
		435					440					445			
Gln	Gly	Met	Lys	Arg	Asn	Ile	Lys	Val	Asn	Asn	Leu	Val	Lys	Ala	Met
	450					455					460				
Arg	Gln	Gly	Lys	Lys	Val	Ser	Arg	Thr	Leu	Ile	Ala	Lys	Val	Leu	Ala
465					470					475					480
Asn	Thr	Ile	Asp	Thr	Asp	Ala	Gly	Tyr	Cys	Phe	Ile	Ser	Pro	Thr	Asp
			485						490					495	
Leu	Ala	Thr	Gln	Leu	Gly	Asn	Ile	Ser	Pro	Arg	Leu	Ser	Lys	Ser	Ile
		500					505						510		
Val	Thr	Ala	Ile	Glu	Gln	Ala	Glu	Gly	Val	Arg	Leu	Asn	Tyr	Ala	Leu
		515					520					525			
Ile	Asp	Lys	Ile	Thr	Tyr	Asn	Ser	Leu	His	Asn	Ile	Leu	Ser	Phe	Ile
	530					535					540				
Phe	Asp	Ile	Asp	Asn	Pro	Leu	Ser	Asp	Gln	Val	Phe	Glu	Arg	Leu	Val

atc aag cgc ttt tta aac cag caa gag cct tat tat ggg gat att ggg	531
Ile Lys Arg Phe Leu Asn Gln Gln Glu Pro Tyr Tyr Gly Asp Ile Gly	
160 165 170	
gtg cgt tta gaa gaa cat cat aag cgt tta gtg gta gtg caa ttt gat	579
Val Arg Leu Glu Glu His His Lys Arg Leu Val Val Val Gln Phe Asp	
175 180 185	
cca ttt ttc cct aaa aac cct ttt tta aaa aac gat gaa atc cta gcg	627
Pro Phe Phe Pro Lys Asn Pro Phe Leu Lys Asn Asp Glu Ile Leu Ala	
190 195 200 205	
atc aac cat caa aag atc cac tca tta gcg gag ttt gaa tgg gtg gtg	675
Ile Asn His Gln Lys Ile His Ser Leu Ala Glu Phe Glu Trp Val Val	
210 215 220	
agc aat ctt aaa tac caa agc ctt gca aaa gtg gaa atc aaa cga aac	723
Ser Asn Leu Lys Tyr Gln Ser Leu Ala Lys Val Glu Ile Lys Arg Asn	
225 230 235	
cat aaa gtc aaa gaa gta acg ctc aaa gtc aat aag cgt tat ggg ggg	771
His Lys Val Lys Glu Val Thr Leu Lys Val Asn Lys Arg Tyr Gly Gly	
240 245 250	
ttt tta ctc aaa gac act ttt tta gag cgc tat ggc atc gct tta gat	819
Phe Leu Leu Lys Asp Thr Phe Leu Glu Arg Tyr Gly Ile Ala Leu Asp	
255 260 265	
gag cgt ttt att atc act aaa ata ggc gct cat ttg ccc aaa ggc ttg	867
Glu Arg Phe Ile Ile Thr Lys Ile Gly Ala His Leu Pro Lys Gly Leu	
270 275 280 285	
gat ttt tta aag ctt ggg gat agg att tta tgg gtg aat tat aaa agc	915
Asp Phe Leu Lys Leu Gly Asp Arg Ile Leu Trp Val Asn Tyr Lys Ser	
290 295 300	
gtg gcg tcc aac cca aag gct tta aga gaa gcg tta agc gcg cct aaa	963
Val Ala Ser Asn Pro Lys Ala Leu Arg Glu Ala Leu Ser Ala Pro Lys	
305 310 315	
att gaa tta tta gtc ttg cgt aaa ggc ttt gaa ttt tac att aaa gtc	1011
Ile Glu Leu Leu Val Leu Arg Lys Gly Phe Glu Phe Tyr Ile Lys Val	
320 325 330	
cg t tgaagtattg atgaaaaatg acgcttatga aattattctt tcttggttt	1063
Arg	

<210> 432

<211> 334

<212> PRT

<213> Helicobacter pylori

<400> 432

Met Phe His Lys Ala Leu Ile Thr Phe Ile Val Leu Trp Phe Phe Leu	
1 5 10 15	
Asn Gly Leu Gly Ala Tyr Asp Phe Lys His Cys Gln Ala Phe Phe Lys	
20 25 30	

Ala	Ile	Leu	Gly	Arg	Phe	Ala	Glu	Phe	Phe	Leu	Tyr	Thr	Leu	His	Ala		
	20					25					30						
caa	ttg	gtg	ttt	aat	agc	gtg	gtc	gct	ttg	gcg	ttc	atg	ctc	ttt	gct	201	
Gln	Leu	Val	Phe	Asn	Ser	Val	Val	Ala	Leu	Ala	Phe	Met	Leu	Phe	Ala		
	35				40					45					50		
tat	agg	agt	ttg	aaa	gaa	cag	aat	ttc	ttc	agc	gct	agc	gcg	cta	aca	249	
Tyr	Arg	Ser	Leu	Lys	Glu	Gln	Asn	Phe	Phe	Ser	Ala	Ser	Ala	Leu	Thr		
				55					60					65			
gaa	gcg	tta	ttg	ttt	gtg	ggg	ttt	ttt	gca	ctt	ttc	aac	tac	gct	tta	297	
Glu	Ala	Leu	Leu	Phe	Val	Gly	Phe	Phe	Ala	Leu	Phe	Asn	Tyr	Ala	Leu		
			70					75					80				
aaa	aat	ccc	atg	cat	ttt	tat	gaa	ttt	ttc	caa	aac	gct	att	ttt	att	345	
Lys	Asn	Pro	Met	His	Phe	Tyr	Glu	Phe	Phe	Gln	Asn	Ala	Ile	Phe	Ile		
		85					90					95					
gcg	cct	aac	atg	atc	gcg	caa	agc	ctc	tct	caa	agc	ttg	agt	aac	ttt	393	
Ala	Pro	Asn	Met	Ile	Ala	Gln	Ser	Leu	Ser	Gln	Ser	Leu	Ser	Asn	Phe		
	100					105					110						
tct	gac	cat	gcg	ctt	tct	tta	gat	ttt	atc	ttt	aat	cat	ggt	ttt	tat	441	
Ser	Asp	His	Ala	Leu	Ser	Leu	Asp	Phe	Ile	Phe	Asn	His	Gly	Phe	Tyr		
	115				120					125					130		
gcc	ctt	agt	ttc	atc	agc	gat	ttg	agc	cat	aat	gaa	atg	tct	gtg	tgg	489	
Ala	Leu	Ser	Phe	Ile	Ser	Asp	Leu	Ser	His	Asn	Glu	Met	Ser	Val	Trp		
				135					140					145			
ctt	ttt	tta	agc	gtt	ttg	caa	ggg	ctt	ttt	ttg	agc	gtg	ctg	ttt	gca	537	
Leu	Phe	Leu	Ser	Val	Leu	Gln	Gly	Leu	Phe	Leu	Ser	Val	Leu	Phe	Ala		
			150				155						160				
atc	atc	att	tta	gtg	tat	tta	gaa	gtg	cat	gtg	tgg	tgc	tct	tta	ggg	585	
Ile	Ile	Ile	Leu	Val	Tyr	Leu	Glu	Val	His	Val	Trp	Cys	Ser	Leu	Gly		
		165					170					175					
gtg	ctg	ttt	tta	gcg	ttt	ggg	ttt	ttt	aaa	acc	tgg	agg	agc	gtt	gtg	633	
Val	Leu	Phe	Leu	Ala	Phe	Gly	Phe	Phe	Lys	Thr	Trp	Arg	Ser	Val	Val		
	180					185					190						
gtt	ata	tgc	cta	aaa	aag	tgc	ttc	gct	ctt	ggg	ttt	tac	aag	cct	ttt	681	
Val	Ile	Cys	Leu	Lys	Lys	Cys	Phe	Ala	Leu	Gly	Phe	Tyr	Lys	Pro	Phe		
	195				200					205					210		
ttg	ttg	ttg	gta	ggg	ttt	ttg	aat	gtg	tcg	gtt	act	aag	gct	tta	ata	729	
Leu	Leu	Leu	Val	Gly	Phe	Leu	Asn	Val	Ser	Val	Thr	Lys	Ala	Leu	Ile		
				215					220					225			
gac	gct	cat	atg	caa	gaa	aaa	caa	gac	tta	agc	ctt	tta	ttg	gtg	gta	777	
Asp	Ala	His	Met	Gln	Glu	Lys	Gln	Asp	Leu	Ser	Leu	Leu	Leu	Val	Val		
			230					235					240				
gcg	tta	ttt	ttg	tgt	tgc	gtt	ttt	atc	atc	ggc	gtg	cct	ttt	ttc	atc	825	
Ala	Leu	Phe	Leu	Cys	Cys	Val	Phe	Ile	Ile	Gly	Val	Pro	Phe	Phe	Ile		
		245					250					255					

aac gct ttg ttt agg gtg caa aac agc ctt aaa gaa act tac aaa ctc	873
Asn Ala Leu Phe Arg Val Gln Asn Ser Leu Lys Glu Thr Tyr Lys Leu	
260 265 270	
gcc acc aat ttg agt gcc aac ctc agc caa aac gcc ctt aat tcc tta	921
Ala Thr Asn Leu Ser Ala Asn Leu Ser Gln Asn Ala Leu Asn Ser Leu	
275 280 285 290	
caa tac atc acg acc cca ccc gct tct tct agc gtt tct tct tct atg	969
Gln Tyr Ile Thr Thr Pro Pro Ala Ser Ser Ser Val Ser Ser Ser Met	
295 300 305	
agt gaa agc gtc tct aaa gaa aaa gaa acg cat tcc ccc aca ttt aag	1017
Ser Glu Ser Val Ser Lys Glu Lys Glu Thr His Ser Pro Thr Phe Lys	
310 315 320	
gta gaa acc act caa tta gat gta aaa atc cca aat ttc aag caa aaa	1065
Val Glu Thr Thr Gln Leu Asp Val Lys Ile Pro Asn Phe Lys Gln Lys	
325 330 335	
aag gtt aaa aag gat aca ata aat aca aaa aat gaa att taaataaata	1114
Lys Val Lys Lys Asp Thr Ile Asn Thr Lys Asn Glu Ile	
340 345 350	
ggaatttaat gagaatttt	1133

<210> 434

<211> 351

<212> PRT

<213> Helicobacter pylori

<400> 434

Met Lys Asn Asp Ala Tyr Glu Ile Ile Leu Ser Trp Phe Ile Thr Pro	
1 5 10 15	
Leu Thr Ala Ile Leu Gly Arg Phe Ala Glu Phe Phe Leu Tyr Thr Leu	
20 25 30	
His Ala Gln Leu Val Phe Asn Ser Val Val Ala Leu Ala Phe Met Leu	
35 40 45	
Phe Ala Tyr Arg Ser Leu Lys Glu Gln Asn Phe Phe Ser Ala Ser Ala	
50 55 60	
Leu Thr Glu Ala Leu Leu Phe Val Gly Phe Phe Ala Leu Phe Asn Tyr	
65 70 75 80	
Ala Leu Lys Asn Pro Met His Phe Tyr Glu Phe Phe Gln Asn Ala Ile	
85 90 95	
Phe Ile Ala Pro Asn Met Ile Ala Gln Ser Leu Ser Gln Ser Leu Ser	
100 105 110	
Asn Phe Ser Asp His Ala Leu Ser Leu Asp Phe Ile Phe Asn His Gly	
115 120 125	
Phe Tyr Ala Leu Ser Phe Ile Ser Asp Leu Ser His Asn Glu Met Ser	
130 135 140	
Val Trp Leu Phe Leu Ser Val Leu Gln Gly Leu Phe Leu Ser Val Leu	
145 150 155 160	
Phe Ala Ile Ile Ile Leu Val Tyr Leu Glu Val His Val Trp Cys Ser	
165 170 175	
Leu Gly Val Leu Phe Leu Ala Phe Gly Phe Phe Lys Thr Trp Arg Ser	
180 185 190	
Val Val Val Ile Cys Leu Lys Lys Cys Phe Ala Leu Gly Phe Tyr Lys	
195 200 205	
Pro Phe Leu Leu Leu Val Gly Phe Leu Asn Val Ser Val Thr Lys Ala	

210	215	220
Leu Ile Asp Ala His Met Gln Glu Lys Gln Asp Leu Ser Leu Leu Leu		
225	230	235
Val Val Ala Leu Phe Leu Cys Cys Val Phe Ile Ile Gly Val Pro Phe		240
	245	250
Phe Ile Asn Ala Leu Phe Arg Val Gln Asn Ser Leu Lys Glu Thr Tyr		255
	260	265
Lys Leu Ala Thr Asn Leu Ser Ala Asn Leu Ser Gln Asn Ala Leu Asn		270
	275	280
Ser Leu Gln Tyr Ile Thr Thr Pro Pro Ala Ser Ser Ser Val Ser Ser		285
	290	295
Ser Met Ser Glu Ser Val Ser Lys Glu Lys Glu Thr His Ser Pro Thr		300
305	310	315
Phe Lys Val Glu Thr Thr Gln Leu Asp Val Lys Ile Pro Asn Phe Lys		320
	325	330
Gln Lys Lys Val Lys Lys Asp Thr Ile Asn Thr Lys Asn Glu Ile		335
	340	345
		350

<210> 435
 <211> 777
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (50)...(748)

<400> 435
 ccctttcaaa caaggcccta aaaattacga agaaaacctg attttcccc atg gat aac 58
 Met Asp Asn
 1

cct aaa ggc att gat ggt ttt act aac ctt aaa gaa aaa gac atc gcc 106
 Pro Lys Gly Ile Asp Gly Phe Thr Asn Leu Lys Glu Lys Asp Ile Ala
 5 10 15

act aat gaa aat aag ctt tta cgc acc att aca gcg gat aaa atg ata 154
 Thr Asn Glu Asn Lys Leu Leu Arg Thr Ile Thr Ala Asp Lys Met Ile
 20 25 30 35

ccc gcc ttt ctc atc acg cct att tct agc cag atc gct ggt aaa gtc 202
 Pro Ala Phe Leu Ile Thr Pro Ile Ser Ser Gln Ile Ala Gly Lys Val
 40 45 50

atc gcg cag gtg gag agc gat att ttt gct cac atg ggc aag gcc gtc 250
 Ile Ala Gln Val Glu Ser Asp Ile Phe Ala His Met Gly Lys Ala Val
 55 60 65

tta atc ccc aaa ggc tct aaa gtc ata ggt tat tac agc aac aat aac 298
 Leu Ile Pro Lys Gly Ser Lys Val Ile Gly Tyr Tyr Ser Asn Asn Asn
 70 75 80

aaa atg ggc gaa tac cgc ttg gat att gta tgg agc cgc atc atc act 346
 Lys Met Gly Glu Tyr Arg Leu Asp Ile Val Trp Ser Arg Ile Ile Thr
 85 90 95

ccc cat ggc atc aat atc atg ctc act aac gct aaa ggg gcg gac att 394
 Pro His Gly Ile Asn Ile Met Leu Thr Asn Ala Lys Gly Ala Asp Ile

100		105		110		115	
aaa ggc tat aac ggc ttg gtg ggg gaa ttg att gaa agg aat ttc cag							442
Lys Gly Tyr Asn Gly Leu Val Gly Glu Leu Ile Glu Arg Asn Phe Gln							
		120		125		130	
cgc tat ggc gtg ccg tta ctg ctt tct act ctc act aac ggc cta ttg							490
Arg Tyr Gly Val Pro Leu Leu Leu Ser Thr Leu Thr Asn Gly Leu Leu							
		135		140		145	
att ggg atc act tcg gct tta aac aac aga ggc aat aaa gaa gga gcc							538
Ile Gly Ile Thr Ser Ala Leu Asn Asn Arg Gly Asn Lys Glu Gly Ala							
		150		155		160	
acc aat ttc ttt ggg gat tat ctt tta atg caa ttg atg agg caa agc							586
Thr Asn Phe Phe Gly Asp Tyr Leu Leu Met Gln Leu Met Arg Gln Ser							
		165		170		175	
ggc atg ggc atc aat caa gta gtc aat caa att tta aga gat aag agc							634
Gly Met Gly Ile Asn Gln Val Val Asn Gln Ile Leu Arg Asp Lys Ser							
		180		185		190	
aaa atc gct cct att gtg gtg att aga gaa ggg agt agg gtc ttc att							682
Lys Ile Ala Pro Ile Val Val Ile Arg Glu Gly Ser Arg Val Phe Ile							
		200		205		210	
tcg ccc aat act gac atc ttt ttc cct ata ccc aga gag aat gaa gtc							730
Ser Pro Asn Thr Asp Ile Phe Phe Pro Ile Pro Arg Glu Asn Glu Val							
		215		220		225	
atc gct gag ttt ttg aag tgactcaaaa atccccaatt aaaaaacgct							777
Ile Ala Glu Phe Leu Lys							
		230					

<210> 436
 <211> 233
 <212> PRT
 <213> *Helicobacter pylori*

<400> 436

Met Asp Asn Pro Lys Gly Ile Asp Gly Phe Thr Asn Leu Lys Glu Lys																
1				5				10					15			
Asp Ile Ala Thr Asn Glu Asn Lys Leu Leu Arg Thr Ile Thr Ala Asp								20					25			
				20									30			
Lys Met Ile Pro Ala Phe Leu Ile Thr Pro Ile Ser Ser Gln Ile Ala								35					40			
													45			
Gly Lys Val Ile Ala Gln Val Glu Ser Asp Ile Phe Ala His Met Gly								50					55			
													60			
Lys Ala Val Leu Ile Pro Lys Gly Ser Lys Val Ile Gly Tyr Tyr Ser								65					70			
													75			
Asn Asn Asn Lys Met Gly Glu Tyr Arg Leu Asp Ile Val Trp Ser Arg								80					85			
													90			
Ile Ile Thr Pro His Gly Ile Asn Ile Met Leu Thr Asn Ala Lys Gly								100					105			
													110			
Ala Asp Ile Lys Gly Tyr Asn Gly Leu Val Gly Glu Leu Ile Glu Arg								115					120			
													125			
Asn Phe Gln Arg Tyr Gly Val Pro Leu Leu Leu Ser Thr Leu Thr Asn								130					135			
													140			

ttg tat ggc gaa gtc tta gaa acc ccg caa aat gaa aac acc ccc ttt	485
Leu Tyr Gly Glu Val Leu Glu Thr Pro Gln Asn Glu Asn Thr Pro Phe	
140 145 150	
aac cca cga agc ccc tat gcg gtc gct aaa atg tat gcc ttt tac atc	533
Asn Pro Arg Ser Pro Tyr Ala Val Ala Lys Met Tyr Ala Phe Tyr Ile	
155 160 165	
acc aaa aat tac aga gag gcc tat aac ttg ttt gcg gtt aat ggc att	581
Thr Lys Asn Tyr Arg Glu Ala Tyr Asn Leu Phe Ala Val Asn Gly Ile	
170 175 180 185	
ctt ttt aac cat gag agc agg gta agg ggc gaa act ttt gta acc cgt	629
Leu Phe Asn His Glu Ser Arg Val Arg Gly Glu Thr Phe Val Thr Arg	
190 195 200	
aaa atc aca cga gcc gct agc gcg ata gcg tat aac tta acg gat tgc	677
Lys Ile Thr Arg Ala Ala Ser Ala Ile Ala Tyr Asn Leu Thr Asp Cys	
205 210 215	
ttg tat tta ggg aat tta gac gct aaa aga gac tgg ggg cat gcc aaa	725
Leu Tyr Leu Gly Asn Leu Asp Ala Lys Arg Asp Trp Gly His Ala Lys	
220 225 230	
gat tac gtg aaa atg atg cat tta atg ctc caa gcg ccc atc cca caa	773
Asp Tyr Val Lys Met Met His Leu Met Leu Gln Ala Pro Ile Pro Gln	
235 240 245	
gat tat gtg atc gcc aca gga aag acc aca agc gtg cgc gat ttt gtg	821
Asp Tyr Val Ile Ala Thr Gly Lys Thr Thr Ser Val Arg Asp Phe Val	
250 255 260 265	
aaa atg agc ttt gaa ttt atc ggt atc aat tta gaa ttt caa aat aca	869
Lys Met Ser Phe Glu Phe Ile Gly Ile Asn Leu Glu Phe Gln Asn Thr	
270 275 280	
ggg att aaa gaa atc ggt ttg att aaa agc gtt gat gaa aaa aga gcg	917
Gly Ile Lys Glu Ile Gly Leu Ile Lys Ser Val Asp Glu Lys Arg Ala	
285 290 295	
aac gct tta aaa ttg aac tta agc cat tta aaa aaa ggc caa atc gtg	965
Asn Ala Leu Lys Leu Asn Leu Ser His Leu Lys Lys Gly Gln Ile Val	
300 305 310	
gtg cgc ata gac gag cgt tat ttc agg cct acc gaa gtg gat ttg ctt	1013
Val Arg Ile Asp Glu Arg Tyr Phe Arg Pro Thr Glu Val Asp Leu Leu	
315 320 325	
tta ggc gat ccc act aag gca gag aaa gag cta gac tgg gtt agg gaa	1061
Leu Gly Asp Pro Thr Lys Ala Glu Lys Glu Leu Asp Trp Val Arg Glu	
330 335 340 345	
tac gat tta aaa gag ttg gtt aag gac atg tta gaa tac gat tta aaa	1109
Tyr Asp Leu Lys Glu Leu Val Lys Asp Met Leu Glu Tyr Asp Leu Lys	
350 355 360	
gaa tgc caa aaa aac ctt tac ttg caa gat ggg ggt tat att tta agg	1157
Glu Cys Gln Lys Asn Leu Tyr Leu Gln Asp Gly Gly Tyr Ile Leu Arg	

365	370	375													
aat ttt tat gaa tgagattatt ttaatcactg gtcgctatgg catgggtgggg			1209												
Asn Phe Tyr Glu															
380															
cagaacacgg cgttgtattt			1229												
<210> 438															
<211> 381															
<212> PRT															
<213> Helicobacter pylori															
<400> 438															
Met	Lys	Glu	Lys	Ile	Ala	Leu	Ile	Thr	Gly	Val	Thr	Gly	Gln	Asp	Gly
1				5					10					15	
Ser	Tyr	Leu	Ala	Glu	Tyr	Leu	Leu	Asn	Leu	Gly	Tyr	Glu	Val	His	Gly
			20					25					30		
Leu	Lys	Arg	Arg	Ser	Ser	Ser	Ile	Asn	Thr	Ser	Arg	Ile	Asp	His	Leu
		35					40					45			
Tyr	Glu	Asp	Leu	His	Ser	Asp	His	Lys	Arg	Arg	Phe	Phe	Leu	His	Tyr
	50					55					60				
Gly	Asp	Met	Thr	Asp	Ser	Ser	Asn	Leu	Ile	His	Leu	Ile	Ala	Thr	Thr
65					70					75					80
Lys	Pro	Thr	Glu	Ile	Tyr	Asn	Leu	Ala	Ala	Gln	Ser	His	Val	Lys	Val
				85					90					95	
Ser	Phe	Glu	Thr	Pro	Glu	Tyr	Thr	Ala	Asn	Ala	Asp	Gly	Ile	Gly	Thr
			100					105					110		
Leu	Arg	Ile	Leu	Glu	Ala	Met	Arg	Ile	Leu	Gly	Leu	Glu	Lys	Lys	Thr
		115					120					125			
Arg	Phe	Tyr	Gln	Ala	Ser	Thr	Ser	Glu	Leu	Tyr	Gly	Glu	Val	Leu	Glu
	130					135					140				
Thr	Pro	Gln	Asn	Glu	Asn	Thr	Pro	Phe	Asn	Pro	Arg	Ser	Pro	Tyr	Ala
145					150					155					160
Val	Ala	Lys	Met	Tyr	Ala	Phe	Tyr	Ile	Thr	Lys	Asn	Tyr	Arg	Glu	Ala
			165					170						175	
Tyr	Asn	Leu	Phe	Ala	Val	Asn	Gly	Ile	Leu	Phe	Asn	His	Glu	Ser	Arg
			180				185					190			
Val	Arg	Gly	Glu	Thr	Phe	Val	Thr	Arg	Lys	Ile	Thr	Arg	Ala	Ala	Ser
	195						200					205			
Ala	Ile	Ala	Tyr	Asn	Leu	Thr	Asp	Cys	Leu	Tyr	Leu	Gly	Asn	Leu	Asp
	210					215					220				
Ala	Lys	Arg	Asp	Trp	Gly	His	Ala	Lys	Asp	Tyr	Val	Lys	Met	Met	His
225					230					235					240
Leu	Met	Leu	Gln	Ala	Pro	Ile	Pro	Gln	Asp	Tyr	Val	Ile	Ala	Thr	Gly
				245					250					255	
Lys	Thr	Thr	Ser	Val	Arg	Asp	Phe	Val	Lys	Met	Ser	Phe	Glu	Phe	Ile
			260					265					270		
Gly	Ile	Asn	Leu	Glu	Phe	Gln	Asn	Thr	Gly	Ile	Lys	Glu	Ile	Gly	Leu
		275					280					285			
Ile	Lys	Ser	Val	Asp	Glu	Lys	Arg	Ala	Asn	Ala	Leu	Lys	Leu	Asn	Leu
	290					295					300				
Ser	His	Leu	Lys	Lys	Gly	Gln	Ile	Val	Val	Arg	Ile	Asp	Glu	Arg	Tyr
305					310					315					320
Phe	Arg	Pro	Thr	Glu	Val	Asp	Leu	Leu	Leu	Gly	Asp	Pro	Thr	Lys	Ala
				325					330					335	
Glu	Lys	Glu	Leu	Asp	Trp	Val	Arg	Glu	Tyr	Asp	Leu	Lys	Glu	Leu	Val
			340					345					350		
Lys	Asp	Met	Leu	Glu	Tyr	Asp	Leu	Lys	Glu	Cys	Gln	Lys	Asn	Leu	Tyr

355 360 365
 Leu Gln Asp Gly Gly Tyr Ile Leu Arg Asn Phe Tyr Glu
 370 375 380

<210> 439
 <211> 1116
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (70)...(1065)

<400> 439
 cagcagtatc cctatcggtc aagccttaat ggcgtatttc aaccctacaa tcatcaaaaa 60
 aggataaaaa atg gat agc gta act cta gca tgc ggg aac gga ggg aaa gaa 111
 Met Asp Ser Val Thr Leu Ala Cys Gly Asn Gly Gly Lys Glu
 1 5 10

 aca aac gct ttg att gag cga gtc ttt atg ccc tat tta aaa gaa tgg 159
 Thr Asn Ala Leu Ile Glu Arg Val Phe Met Pro Tyr Leu Lys Glu Trp
 15 20 25 30

 att gtt gca ttt gat gaa gac gcc cct aaa ttt gaa gct agt ggg gaa 207
 Ile Val Ala Phe Asp Glu Asp Ala Pro Lys Phe Glu Ala Ser Gly Glu
 35 40 45

 tat tgc gtg agc acg gat agt ttt gtc atc acg ccc tta att ttt aat 255
 Tyr Cys Val Ser Thr Asp Ser Phe Val Ile Thr Pro Leu Ile Phe Asn
 50 55 60

 ggg ggc gat ata ggc aag ctt tgc gtt tgc ggg agt gcg aat gat gtg 303
 Gly Gly Asp Ile Gly Lys Leu Cys Val Cys Gly Ser Ala Asn Asp Val
 65 70 75

 agc gtg caa ggg ggc gaa cct ttg tat ttg aat atg ggt ttt att tta 351
 Ser Val Gln Gly Gly Glu Pro Leu Tyr Leu Asn Met Gly Phe Ile Leu
 80 85 90

 gaa gaa ggc tta gaa att tct ctt tta aaa caa att tta caa tcc ata 399
 Glu Glu Gly Leu Glu Ile Ser Leu Leu Lys Gln Ile Leu Gln Ser Ile
 95 100 105 110

 caa aaa gaa ttg ttt aaa gcc aac ctg aaa ctc ctc tcc cta gac act 447
 Gln Lys Glu Leu Phe Lys Ala Asn Leu Lys Leu Leu Ser Leu Asp Thr
 115 120 125

 aaa gtc gtg cca aag ggg agc gtg gat aag ctt ttt atc aac aca acc 495
 Lys Val Val Pro Lys Gly Ser Val Asp Lys Leu Phe Ile Asn Thr Thr
 130 135 140

 tgc att ggt aaa atc atc aag cca ggg att tct tcg tac cat tta caa 543
 Cys Ile Gly Lys Ile Ile Lys Pro Gly Ile Ser Ser Tyr His Leu Gln
 145 150 155

 caa ggg caa gcc att atc cta agc gac act atc gcc aat cat ggg gca 591
 Gln Gly Gln Ala Ile Ile Leu Ser Asp Thr Ile Ala Asn His Gly Ala
 160 165 170

agc tta ttt gcg atg cgt aat gaa atc aag ctt aaa acg aat cta gaa 639
 Ser Leu Phe Ala Met Arg Asn Glu Ile Lys Leu Lys Thr Asn Leu Glu
 175 180 185 190

agc gat tgc caa ctg ctc tat ccc tta tta aaa ccc cta ttt tta agc 687
 Ser Asp Cys Gln Leu Leu Tyr Pro Leu Leu Lys Pro Leu Phe Leu Ser
 195 200 205

gat ctc aaa att gat gct tta aga gat gcg act agg ggc ggg tta gcg 735
 Asp Leu Lys Ile Asp Ala Leu Arg Asp Ala Thr Arg Gly Gly Leu Ala
 210 215 220

agc gtg ctg aac gaa tgg gcg aac agc tct aga gtg aaa atc gtt ata 783
 Ser Val Leu Asn Glu Trp Ala Asn Ser Ser Arg Val Lys Ile Val Ile
 225 230 235

gaa gaa gaa aaa atc ccc tta aaa gaa gaa acg aaa ggg att tgt gag 831
 Glu Glu Glu Lys Ile Pro Leu Lys Glu Glu Thr Lys Gly Ile Cys Glu
 240 245 250

att tta ggg tta gaa ccc tac gcg cta gcc aat gag ggg gtg ttt gtt 879
 Ile Leu Gly Leu Glu Pro Tyr Ala Leu Ala Asn Glu Gly Val Phe Val
 255 260 265 270

tta gcg ctc aat caa aaa gac gcc cct aaa gcc tta gaa att tta aaa 927
 Leu Ala Leu Asn Gln Lys Asp Ala Pro Lys Ala Leu Glu Ile Leu Lys
 275 280 285

agt aac gaa aaa gct aaa aac gct tgc gtg att ggc aaa gtg ttt gaa 975
 Ser Asn Glu Lys Ala Lys Asn Ala Cys Val Ile Gly Lys Val Phe Glu
 290 295 300

aac cct tat cct agc gtg gtt tta aag aac gca tgg ggt ttt gaa agg 1023
 Asn Pro Tyr Pro Ser Val Val Leu Lys Asn Ala Trp Gly Phe Glu Arg
 305 310 315

att tta gag gtg cca gag ggc gaa tta ttg cct agg att tgt 1065
 Ile Leu Glu Val Pro Glu Gly Glu Leu Leu Pro Arg Ile Cys
 320 325 330

taacacgccg tcatttttta atcgttttaa gcctgcccta aaaatggttt a 1116

<210> 440

<211> 332

<212> PRT

<213> Helicobacter pylori

<400> 440

Met Asp Ser Val Thr Leu Ala Cys Gly Asn Gly Gly Lys Glu Thr Asn
 1 5 10 15
 Ala Leu Ile Glu Arg Val Phe Met Pro Tyr Leu Lys Glu Trp Ile Val
 20 25 30
 Ala Phe Asp Glu Asp Ala Pro Lys Phe Glu Ala Ser Gly Glu Tyr Cys
 35 40 45
 Val Ser Thr Asp Ser Phe Val Ile Thr Pro Leu Ile Phe Asn Gly Gly
 50 55 60
 Asp Ile Gly Lys Leu Cys Val Cys Gly Ser Ala Asn Asp Val Ser Val
 65 70 75 80

Gln	Gly	Gly	Glu	Pro	Leu	Tyr	Leu	Asn	Met	Gly	Phe	Ile	Leu	Glu	Glu	
				85					90					95		
Gly	Leu	Glu	Ile	Ser	Leu	Leu	Lys	Gln	Ile	Leu	Gln	Ser	Ile	Gln	Lys	
			100					105					110			
Glu	Leu	Phe	Lys	Ala	Asn	Leu	Lys	Leu	Leu	Ser	Leu	Asp	Thr	Lys	Val	
		115					120					125				
Val	Pro	Lys	Gly	Ser	Val	Asp	Lys	Leu	Phe	Ile	Asn	Thr	Thr	Cys	Ile	
	130					135					140					
Gly	Lys	Ile	Ile	Lys	Pro	Gly	Ile	Ser	Ser	Tyr	His	Leu	Gln	Gln	Gly	
145					150					155					160	
Gln	Ala	Ile	Ile	Leu	Ser	Asp	Thr	Ile	Ala	Asn	His	Gly	Ala	Ser	Leu	
				165					170					175		
Phe	Ala	Met	Arg	Asn	Glu	Ile	Lys	Leu	Lys	Thr	Asn	Leu	Glu	Ser	Asp	
			180					185					190			
Cys	Gln	Leu	Leu	Tyr	Pro	Leu	Leu	Lys	Pro	Leu	Phe	Leu	Ser	Asp	Leu	
	195					200						205				
Lys	Ile	Asp	Ala	Leu	Arg	Asp	Ala	Thr	Arg	Gly	Gly	Leu	Ala	Ser	Val	
	210					215					220					
Leu	Asn	Glu	Trp	Ala	Asn	Ser	Ser	Arg	Val	Lys	Ile	Val	Ile	Glu	Glu	
225					230					235					240	
Glu	Lys	Ile	Pro	Leu	Lys	Glu	Glu	Thr	Lys	Gly	Ile	Cys	Glu	Ile	Leu	
			245						250					255		
Gly	Leu	Glu	Pro	Tyr	Ala	Leu	Ala	Asn	Glu	Gly	Val	Phe	Val	Leu	Ala	
			260					265					270			
Leu	Asn	Gln	Lys	Asp	Ala	Pro	Lys	Ala	Leu	Glu	Ile	Leu	Lys	Ser	Asn	
	275					280						285				
Glu	Lys	Ala	Lys	Asn	Ala	Cys	Val	Ile	Gly	Lys	Val	Phe	Glu	Asn	Pro	
	290					295				300						
Tyr	Pro	Ser	Val	Val	Leu	Lys	Asn	Ala	Trp	Gly	Phe	Glu	Arg	Ile	Leu	
305					310					315					320	
Glu	Val	Pro	Glu	Gly	Glu	Leu	Leu	Pro	Arg	Ile	Cys					
				325					330							

<210> 441
 <211> 1033
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (16)...(1005)

<400> 441																
aaaaggatat	tttga	atg	aaa	aga	atg	tta	gcg	gag	ttt	gaa	aaa	atc	caa		51	
					Met	Lys	Arg	Met	Leu	Ala	Glu	Phe	Glu	Lys	Ile	Gln
					1				5					10		
gcg	att	cta	atg	gct	ttc	ccc	cat	gag	ttt	agc	gac	tg	gcg	tat	tgt	99
Ala	Ile	Leu	Met	Ala	Phe	Pro	His	Glu	Phe	Ser	Asp	Trp	Ala	Tyr	Cys	
		15					20					25				
atc	aaa	gag	gct	agg	gaa	agt	ttt	tta	aac	atc	att	caa	acc	ata	gcc	147
Ile	Lys	Glu	Ala	Arg	Glu	Ser	Phe	Leu	Asn	Ile	Ile	Gln	Thr	Ile	Ala	
	30					35					40					
aaa	cac	gct	aaa	gtg	cta	gtg	tgc	gtc	cac	act	aac	gat	att	atc	gg	195
Lys	His	Ala	Lys	Val	Leu	Val	Cys	Val	His	Thr	Asn	Asp	Ile	Ile	Gly	
	45				50					55					60	

tat gaa acg ctt aaa aac tta ccc ggt gta gag atc gca agg att gac	243
Tyr Glu Thr Leu Lys Asn Leu Pro Gly Val Glu Ile Ala Arg Ile Asp	
65 70 75	
act aac gac aca tgg gct agg gat ttt gga gcg atc agc gtt gaa aat	291
Thr Asn Asp Thr Trp Ala Arg Asp Phe Gly Ala Ile Ser Val Glu Asn	
80 85 90	
cat ggc gtt tta gag tgc ttg gat ttt ggc ttt aat ggc tgg ggg tta	339
His Gly Val Leu Glu Cys Leu Asp Phe Gly Phe Asn Gly Trp Gly Leu	
95 100 105	
aaa tac ccg tcc aat tta gac aat caa gtg aat ttc aaa ctc aaa agt	387
Lys Tyr Pro Ser Asn Leu Asp Asn Gln Val Asn Phe Lys Leu Lys Ser	
110 115 120	
tta ggg ttt tta aaa cac cct tta aaa acg atg ccc tat att tta gag	435
Leu Gly Phe Leu Lys His Pro Leu Lys Thr Met Pro Tyr Ile Leu Glu	
125 130 135 140	
ggc ggg agt ata gaa agc gat ggg gct ggg agc gtt tta acc aac acc	483
Gly Gly Ser Ile Glu Ser Asp Gly Ala Gly Ser Val Leu Thr Asn Thr	
145 150 155	
caa tgc ctg tta gaa aaa aat cgt aac ccc cat ttg aat caa aat gga	531
Gln Cys Leu Leu Glu Lys Asn Arg Asn Pro His Leu Asn Gln Asn Gly	
160 165 170	
ata gaa aac atg ctt aaa aag gaa tta ggg gct aaa caa gtg ctg tgg	579
Ile Glu Asn Met Leu Lys Lys Glu Leu Gly Ala Lys Gln Val Leu Trp	
175 180 185	
tat tct tat ggc tat ctc aaa ggc gat gat acc gat agc cat acc gac	627
Tyr Ser Tyr Gly Tyr Leu Lys Gly Asp Asp Thr Asp Ser His Thr Asp	
190 195 200	
acg ctc gct cgt ttt tta gat aaa gac acc att gtt tat agc aca tgc	675
Thr Leu Ala Arg Phe Leu Asp Lys Asp Thr Ile Val Tyr Ser Thr Cys	
205 210 215 220	
gaa gat gaa aac gat gag cac tac aca gcc tta aaa aaa atg caa gaa	723
Glu Asp Glu Asn Asp Glu His Tyr Thr Ala Leu Lys Lys Met Gln Glu	
225 230 235	
gaa tta aaa acc ttt aaa aaa cta gac ggc acg ccc tat aaa ctc atc	771
Glu Leu Lys Thr Phe Lys Lys Leu Asp Gly Thr Pro Tyr Lys Leu Ile	
240 245 250	
ccc cta gaa atc cct aaa gcc att ttt gat gaa aac caa caa cgc ttg	819
Pro Leu Glu Ile Pro Lys Ala Ile Phe Asp Glu Asn Gln Gln Arg Leu	
255 260 265	
ccg gca act tat gtg aat ttt tta ttg tgc aat aac gct tta atc gtg	867
Pro Ala Thr Tyr Val Asn Phe Leu Leu Cys Asn Asn Ala Leu Ile Val	
270 275 280	
ccc act tac aac gac cct aaa gac gcg ctc att tta gaa acc ttg aaa	915
Pro Thr Tyr Asn Asp Pro Lys Asp Ala Leu Ile Leu Glu Thr Leu Lys	

285		290		295		300	
caa cac acg ccc tta gaa gtg ata ggg gtt gat tgc aac acc tta atc							963
Gln His Thr Pro Leu Glu Val Ile Gly Val Asp Cys Asn Thr Leu Ile							
	305			310		315	
aaa cag cat gga agt ttg cat tgt gta acg atg caa ctt tat							1005
Lys Gln His Gly Ser Leu His Cys Val Thr Met Gln Leu Tyr							
	320			325		330	
tgaacaaaat cacgcttttt ggcgtggt							1033

<210> 442

<211> 330

<212> PRT

<213> *Helicobacter pylori*

<400> 442

Met	Lys	Arg	Met	Leu	Ala	Glu	Phe	Glu	Lys	Ile	Gln	Ala	Ile	Leu	Met
1				5				10						15	
Ala	Phe	Pro	His	Glu	Phe	Ser	Asp	Trp	Ala	Tyr	Cys	Ile	Lys	Glu	Ala
		20					25					30			
Arg	Glu	Ser	Phe	Leu	Asn	Ile	Ile	Gln	Thr	Ile	Ala	Lys	His	Ala	Lys
		35				40					45				
Val	Leu	Val	Cys	Val	His	Thr	Asn	Asp	Ile	Ile	Gly	Tyr	Glu	Thr	Leu
	50				55					60					
Lys	Asn	Leu	Pro	Gly	Val	Glu	Ile	Ala	Arg	Ile	Asp	Thr	Asn	Asp	Thr
65				70				75						80	
Trp	Ala	Arg	Asp	Phe	Gly	Ala	Ile	Ser	Val	Glu	Asn	His	Gly	Val	Leu
			85					90					95		
Glu	Cys	Leu	Asp	Phe	Gly	Phe	Asn	Gly	Trp	Gly	Leu	Lys	Tyr	Pro	Ser
		100					105					110			
Asn	Leu	Asp	Asn	Gln	Val	Asn	Phe	Lys	Leu	Lys	Ser	Leu	Gly	Phe	Leu
		115				120					125				
Lys	His	Pro	Leu	Lys	Thr	Met	Pro	Tyr	Ile	Leu	Glu	Gly	Gly	Ser	Ile
	130				135					140					
Glu	Ser	Asp	Gly	Ala	Gly	Ser	Val	Leu	Thr	Asn	Thr	Gln	Cys	Leu	Leu
145				150				155						160	
Glu	Lys	Asn	Arg	Asn	Pro	His	Leu	Asn	Gln	Asn	Gly	Ile	Glu	Asn	Met
		165						170					175		
Leu	Lys	Lys	Glu	Leu	Gly	Ala	Lys	Gln	Val	Leu	Trp	Tyr	Ser	Tyr	Gly
		180						185				190			
Tyr	Leu	Lys	Gly	Asp	Asp	Thr	Asp	Ser	His	Thr	Asp	Thr	Leu	Ala	Arg
	195					200					205				
Phe	Leu	Asp	Lys	Asp	Thr	Ile	Val	Tyr	Ser	Thr	Cys	Glu	Asp	Glu	Asn
	210				215					220					
Asp	Glu	His	Tyr	Thr	Ala	Leu	Lys	Lys	Met	Gln	Glu	Glu	Leu	Lys	Thr
225				230				235						240	
Phe	Lys	Lys	Leu	Asp	Gly	Thr	Pro	Tyr	Lys	Leu	Ile	Pro	Leu	Glu	Ile
		245						250					255		
Pro	Lys	Ala	Ile	Phe	Asp	Glu	Asn	Gln	Arg	Leu	Pro	Ala	Thr	Tyr	
		260					265					270			
Val	Asn	Phe	Leu	Leu	Cys	Asn	Asn	Ala	Leu	Ile	Val	Pro	Thr	Tyr	Asn
	275					280					285				
Asp	Pro	Lys	Asp	Ala	Leu	Ile	Leu	Glu	Thr	Leu	Lys	Gln	His	Thr	Pro
	290				295					300					
Leu	Glu	Val	Ile	Gly	Val	Asp	Cys	Asn	Thr	Leu	Ile	Lys	Gln	His	Gly
305				310						315					320
Ser	Leu	His	Cys	Val	Thr	Met	Gln	Leu	Tyr						

<210> 443
 <211> 449
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (73) ... (408)

<400> 443
 gctttattca aaagagcgag gagtttagac gagatagcaa aatcatcaat ctttatcgcc 60
 tttcaacgcc ta atg ttt gca gtg cat gct gcg atg att acg aca tta aag 111
 Met Phe Ala Val His Ala Ala Met Ile Thr Thr Leu Lys
 1 5 10

aaa gaa gtt ttc ttt ctt tac ctt tat atc aaa tca ctc aaa atc ccg 159
 Lys Glu Val Phe Phe Leu Tyr Leu Tyr Ile Lys Ser Leu Lys Ile Pro
 15 20 25

att cct act aca ctg aaa tac atg att tct tta ggc aaa atc aga gaa 207
 Ile Pro Thr Thr Leu Lys Tyr Met Ile Ser Leu Gly Lys Ile Arg Glu
 30 35 40 45

tta gat gtt tta gca aat ctt gct aaa ctt tgc cct act tgt cat agg 255
 Leu Asp Val Leu Ala Asn Leu Ala Lys Leu Cys Pro Thr Cys His Arg
 50 55 60

gct tta aaa aaa gga tct agc gaa gag gag ttt caa aaa cgc ttg att 303
 Ala Leu Lys Lys Gly Ser Ser Glu Glu Glu Phe Gln Lys Arg Leu Ile
 65 70 75

aga aac att ctc aat cgc aat aaa gac aat tta gag ttt gcg caa ttg 351
 Arg Asn Ile Leu Asn Arg Asn Lys Asp Asn Leu Glu Phe Ala Gln Leu
 80 85 90

cgt ttt gaa acc gat gat ttt tca acg ctt att gat cgt att tgt gaa 399
 Arg Phe Glu Thr Asp Asp Phe Ser Thr Leu Ile Asp Arg Ile Cys Glu
 95 100 105

agc ttg aaa tgaattataa aatttttagat ttattttgtg gggctggggg 448
 Ser Leu Lys
 110

t 449

<210> 444
 <211> 112
 <212> PRT
 <213> *Helicobacter pylori*

<400> 444
 Met Phe Ala Val His Ala Ala Met Ile Thr Thr Leu Lys Lys Glu Val
 1 5 10 15
 Phe Phe Leu Tyr Leu Tyr Ile Lys Ser Leu Lys Ile Pro Ile Pro Thr
 20 25 30
 Thr Leu Lys Tyr Met Ile Ser Leu Gly Lys Ile Arg Glu Leu Asp Val

[illegible]

<213> Helicobacter pylori

<222> (43) ... (627)

ggtg	cg	tttg	ttgtaaaaaat	ttttgttttg	aaggaaaagg	ca	atg	cta	gga	ctt							54
											Met	Leu	Gly	Leu			
											1						
gta	ttg	tta	tat	gtt	ggg	att	gtt	tta	atc	agc	aat	ggg	att	tgc	ggg		102
Val	Leu	Leu	Tyr	Val	Gly	Ile	Val	Leu	Ile	Ser	Asn	Gly	Ile	Cys	Gly		
5					10					15					20		
tta	acc	aaa	gtc	gat	cct	aaa	agc	act	gcg	gtg	atg	aac	ttt	ttt	gtg		150
Leu	Thr	Lys	Val	Asp	Pro	Lys	Ser	Thr	Ala	Val	Met	Asn	Phe	Phe	Val		
				25					30					35			
ggc	gga	ctt	tcc	att	att	tgt	aat	ata	gtt	gtc	atc	act	tat	tct	gca		198
Gly	Gly	Leu	Ser	Ile	Ile	Cys	Asn	Ile	Val	Val	Ile	Thr	Tyr	Ser	Ala		
			40					45					50				
ctc	cac	cct	aca	gcc	cct	gta	gaa	ggt	gct	gaa	gat	att	gct	caa	gta		246
Leu	His	Pro	Thr	Ala	Pro	Val	Glu	Gly	Ala	Glu	Asp	Ile	Ala	Gln	Val		
		55					60					65					
tcg	cac	cat	ttg	act	agt	ttc	tat	gga	cca	gcg	act	ggg	tta	ttg	ttt		294
Ser	His	His	Leu	Thr	Ser	Phe	Tyr	Gly	Pro	Ala	Thr	Gly	Leu	Leu	Phe		
	70					75					80						
ggt	ttc	acc	tac	ttg	tat	gcg	gct	atc	aac	cac	act	ttt	ggg	ttg	gat		342
Gly	Phe	Thr	Tyr	Leu	Tyr	Ala	Ala	Ile	Asn	His	Thr	Phe	Gly	Leu	Asp		
85					90					95					100		
tgg	agg	ccc	tac	tct	tgg	tat	agc	tta	ttc	gta	gcg	atc	aac	acg	att		390
Trp	Arg	Pro	Tyr	Ser	Trp	Tyr	Ser	Leu	Phe	Val	Ala	Ile	Asn	Thr	Ile		

105										110					115					
cct	gct	gcg	att	tta	tcc	cac	tat	agc	gat	atg	ctt	gat	gac	cac	aaa	438				
Pro	Ala	Ala	Ile	Leu	Ser	His	Tyr	Ser	Asp	Met	Leu	Asp	Asp	His	Lys					
			120						125				130							
gtg	tta	ggc	atc	act	gaa	ggc	gat	tgg	tgg	gcg	atc	att	tgg	ttg	gct	486				
Val	Leu	Gly	Ile	Thr	Glu	Gly	Asp	Trp	Trp	Ala	Ile	Ile	Trp	Leu	Ala					
		135					140					145								
tgg	ggt	ggt	ttg	tgg	ctt	acc	gct	ttc	att	gaa	aac	atc	ttg	aaa	atc	534				
Trp	Gly	Val	Leu	Trp	Leu	Thr	Ala	Phe	Ile	Glu	Asn	Ile	Leu	Lys	Ile					
	150					155					160									
cct	tta	ggg	aaa	ttc	act	cca	tgg	ctt	gct	atc	att	gag	ggt	att	tta	582				
Pro	Leu	Gly	Lys	Phe	Thr	Pro	Trp	Leu	Ala	Ile	Ile	Glu	Gly	Ile	Leu					
165					170					175					180					
acc	gct	tgg	atc	cct	gct	tgg	ttg	ctc	ttt	atc	caa	cac	tgg	gtg		627				
Thr	Ala	Trp	Ile	Pro	Ala	Trp	Leu	Leu	Phe	Ile	Gln	His	Trp	Val						
			185						190					195						
tgagatgatac	atagagcggtt	tagt														651				

<210> 448
 <211> 195
 <212> PRT
 <213> *Helicobacter pylori*

<400> 448

Met	Leu	Gly	Leu	Val	Leu	Leu	Tyr	Val	Gly	Ile	Val	Leu	Ile	Ser	Asn
1				5					10					15	
Gly	Ile	Cys	Gly	Leu	Thr	Lys	Val	Asp	Pro	Lys	Ser	Thr	Ala	Val	Met
			20					25					30		
Asn	Phe	Phe	Val	Gly	Gly	Leu	Ser	Ile	Ile	Cys	Asn	Ile	Val	Val	Ile
			35				40					45			
Thr	Tyr	Ser	Ala	Leu	His	Pro	Thr	Ala	Pro	Val	Glu	Gly	Ala	Glu	Asp
	50					55					60				
Ile	Ala	Gln	Val	Ser	His	His	Leu	Thr	Ser	Phe	Tyr	Gly	Pro	Ala	Thr
65					70					75				80	
Gly	Leu	Leu	Phe	Gly	Phe	Thr	Tyr	Leu	Tyr	Ala	Ala	Ile	Asn	His	Thr
			85						90				95		
Phe	Gly	Leu	Asp	Trp	Arg	Pro	Tyr	Ser	Trp	Tyr	Ser	Leu	Phe	Val	Ala
			100					105					110		
Ile	Asn	Thr	Ile	Pro	Ala	Ala	Ile	Leu	Ser	His	Tyr	Ser	Asp	Met	Leu
			115				120					125			
Asp	Asp	His	Lys	Val	Leu	Gly	Ile	Thr	Glu	Gly	Asp	Trp	Trp	Ala	Ile
	130					135					140				
Ile	Trp	Leu	Ala	Trp	Gly	Val	Leu	Trp	Leu	Thr	Ala	Phe	Ile	Glu	Asn
145					150					155					160
Ile	Leu	Lys	Ile	Pro	Leu	Gly	Lys	Phe	Thr	Pro	Trp	Leu	Ala	Ile	Ile
				165					170					175	
Glu	Gly	Ile	Leu	Thr	Ala	Trp	Ile	Pro	Ala	Trp	Leu	Leu	Phe	Ile	Gln
			180					185					190		
His	Trp	Val													
		195													

<210> 449

```
<211> 526
<212> DNA
<213> Helicobacter pylori
```

<400> 449																
gaaggggcatt	tgtgctaaaa	accactaaaa	aaagcctgtt	ggttttt	atg	ggg	ggt	56								
					Met	Gly	Val									
					1											
ttt	ttc	ctt	att	ttt	ggc	gtg	gat	caa	gcg	att	aaa	tac	gct	att	tta	104
Phe	Phe	Leu	Ile	Phe	Gly	Val	Asp	Gln	Ala	Ile	Lys	Tyr	Ala	Ile	Leu	
	5					10					15					
gaa	ggg	ttt	cgc	tat	gaa	agt	ttg	atg	ata	gat	att	gtt	tta	gtg	ttc	152
Glu	Gly	Phe	Arg	Tyr	Glu	Ser	Leu	Met	Ile	Asp	Ile	Val	Leu	Val	Phe	
	20				25					30					35	
aat	aaa	ggc	gtg	gcg	ttt	tcc	ttg	ctc	agt	ttt	tta	gag	ggg	ggt	ttg	200
Asn	Lys	Gly	Val	Ala	Phe	Ser	Leu	Leu	Ser	Phe	Leu	Glu	Gly	Gly	Leu	
				40					45					50		
aaa	tac	ttg	caa	atc	ctt	ttg	att	tta	ggg	ctt	ttt	atc	ttt	tta	atg	248
Lys	Tyr	Leu	Gln	Ile	Leu	Leu	Ile	Leu	Gly	Leu	Phe	Ile	Phe	Leu	Met	
			55					60					65			
cgc	caa	agg	gag	ctt	ttt	aaa	aac	cat	gcg	ata	gag	ttt	ggc	atg	gtg	296
Arg	Gln	Arg	Glu	Leu	Phe	Lys	Asn	His	Ala	Ile	Glu	Phe	Gly	Met	Val	
		70					75					80				
ttt	ggc	gcc	ggg	ggt	tct	aat	ggt	tta	gac	cgg	ttt	gtg	cat	ggg	ggc	344
Phe	Gly	Ala	Gly	Val	Ser	Asn	Val	Leu	Asp	Arg	Phe	Val	His	Gly	Gly	
	85					90					95					
gtg	gtg	gat	tat	gtg	tat	tat	cat	tat	ggc	ttt	gat	ttt	gcc	att	ttt	392
Val	Val	Asp	Tyr	Val	Tyr	Tyr	His	Tyr	Gly	Phe	Asp	Phe	Ala	Ile	Phe	
100					105					110					115	
aat	ttc	gct	gat	gtc	atg	ata	gat	gtg	ggc	gtg	ggc	ggt	tta	ttg	ttg	440
Asn	Phe	Ala	Asp	Val	Met	Ile	Asp	Val	Gly	Val	Gly	Val	Leu	Leu	Leu	
				120					125					130		
aaa	caa	ttc	ttt	ttt	aag	caa	aaa	caa	aac	aaa	att	aag	gca			482
Lys	Gln	Phe	Phe	Phe	Lys	Gln	Lys	Gln	Asn	Lys	Ile	Lys	Ala			
			135					140					145			
taatcactct ttttaaaatg aaaggtcgcg tagctcagtt ggta																526

<400> 450
Met Gly Val Phe Phe Leu Ile Phe Gly Val Asp Gln Ala Ile Lys Tyr
1 5 10 15

Ala Ile Leu Glu Gly Phe Arg Tyr Glu Ser Leu Met Ile Asp Ile Val
20 25 30
Leu Val Phe Asn Lys Gly Val Ala Phe Ser Leu Leu Ser Phe Leu Glu
35 40 45
Gly Gly Leu Lys Tyr Leu Gln Ile Leu Leu Ile Leu Gly Leu Phe Ile
50 55 60
Phe Leu Met Arg Gln Arg Glu Leu Phe Lys Asn His Ala Ile Glu Phe
65 70 75 80
Gly Met Val Phe Gly Ala Gly Val Ser Asn Val Leu Asp Arg Phe Val
85 90 95
His Gly Gly Val Val Asp Tyr Val Tyr Tyr His Tyr Gly Phe Asp Phe
100 105 110
Ala Ile Phe Asn Phe Ala Asp Val Met Ile Asp Val Gly Val Gly Val
115 120 125
Leu Leu Leu Lys Gln Phe Phe Lys Gln Lys Gln Asn Lys Ile Lys
130 135 140
Ala
145

<210> 451
<211> 1392
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (22)...(1356)

<400> 451
ttttaaagggt attttataac g atg aaa att ttt ggg act gat ggc gtg agg 51
Met Lys Ile Phe Gly Thr Asp Gly Val Arg
1 5 10
ggg aaa gca ggg gtg aaa ctc acc ccc atg ttt gtg atg cgt tta ggc 99
Gly Lys Ala Gly Val Lys Leu Thr Pro Met Phe Val Met Arg Leu Gly
15 20 25
att gct gcc gga ttg tat ttt aaa aaa cat tct caa acg aat aaa att 147
Ile Ala Ala Gly Leu Tyr Phe Lys Lys His Ser Gln Thr Asn Lys Ile
30 35 40
cta atc ggt aaa gac acc aga aaa agc ggc tat atg gta gaa aac gct 195
Leu Ile Gly Lys Asp Thr Arg Lys Ser Gly Tyr Met Val Glu Asn Ala
45 50 55
tta gtg agc gct cta act tcc ata ggc tat aat gtg att caa ata ggg 243
Leu Val Ser Ala Leu Thr Ser Ile Gly Tyr Asn Val Ile Gln Ile Gly
60 65 70
cct atg ccc acc cct gcg att gcg ttt tta act gaa gac atg cgc tgt 291
Pro Met Pro Thr Pro Ala Ile Ala Phe Leu Thr Glu Asp Met Arg Cys
75 80 85 90
gat gcg ggt att atg ata agc gcg agc cac aac cct ttt gaa gat aat 339
Asp Ala Gly Ile Met Ile Ser Ala Ser His Asn Pro Phe Glu Asp Asn
95 100 105
ggc att aag ttt ttc aat tct tat ggc tat aag ctt aaa gaa gaa gaa 387

Gly	Ile	Lys	Phe	Phe	Asn	Ser	Tyr	Gly	Tyr	Lys	Leu	Lys	Glu	Glu	Glu	
			110					115					120			
gaa	aaa	gcg	att	gaa	gaa	atc	ttt	cat	gat	gaa	gaa	tta	ctg	cat	tct	435
Glu	Lys	Ala	Ile	Glu	Glu	Ile	Phe	His	Asp	Glu	Glu	Leu	Leu	His	Ser	
		125					130					135				
agc	tat	aaa	gtg	ggg	gag	agc	gtc	ggg	agc	gct	aaa	agg	ata	gac	gat	483
Ser	Tyr	Lys	Val	Gly	Glu	Ser	Val	Gly	Ser	Ala	Lys	Arg	Ile	Asp	Asp	
	140					145					150					
gtc	ata	ggg	cgc	tat	att	gca	cat	tta	aaa	cac	tct	ttc	ccc	aaa	cat	531
Val	Ile	Gly	Arg	Tyr	Ile	Ala	His	Leu	Lys	His	Ser	Phe	Pro	Lys	His	
155					160					165					170	
ttg	aat	tta	cag	agt	tta	agg	atc	gtg	cta	gat	acg	gct	aat	ggc	gcg	579
Leu	Asn	Leu	Gln	Ser	Leu	Arg	Ile	Val	Leu	Asp	Thr	Ala	Asn	Gly	Ala	
			175					180						185		
gct	tat	aag	gtg	gct	ccg	gtc	gtt	ttt	agc	gag	ctt	ggg	gct	gat	gtg	627
Ala	Tyr	Lys	Val	Ala	Pro	Val	Val	Phe	Ser	Glu	Leu	Gly	Ala	Asp	Val	
		190						195					200			
tta	gtg	att	aat	gat	gag	cct	aac	ggg	tgt	aac	att	aat	gat	caa	tgc	675
Leu	Val	Ile	Asn	Asp	Glu	Pro	Asn	Gly	Cys	Asn	Ile	Asn	Asp	Gln	Cys	
		205					210					215				
ggg	gct	tta	cac	ccc	aac	caa	tta	agc	cag	gaa	gtg	aaa	aaa	tac	cgc	723
Gly	Ala	Leu	His	Pro	Asn	Gln	Leu	Ser	Gln	Glu	Val	Lys	Lys	Tyr	Arg	
	220					225					230					
gca	gat	tta	ggc	ttt	gct	ttt	gat	ggc	gat	gct	gac	agg	cta	gtg	gtg	771
Ala	Asp	Leu	Gly	Phe	Ala	Phe	Asp	Gly	Asp	Ala	Asp	Arg	Leu	Val	Val	
235					240				245						250	
gtg	gat	aat	tta	ggg	aat	atc	gtg	cat	ggg	gat	aag	ctt	tta	ggg	gtg	819
Val	Asp	Asn	Leu	Gly	Asn	Ile	Val	His	Gly	Asp	Lys	Leu	Leu	Gly	Val	
				255					260					265		
tta	ggg	gtt	tat	caa	aaa	tct	aaa	aac	gcc	ctt	tct	tct	caa	gcg	gtt	867
Leu	Gly	Val	Tyr	Gln	Lys	Ser	Lys	Asn	Ala	Leu	Ser	Ser	Gln	Ala	Val	
		270					275						280			
gtc	gcc	aca	aac	atg	agc	aat	tta	gcc	ctt	aaa	gaa	tat	tta	aaa	tcc	915
Val	Ala	Thr	Asn	Met	Ser	Asn	Leu	Ala	Leu	Lys	Glu	Tyr	Leu	Lys	Ser	
		285					290					295				
caa	gat	ttg	gaa	ttg	aag	cat	tgc	gcg	att	ggg	gat	aag	ttt	gtg	agc	963
Gln	Asp	Leu	Glu	Leu	Lys	His	Cys	Ala	Ile	Gly	Asp	Lys	Phe	Val	Ser	
	300					305					310					
gaa	tgc	atg	caa	ttg	aat	aaa	gcc	aat	ttt	gga	ggc	gag	caa	agc	ggg	1011
Glu	Cys	Met	Gln	Leu	Asn	Lys	Ala	Asn	Phe	Gly	Gly	Glu	Gln	Ser	Gly	
315					320					325					330	
cat	atc	att	ttt	agc	gat	tac	gct	aaa	aca	ggc	gat	ggt	ttg	gtg	tgc	1059
His	Ile	Ile	Phe	Ser	Asp	Tyr	Ala	Lys	Thr	Gly	Asp	Gly	Leu	Val	Cys	
				335					340					345		

gct ttg caa gtg agc gcg tta gtg tta gaa agc aag cag gta agc tct	1107
Ala Leu Gln Val Ser Ala Leu Val Leu Glu Ser Lys Gln Val Ser Ser	
350 355 360	
gtt gcg tta aac ccc ttt gaa tta tac ccc caa agc cta gtg aat ttg	1155
Val Ala Leu Asn Pro Phe Glu Leu Tyr Pro Gln Ser Leu Val Asn Leu	
365 370 375	
aat gtc caa aaa aag ccc cct tta gaa agc ctg aaa ggt tat agc gct	1203
Asn Val Gln Lys Lys Pro Pro Leu Glu Ser Leu Lys Gly Tyr Ser Ala	
380 385 390	
ctt tta aaa gaa tta gac aag cta gaa atc cgc cat ttg atc cgt tat	1251
Leu Leu Lys Glu Leu Asp Lys Leu Glu Ile Arg His Leu Ile Arg Tyr	
395 400 405 410	
agc ggc act gaa aac aaa ttg cga atc ctt tta gaa gct aaa gat gaa	1299
Ser Gly Thr Glu Asn Lys Leu Arg Ile Leu Leu Glu Ala Lys Asp Glu	
415 420 425	
aag ctt tta gaa tcc aaa atg caa gaa tta aaa gag ttt ttt gaa ggg	1347
Lys Leu Leu Glu Ser Lys Met Gln Glu Leu Lys Glu Phe Phe Glu Gly	
430 435 440	
cat ttg tgc taaaaaccac taaaaaaagc ctgttggttt ttatgg	1392
His Leu Cys	
445	

<210> 452

<211> 445

<212> PRT

<213> Helicobacter pylori

<400> 452

Met Lys Ile Phe Gly Thr Asp Gly Val Arg Gly Lys Ala Gly Val Lys	
1 5 10 15	
Leu Thr Pro Met Phe Val Met Arg Leu Gly Ile Ala Ala Gly Leu Tyr	
20 25 30	
Phe Lys Lys His Ser Gln Thr Asn Lys Ile Leu Ile Gly Lys Asp Thr	
35 40 45	
Arg Lys Ser Gly Tyr Met Val Glu Asn Ala Leu Val Ser Ala Leu Thr	
50 55 60	
Ser Ile Gly Tyr Asn Val Ile Gln Ile Gly Pro Met Pro Thr Pro Ala	
65 70 75 80	
Ile Ala Phe Leu Thr Glu Asp Met Arg Cys Asp Ala Gly Ile Met Ile	
85 90 95	
Ser Ala Ser His Asn Pro Phe Glu Asp Asn Gly Ile Lys Phe Phe Asn	
100 105 110	
Ser Tyr Gly Tyr Lys Leu Lys Glu Glu Glu Lys Ala Ile Glu Glu	
115 120 125	
Ile Phe His Asp Glu Glu Leu Leu His Ser Ser Tyr Lys Val Gly Glu	
130 135 140	
Ser Val Gly Ser Ala Lys Arg Ile Asp Asp Val Ile Gly Arg Tyr Ile	
145 150 155 160	
Ala His Leu Lys His Ser Phe Pro Lys His Leu Asn Leu Gln Ser Leu	
165 170 175	
Arg Ile Val Leu Asp Thr Ala Asn Gly Ala Ala Tyr Lys Val Ala Pro	
180 185 190	

Val	Val	Phe	Ser	Glu	Leu	Gly	Ala	Asp	Val	Leu	Val	Ile	Asn	Asp	Glu	
		195					200					205				
Pro	Asn	Gly	Cys	Asn	Ile	Asn	Asp	Gln	Cys	Gly	Ala	Leu	His	Pro	Asn	
	210					215					220					
Gln	Leu	Ser	Gln	Glu	Val	Lys	Lys	Tyr	Arg	Ala	Asp	Leu	Gly	Phe	Ala	
225					230					235					240	
Phe	Asp	Gly	Asp	Ala	Asp	Arg	Leu	Val	Val	Val	Asp	Asn	Leu	Gly	Asn	
				245					250					255		
Ile	Val	His	Gly	Asp	Lys	Leu	Leu	Gly	Val	Leu	Gly	Val	Tyr	Gln	Lys	
			260					265					270			
Ser	Lys	Asn	Ala	Leu	Ser	Ser	Gln	Ala	Val	Val	Ala	Thr	Asn	Met	Ser	
		275					280					285				
Asn	Leu	Ala	Leu	Lys	Glu	Tyr	Leu	Lys	Ser	Gln	Asp	Leu	Glu	Leu	Lys	
	290					295					300					
His	Cys	Ala	Ile	Gly	Asp	Lys	Phe	Val	Ser	Glu	Cys	Met	Gln	Leu	Asn	
305				310						315					320	
Lys	Ala	Asn	Phe	Gly	Gly	Glu	Gln	Ser	Gly	His	Ile	Ile	Phe	Ser	Asp	
				325					330					335		
Tyr	Ala	Lys	Thr	Gly	Asp	Gly	Leu	Val	Cys	Ala	Leu	Gln	Val	Ser	Ala	
			340				345						350			
Leu	Val	Leu	Glu	Ser	Lys	Gln	Val	Ser	Ser	Val	Ala	Leu	Asn	Pro	Phe	
		355				360						365				
Glu	Leu	Tyr	Pro	Gln	Ser	Leu	Val	Asn	Leu	Asn	Val	Gln	Lys	Lys	Pro	
	370					375					380					
Pro	Leu	Glu	Ser	Leu	Lys	Gly	Tyr	Ser	Ala	Leu	Leu	Lys	Glu	Leu	Asp	
385					390					395					400	
Lys	Leu	Glu	Ile	Arg	His	Leu	Ile	Arg	Tyr	Ser	Gly	Thr	Glu	Asn	Lys	
				405					410					415		
Leu	Arg	Ile	Leu	Leu	Glu	Ala	Lys	Asp	Glu	Lys	Leu	Leu	Glu	Ser	Lys	
			420					425					430			
Met	Gln	Glu	Leu	Lys	Glu	Phe	Phe	Glu	Gly	His	Leu	Cys				
		435					440					445				

<210> 453
 <211> 483
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (19)...(441)

<400> 453																
ttttatcaaa	ggattctt	atg	aca	aag	acc	gct	aaa	gtc	aat	gac	atc	gtt				51
		Met	Thr	Lys	Thr	Ala	Lys	Val	Asn	Asp	Ile	Val				
		1				5					10					
cgt	gat	tgg	gtc	gtt	tta	gac	gcc	aaa	gac	aag	gtt	ttt	ggc	cgc	ttg	99
Arg	Asp	Trp	Val	Val	Leu	Asp	Ala	Lys	Asp	Lys	Val	Phe	Gly	Arg	Leu	
			15					20					25			
atc	act	gaa	atc	gct	gtg	ctt	tta	aga	ggg	aaa	cac	cgc	cct	ttt	tac	147
Ile	Thr	Glu	Ile	Ala	Val	Leu	Leu	Arg	Gly	Lys	His	Arg	Pro	Phe	Tyr	
		30				35						40				
acc	cct	aat	gtg	gat	tgt	ggg	gat	ttt	gtg	gtg	gtt	atc	aac	gct	aat	195
Thr	Pro	Asn	Val	Asp	Cys	Gly	Asp	Phe	Val	Val	Val	Ile	Asn	Ala	Asn	
		45				50					55					

aag gtt aaa ttt tca ggc atg aaa tta gag gat aaa gag tat ttt acc 243
Lys Val Lys Phe Ser Gly Met Lys Leu Glu Asp Lys Glu Tyr Phe Thr
60 65 70 75
cat tca ggc tat ttt ggc agc act aag agc aag act ctc caa gaa atg 291
His Ser Gly Tyr Phe Gly Ser Thr Lys Ser Lys Thr Leu Gln Glu Met
80 85 90
cta gaa aaa gcc cct gaa aag ctc tac cac tta gcc gtt agg ggc atg 339
Leu Glu Lys Ala Pro Glu Lys Leu Tyr His Leu Ala Val Arg Gly Met
95 100 105
ctc cct aaa acg aaa tta ggg aaa gcg atg att aaa aaa ctc aaa gtt 387
Leu Pro Lys Thr Lys Leu Gly Lys Ala Met Ile Lys Lys Leu Lys Val
110 115 120
tat cgt gat gat aag cac cct cac acc gca caa act agc aaa aag gac 435
Tyr Arg Asp Asp Lys His Pro His Thr Ala Gln Thr Ser Lys Lys Asp
125 130 135
gct aaa tgagaaaaat ctatgctacc ggtaaaagaa aaaccgctat cg 483
Ala Lys
140

<210> 454
<211> 141
<212> PRT
<213> Helicobacter pylori

<400> 454
Met Thr Lys Thr Ala Lys Val Asn Asp Ile Val Arg Asp Trp Val Val
1 5 10 15
Leu Asp Ala Lys Asp Lys Val Phe Gly Arg Leu Ile Thr Glu Ile Ala
20 25 30
Val Leu Leu Arg Gly Lys His Arg Pro Phe Tyr Thr Pro Asn Val Asp
35 40 45
Cys Gly Asp Phe Val Val Val Ile Asn Ala Asn Lys Val Lys Phe Ser
50 55 60
Gly Met Lys Leu Glu Asp Lys Glu Tyr Phe Thr His Ser Gly Tyr Phe
65 70 75 80
Gly Ser Thr Lys Ser Lys Thr Leu Gln Glu Met Leu Glu Lys Ala Pro
85 90 95
Glu Lys Leu Tyr His Leu Ala Val Arg Gly Met Leu Pro Lys Thr Lys
100 105 110
Leu Gly Lys Ala Met Ile Lys Lys Leu Lys Val Tyr Arg Asp Asp Lys
115 120 125
His Pro His Thr Ala Gln Thr Ser Lys Lys Asp Ala Lys
130 135 140

<210> 455
<211> 2107
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS

<222> (19)...(2058)

<400> 455

tagcttttga	ttgaaagc	atg	ggt	tct	tac	ttt	atg	gag	tgt	cca	atg	aaa	51			
		Met	Gly	Ser	Tyr	Phe	Met	Glu	Cys	Pro	Met	Lys				
		1				5					10					
aag	aaa	gct	aac	gaa	gaa	aaa	gcc	caa	aaa	aga	gct	aaa	aca	gaa	gcc	99
Lys	Lys	Ala	Asn	Glu	Glu	Lys	Ala	Gln	Lys	Arg	Ala	Lys	Thr	Glu	Ala	
			15					20					25			
aaa	gca	gaa	gcc	aca	caa	gaa	aat	aaa	act	aaa	gaa	aac	aat	aaa	gcc	147
Lys	Ala	Glu	Ala	Thr	Gln	Glu	Asn	Lys	Thr	Lys	Glu	Asn	Asn	Lys	Ala	
		30					35					40				
aaa	gaa	agc	aaa	att	aaa	gaa	agc	aaa	atc	aaa	gaa	gct	aaa	gcg	aaa	195
Lys	Glu	Ser	Lys	Ile	Lys	Glu	Ser	Lys	Ile	Lys	Glu	Ala	Lys	Ala	Lys	
	45					50					55					
gaa	cct	att	cct	gtt	aaa	aag	ctt	agt	ttt	aat	gaa	gcg	tta	gaa	gaa	243
Glu	Pro	Ile	Pro	Val	Lys	Lys	Leu	Ser	Phe	Asn	Glu	Ala	Leu	Glu	Glu	
	60				65					70					75	
ttg	ttc	gct	aat	tcc	tta	agc	gat	tgc	gtt	tct	tat	gag	tcc	atc	att	291
Leu	Phe	Ala	Asn	Ser	Leu	Ser	Asp	Cys	Val	Ser	Tyr	Glu	Ser	Ile	Ile	
			80						85					90		
caa	atc	agc	gcg	aaa	gtc	ccc	act	cta	gcc	caa	atc	aaa	aaa	atc	aaa	339
Gln	Ile	Ser	Ala	Lys	Val	Pro	Thr	Leu	Ala	Gln	Ile	Lys	Lys	Ile	Lys	
			95					100					105			
gaa	ttg	tgc	caa	aaa	tac	caa	aag	aaa	tta	gtc	agc	tct	tca	gaa	tac	387
Glu	Leu	Cys	Gln	Lys	Tyr	Gln	Lys	Lys	Leu	Val	Ser	Ser	Ser	Glu	Tyr	
		110					115					120				
gct	aaa	aaa	ctc	aat	gcg	att	gac	aag	att	aaa	aaa	acc	gaa	gaa	aag	435
Ala	Lys	Lys	Leu	Asn	Ala	Ile	Asp	Lys	Ile	Lys	Lys	Thr	Glu	Glu	Lys	
	125					130					135					
caa	aaa	gtt	tta	gat	gaa	gaa	tta	gaa	gat	ggc	tat	gac	ttt	ttg	aaa	483
Gln	Lys	Val	Leu	Asp	Glu	Glu	Leu	Glu	Asp	Gly	Tyr	Asp	Phe	Leu	Lys	
	140				145				150						155	
gaa	aag	gat	ttt	tta	gag	tgg	agc	aga	agc	gat	agc	cca	gtg	cgc	atg	531
Glu	Lys	Asp	Phe	Leu	Glu	Trp	Ser	Arg	Ser	Asp	Ser	Pro	Val	Arg	Met	
			160						165					170		
tat	ttg	cgc	gaa	atg	ggg	gat	ata	aaa	ctt	tta	agc	aaa	gat	gaa	gag	579
Tyr	Leu	Arg	Glu	Met	Gly	Asp	Ile	Lys	Leu	Leu	Ser	Lys	Asp	Glu	Glu	
			175					180					185			
att	gaa	ttg	agc	aag	caa	atc	cgc	ttg	ggt	gaa	gac	att	att	tta	gac	627
Ile	Glu	Leu	Ser	Lys	Gln	Ile	Arg	Leu	Gly	Glu	Asp	Ile	Ile	Leu	Asp	
		190					195					200				
gcg	atc	tgc	tcg	gtg	ccg	tat	ttg	att	gat	ttt	atc	tat	gcg	tat	aaa	675
Ala	Ile	Cys	Ser	Val	Pro	Tyr	Leu	Ile	Asp	Phe	Ile	Tyr	Ala	Tyr	Lys	
	205					210					215					

gac gct tta atc aat cgt gaa aga agg gtt aaa gag ctt ttc agg agc Asp Ala Leu Ile Asn Arg Glu Arg Arg Val Lys Glu Leu Phe Arg Ser 220 225 230 235	723
ttt gat gat gac gat gaa aat agc gtg agc gat tct aaa aaa gat gaa Phe Asp Asp Asp Asp Glu Asn Ser Val Ser Asp Ser Lys Lys Asp Glu 240 245 250	771
gac aac gaa gaa gat gaa gaa aac gaa gaa agg aaa aaa gtc gtt tct Asp Asn Glu Glu Asp Glu Glu Asn Glu Glu Arg Lys Lys Val Val Ser 255 260 265	819
gaa aaa gac aag aag cgt gta gaa aag gtt caa gaa agc ttt aaa gcc Glu Lys Asp Lys Lys Arg Val Glu Lys Val Gln Glu Ser Phe Lys Ala 270 275 280	867
cta gac aag gct aaa aaa gaa tgg ctt aaa gcc ctt gaa gcc ccc ata Leu Asp Lys Ala Lys Lys Glu Trp Leu Lys Ala Leu Glu Ala Pro Ile 285 290 295	915
gat gaa aga gaa gac gaa ttg gtg cgt tca ttg acc cta gct tac aaa Asp Glu Arg Glu Asp Glu Leu Val Arg Ser Leu Thr Leu Ala Tyr Lys 300 305 310 315	963
cgc caa aca ctc aaa gac aga ctc tat gat tta gaa cct acc agc aaa Arg Gln Thr Leu Lys Asp Arg Leu Tyr Asp Leu Glu Pro Thr Ser Lys 320 325 330	1011
ctg att aat gaa tta gtc aaa acg atg gaa acc act tta aaa agc ggc Leu Ile Asn Glu Leu Val Lys Thr Met Glu Thr Thr Leu Lys Ser Gly 335 340 345	1059
gat ggg ttt gaa aaa gag ttg aaa cgc ttg gaa tac aaa ctg ccc tta Asp Gly Phe Glu Lys Glu Leu Lys Arg Leu Glu Tyr Lys Leu Pro Leu 350 355 360	1107
ttc aat gac act ctc atc gca aac cat aaa aaa atc ctt gcc aat atc Phe Asn Asp Thr Leu Ile Ala Asn His Lys Lys Ile Leu Ala Asn Ile 365 370 375	1155
act aac atg act aaa gaa gat att atc gct caa gtg cca gaa gcg act Thr Asn Met Thr Lys Glu Asp Ile Ile Ala Gln Val Pro Glu Ala Thr 380 385 390 395	1203
atg gtg agc gtg tat atg gat ctt aaa aag ctt ttt ttg act aaa gaa Met Val Ser Val Tyr Met Asp Leu Lys Lys Leu Phe Leu Thr Lys Glu 400 405 410	1251
gcg agc gaa gaa ggc ttt gat cta gcc ccc aac aag cta aaa gaa att Ala Ser Glu Glu Gly Phe Asp Leu Ala Pro Asn Lys Leu Lys Glu Ile 415 420 425	1299
tta gag caa atc aaa aga ggg aag ttg att tcc gat cgc gct aaa aac Leu Glu Gln Ile Lys Arg Gly Lys Leu Ile Ser Asp Arg Ala Lys Asn 430 435 440	1347
aaa atg gct aaa tcc aat tta agg ttg gtg gtg agc atc gct aaa cga Lys Met Ala Lys Ser Asn Leu Arg Leu Val Val Ser Ile Ala Lys Arg 445 450 455	1395

ttc acg agc aga ggc tta cca ttc ttg gat ttg att caa gag ggc aat	1443
Phe Thr Ser Arg Gly Leu Pro Phe Leu Asp Leu Ile Gln Glu Gly Asn	
460 465 470 475	
att ggc ttg atg aaa gcg gtg gat aag ttt gag cat gaa aag ggc ttc	1491
Ile Gly Leu Met Lys Ala Val Asp Lys Phe Glu His Glu Lys Gly Phe	
480 485 490	
aag ttt tct acc tat gcg acc tgg tgg atc aaa caa gct atc agc aga	1539
Lys Phe Ser Thr Tyr Ala Thr Trp Trp Ile Lys Gln Ala Ile Ser Arg	
495 500 505	
gcc ata gcc gat cag gcc cgc act atc cgc atc ccc att cac atg att	1587
Ala Ile Ala Asp Gln Ala Arg Thr Ile Arg Ile Pro Ile His Met Ile	
510 515 520	
gat acg att aat cgc atc aat aaa gtc atg cgc aaa cac att caa gaa	1635
Asp Thr Ile Asn Arg Ile Asn Lys Val Met Arg Lys His Ile Gln Glu	
525 530 535	
aac ggc aaa gag cct gat tta gaa gtg gtg gct gaa gaa gtg ggg ctt	1683
Asn Gly Lys Glu Pro Asp Leu Glu Val Val Ala Glu Glu Val Gly Leu	
540 545 550 555	
tcg tta gat aaa gtg aag aat gtg att aag gtg act aaa gag cct atc	1731
Ser Leu Asp Lys Val Lys Asn Val Ile Lys Val Thr Lys Glu Pro Ile	
560 565 570	
agt ttg gaa acc cca gtc ggc aat gat gat gat ggc aag ttt ggg gat	1779
Ser Leu Glu Thr Pro Val Gly Asn Asp Asp Asp Gly Lys Phe Gly Asp	
575 580 585	
ttc gtg gaa gat aag aat atc gtc agc tcc att gat cac atc atg cga	1827
Phe Val Glu Asp Lys Asn Ile Val Ser Ser Ile Asp His Ile Met Arg	
590 595 600	
gaa gat ttg aaa gca caa att gaa agc gtt ttg gat cag ttg aat gag	1875
Glu Asp Leu Lys Ala Gln Ile Glu Ser Val Leu Asp Gln Leu Asn Glu	
605 610 615	
cga gaa aaa gcg gtg atc cgc atg cgt ttt ggg ctt tta gac gat gaa	1923
Arg Glu Lys Ala Val Ile Arg Met Arg Phe Gly Leu Leu Asp Asp Glu	
620 625 630 635	
agc gat cga act tta gaa gaa att ggc aag gaa ttg aat gtt act aga	1971
Ser Asp Arg Thr Leu Glu Glu Ile Gly Lys Glu Leu Asn Val Thr Arg	
640 645 650	
gaa agg gtg cgc cag att gaa agc tct gcg att aaa aaa ttg aga agc	2019
Glu Arg Val Arg Gln Ile Glu Ser Ser Ala Ile Lys Lys Leu Arg Ser	
655 660 665	
ccg cag tac ggg cgc att tta aga aac tat ttg cgc att tgatgttaag	2068
Pro Gln Tyr Gly Arg Ile Leu Arg Asn Tyr Leu Arg Ile	
670 675 680	
gtttctctaa agcatgcggtt attttcttgt agttttctt	2107

<210> 456
 <211> 680
 <212> PRT
 <213> Helicobacter pylori

<400> 456
 Met Gly Ser Tyr Phe Met Glu Cys Pro Met Lys Lys Lys Ala Asn Glu
 1 5 10 15
 Glu Lys Ala Gln Lys Arg Ala Lys Thr Glu Ala Lys Ala Glu Ala Thr
 20 25 30
 Gln Glu Asn Lys Thr Lys Glu Asn Asn Lys Ala Lys Glu Ser Lys Ile
 35 40 45
 Lys Glu Ser Lys Ile Lys Glu Ala Lys Ala Lys Glu Pro Ile Pro Val
 50 55 60
 Lys Lys Leu Ser Phe Asn Glu Ala Leu Glu Glu Leu Phe Ala Asn Ser
 65 70 75 80
 Leu Ser Asp Cys Val Ser Tyr Glu Ser Ile Ile Gln Ile Ser Ala Lys
 85 90 95
 Val Pro Thr Leu Ala Gln Ile Lys Lys Ile Lys Glu Leu Cys Gln Lys
 100 105 110
 Tyr Gln Lys Lys Leu Val Ser Ser Ser Glu Tyr Ala Lys Lys Leu Asn
 115 120 125
 Ala Ile Asp Lys Ile Lys Lys Thr Glu Glu Lys Gln Lys Val Leu Asp
 130 135 140
 Glu Glu Leu Glu Asp Gly Tyr Asp Phe Leu Lys Glu Lys Asp Phe Leu
 145 150 155 160
 Glu Trp Ser Arg Ser Asp Ser Pro Val Arg Met Tyr Leu Arg Glu Met
 165 170 175
 Gly Asp Ile Lys Leu Leu Ser Lys Asp Glu Glu Ile Glu Leu Ser Lys
 180 185 190
 Gln Ile Arg Leu Gly Glu Asp Ile Ile Leu Asp Ala Ile Cys Ser Val
 195 200 205
 Pro Tyr Leu Ile Asp Phe Ile Tyr Ala Tyr Lys Asp Ala Leu Ile Asn
 210 215 220
 Arg Glu Arg Arg Val Lys Glu Leu Phe Arg Ser Phe Asp Asp Asp
 225 230 235 240
 Glu Asn Ser Val Ser Asp Ser Lys Lys Asp Glu Asp Asn Glu Glu Asp
 245 250 255
 Glu Glu Asn Glu Glu Arg Lys Lys Val Val Ser Glu Lys Asp Lys Lys
 260 265 270
 Arg Val Glu Lys Val Gln Glu Ser Phe Lys Ala Leu Asp Lys Ala Lys
 275 280 285
 Lys Glu Trp Leu Lys Ala Leu Glu Ala Pro Ile Asp Glu Arg Glu Asp
 290 295 300
 Glu Leu Val Arg Ser Leu Thr Leu Ala Tyr Lys Arg Gln Thr Leu Lys
 305 310 315 320
 Asp Arg Leu Tyr Asp Leu Glu Pro Thr Ser Lys Leu Ile Asn Glu Leu
 325 330 335
 Val Lys Thr Met Glu Thr Thr Leu Lys Ser Gly Asp Gly Phe Glu Lys
 340 345 350
 Glu Leu Lys Arg Leu Glu Tyr Lys Leu Pro Leu Phe Asn Asp Thr Leu
 355 360 365
 Ile Ala Asn His Lys Lys Ile Leu Ala Asn Ile Thr Asn Met Thr Lys
 370 375 380
 Glu Asp Ile Ile Ala Gln Val Pro Glu Ala Thr Met Val Ser Val Tyr
 385 390 395 400
 Met Asp Leu Lys Lys Leu Phe Leu Thr Lys Glu Ala Ser Glu Glu Gly
 405 410 415
 Phe Asp Leu Ala Pro Asn Lys Leu Lys Glu Ile Leu Glu Gln Ile Lys

45					50					55						
tcc	act	tta	acc	aca	acg	agc	atg	att	tta	gcg	ttt	ggc	ggt	caa	aag	243
Ser	Thr	Leu	Thr	Thr	Thr	Ser	Met	Ile	Leu	Ala	Phe	Gly	Val	Gln	Lys	
		60					65					70				
gtg	ctt	ttt	agc	ggg	gtg	gct	gga	agc	tta	ggt	aaa	gat	tta	aaa	atc	291
Val	Leu	Phe	Ser	Gly	Val	Ala	Gly	Ser	Leu	Val	Lys	Asp	Leu	Lys	Ile	
		75				80					85					
aat	gat	tta	cta	gtg	gct	att	caa	tta	gtc	cag	cat	gat	gtg	gat	ttg	339
Asn	Asp	Leu	Leu	Val	Ala	Ile	Gln	Leu	Val	Gln	His	Asp	Val	Asp	Leu	
		90			95				100						105	
agc	gcg	ttt	gat	cac	cct	tta	ggg	ttc	atc	cca	gaa	agc	gcg	att	ttt	387
Ser	Ala	Phe	Asp	His	Pro	Leu	Gly	Phe	Ile	Pro	Glu	Ser	Ala	Ile	Phe	
				110					115					120		
att	gaa	acg	agc	gaa	agt	ttg	aac	gct	ttg	gct	aaa	gaa	gtc	gct	aat	435
Ile	Glu	Thr	Ser	Glu	Ser	Leu	Asn	Ala	Leu	Ala	Lys	Glu	Val	Ala	Asn	
			125					130					135			
gaa	cag	cat	atc	gtg	ctc	aaa	gaa	ggc	gtc	atc	gca	tca	ggc	gat	cag	483
Glu	Gln	His	Ile	Val	Leu	Lys	Glu	Gly	Val	Ile	Ala	Ser	Gly	Asp	Gln	
			140				145					150				
ttt	gtg	cat	agc	aaa	gaa	agg	aaa	gag	ttt	tta	ggt	agc	gag	ttt	aaa	531
Phe	Val	His	Ser	Lys	Glu	Arg	Lys	Glu	Phe	Leu	Val	Ser	Glu	Phe	Lys	
		155				160					165					
gcg	agc	gcg	gtg	gaa	atg	gag	ggg	gcg	agc	gtg	gcg	ttt	gtg	tgc	caa	579
Ala	Ser	Ala	Val	Glu	Met	Glu	Gly	Ala	Ser	Val	Ala	Phe	Val	Cys	Gln	
					175					180					185	
aaa	ttt	ggc	gtg	cca	tgc	tgt	gtg	tta	agg	agc	att	agc	gat	aac	gct	627
Lys	Phe	Gly	Val	Pro	Cys	Cys	Val	Leu	Arg	Ser	Ile	Ser	Asp	Asn	Ala	
				190					195					200		
gat	gag	gaa	gct	aac	atg	agc	ttt	gat	gcg	ttt	tta	gaa	aaa	agc	gct	675
Asp	Glu	Glu	Ala	Asn	Met	Ser	Phe	Asp	Ala	Phe	Leu	Glu	Lys	Ser	Ala	
			205					210					215			
caa	act	tca	gcg	aaa	ttc	tta	aaa	agc	atg	gtg	gat	gag	ctt			717
Gln	Thr	Ser	Ala	Lys	Phe	Leu	Lys	Ser	Met	Val	Asp	Glu	Leu			
			220				225					230				
taggg	ttt	gt	ttt	atagag	gggt	ggaa										745

<210> 458
 <211> 231
 <212> PRT
 <213> Helicobacter pylori

<400> 458
 Met Val Gln Lys Ile Gly Ile Leu Gly Ala Met Arg Glu Glu Ile Thr
 1 5 10 15
 Pro Ile Leu Glu Leu Phe Gly Val Asp Phe Glu Glu Ile Pro Leu Gly
 20 25 30
 Gly Asn Val Phe His Lys Gly Val Tyr His Asn Lys Glu Ile Ile Val

<400> 459																
ggtgtcctta aacagcaggg tgaaagagat tttaaaagaa agcgcctctgc attct atg																58
																Met
																1
caa gat agt ttg cat ttt aag gtt aat gaa gtg caa ggg gtt tta gaa																106
Gln Asp Ser Leu His Phe Lys Val Asn Glu Val Gln Gly Val Leu Glu																
																5
																10
																15
aac act tat acg agc atg ggc att gtt aaa gaa atg ctc cct aaa gac																154
Asn Thr Tyr Thr Ser Met Gly Ile Val Lys Glu Met Leu Pro Lys Asp																
																20
																25
																30
acc aaa aga gaa atc aaa atc ggc ttg tta aaa aac ttc att tta gcc																202
Thr Lys Arg Glu Ile Lys Ile Gly Leu Leu Lys Asn Phe Ile Leu Ala																
																35
																40
																45
aat tcg cat gtc gct ggg gtg agc atg ttt ttt aaa ggc aga gaa gat																250
Asn Ser His Val Ala Gly Val Ser Met Phe Phe Lys Gly Arg Glu Asp																
																50
																55
																60
																65
tta aga tta acg ctt tta agg gat aac aat acg att aag cta gtg gaa																298
Leu Arg Leu Thr Leu Leu Arg Asp Asn Asn Thr Ile Lys Leu Val Glu																

70					75					80						
aat	ccg	tca	tta	gag	aat	agc	cct	tta	gcg	caa	aaa	gcg	atg	aaa	aat	346
Asn	Pro	Ser	Leu	Glu	Asn	Ser	Pro	Leu	Ala	Gln	Lys	Ala	Met	Lys	Asn	
			85					90					95			
aaa	gaa	att	tct	aaa	agt	ttg	ggg	tat	tat	agg	aaa	atg	cct	aat	ggg	394
Lys	Glu	Ile	Ser	Lys	Ser	Leu	Gly	Tyr	Tyr	Arg	Lys	Met	Pro	Asn	Gly	
		100					105					110				
gcg	gaa	gtt	tat	ggg	gtg	gat	att	ctt	tta	cct	tta	ttg	aat	gag	aac	442
Ala	Glu	Val	Tyr	Gly	Val	Asp	Ile	Leu	Leu	Pro	Leu	Leu	Asn	Glu	Asn	
		115				120					125					
gct	caa	gag	gtt	gta	ggg	gct	ttg	atg	att	ttt	att	tcc	att	gac	agc	490
Ala	Gln	Glu	Val	Val	Gly	Ala	Leu	Met	Ile	Phe	Ile	Ser	Ile	Asp	Ser	
					135					140					145	
ttc	agc	aat	gaa	atc	act	aaa	aac	agg	agc	gat	tta	ttt	tta	att	ggc	538
Phe	Ser	Asn	Glu	Ile	Thr	Lys	Asn	Arg	Ser	Asp	Leu	Phe	Leu	Ile	Gly	
				150					155						160	
act	aaa	ggg	aaa	gtg	ctt	ttg	agc	gcg	aat	aag	agt	ttg	caa	gac	aaa	586
Thr	Lys	Gly	Lys	Val	Leu	Leu	Ser	Ala	Asn	Lys	Ser	Leu	Gln	Asp	Lys	
			165				170						175			
cct	atc	gca	gaa	att	tat	aag	agc	gtg	cct	aaa	gcc	acc	aac	gaa	gtg	634
Pro	Ile	Ala	Glu	Ile	Tyr	Lys	Ser	Val	Pro	Lys	Ala	Thr	Asn	Glu	Val	
			180				185					190				
atg	gct	att	tta	gaa	aac	ggc	tct	aaa	gcg	act	tta	gaa	tac	tta	gat	682
Met	Ala	Ile	Leu	Glu	Asn	Gly	Ser	Lys	Ala	Thr	Leu	Glu	Tyr	Leu	Asp	
					200						205					
ccc	ttt	agc	cat	aag	gaa	aat	ttt	tta	gcc	gtt	gaa	acc	ttt	aaa	atg	730
Pro	Phe	Ser	His	Lys	Glu	Asn	Phe	Leu	Ala	Val	Glu	Thr	Phe	Lys	Met	
					215					220					225	
cta	ggc	aaa	aca	gaa	agt	aaa	gac	aat	ctt	aat	tgg	atg	atc	gct	tta	778
Leu	Gly	Lys	Thr	Glu	Ser	Lys	Asp	Asn	Leu	Asn	Trp	Met	Ile	Ala	Leu	
				230					235					240		
atc	att	gaa	aaa	gac	aag	gtc	tat	gag	caa	gta	ggc	tcg	gtg	cgt	ttt	826
Ile	Ile	Glu	Lys	Asp	Lys	Val	Tyr	Glu	Gln	Val	Gly	Ser	Val	Arg	Phe	
			245					250					255			
gtg	gtg	atc	ata	gcg	agc	gca	atc	atg	gtg	tta	gcc	ttg	att	ata	gcg	874
Val	Val	Ile	Ile	Ala	Ser	Ala	Ile	Met	Val	Leu	Ala	Leu	Ile	Ile	Ala	
			260			265					270					
atc	act	ctc	tta	atg	cga	gcg	atc	gtg	agc	agt	cgt	ttg	gaa	gcc	gtt	922
Ile	Thr	Leu	Leu	Met	Arg	Ala	Ile	Val	Ser	Ser	Arg	Leu	Glu	Ala	Val	
			275			280					285					
tct	agc	acc	ttg	tct	cat	ttc	ttt	aaa	tta	ttg	aac	aat	caa	gcc	aat	970
Ser	Ser	Thr	Leu	Ser	His	Phe	Phe	Lys	Leu	Leu	Asn	Asn	Gln	Ala	Asn	
					295				300						305	
tct	agc	ggg	att	aaa	ttg	att	gaa	gcg	aaa	tcc	aat	gac	gag	tta	ggc	1018

Ser	Ser	Gly	Ile	Lys	Leu	Ile	Glu	Ala	Lys	Ser	Asn	Asp	Glu	Leu	Gly	
				310					315					320		
cgc	atg	caa	aca	gcg	atc	aat	aaa	aat	atc	ttg	caa	acc	caa	aaa	atc	1066
Arg	Met	Gln	Thr	Ala	Ile	Asn	Lys	Asn	Ile	Leu	Gln	Thr	Gln	Lys	Ile	
			325					330					335			
atg	caa	gaa	gac	agg	caa	gcc	gtc	caa	gac	acc	att	aaa	gtg	gtt	tca	1114
Met	Gln	Glu	Asp	Arg	Gln	Ala	Val	Gln	Asp	Thr	Ile	Lys	Val	Val	Ser	
			340				345					350				
gat	gtg	aaa	gca	ggg	aat	ttt	gcg	gtg	cgc	atc	acg	gct	gag	ccc	gca	1162
Asp	Val	Lys	Ala	Gly	Asn	Phe	Ala	Val	Arg	Ile	Thr	Ala	Glu	Pro	Ala	
			355			360					365					
agc	cct	gat	ttg	aaa	gaa	ttg	agg	gac	gcg	cta	aat	ggg	atc	atg	gat	1210
Ser	Pro	Asp	Leu	Lys	Glu	Leu	Arg	Asp	Ala	Leu	Asn	Gly	Ile	Met	Asp	
					375					380					385	
tat	ttg	caa	gaa	agc	gta	ggg	act	cac	atg	cca	agc	att	ttc	aaa	atc	1256
Tyr	Leu	Gln	Glu	Ser	Val	Gly	Thr	His	Met	Pro	Ser	Ile	Phe	Lys	Ile	
				390				395					400			
ttt	gaa	agc	tat	tct	ggt	ttg	gat	ttt	aga	ggc	cgg	atc	caa	aac	gct	1306
Phe	Glu	Ser	Tyr	Ser	Gly	Leu	Asp	Phe	Arg	Gly	Arg	Ile	Gln	Asn	Ala	
			405					410					415			
tcg	ggt	agg	gtg	gaa	ctg	gtt	act	aac	gct	tta	ggg	caa	gaa	atc	caa	1354
Ser	Gly	Arg	Val	Glu	Leu	Val	Thr	Asn	Ala	Leu	Gly	Gln	Glu	Ile	Gln	
			420				425					430				
aaa	atg	cta	gaa	act	tcg	tct	aat	ttt	gcc	aaa	gat	tta	gcg	aac	gat	1402
Lys	Met	Leu	Glu	Thr	Ser	Ser	Asn	Phe	Ala	Lys	Asp	Leu	Ala	Asn	Asp	
			435			440					445					
agc	gcg	aat	tta	aaa	gag	tgc	gtg	caa	aat	tta	gaa	aaa	gct	tca	aac	1450
Ser	Ala	Asn	Leu	Lys	Glu	Cys	Val	Gln	Asn	Leu	Glu	Lys	Ala	Ser	Asn	
					455					460					465	
tcc	caa	cac	aaa	agc	ttg	atg	gaa	act	tcc	aaa	acg	ata	gaa	aat	atc	1498
Ser	Gln	His	Lys	Ser	Leu	Met	Glu	Thr	Ser	Lys	Thr	Ile	Glu	Asn	Ile	
				470					475					480		
acc	act	tcc	att	caa	ggc	gtg	agc	tct	caa	agt	gaa	gcc	atg	att	gaa	1546
Thr	Thr	Ser	Ile	Gln	Gly	Val	Ser	Ser	Gln	Ser	Glu	Ala	Met	Ile	Glu	
			485					490					495			
caa	ggg	caa	gac	att	aaa	agc	att	gta	gaa	atc	att	aga	gat	att	gct	1594
Gln	Gly	Gln	Asp	Ile	Lys	Ser	Ile	Val	Glu	Ile	Ile	Arg	Asp	Ile	Ala	
			500				505					510				
gat	caa	acc	aat	ctt	tta	gcc	tta	aac	gcc	gct	att	gaa	gcc	gca	agg	1642
Asp	Gln	Thr	Asn	Leu	Leu	Ala	Leu	Asn	Ala	Ala	Ile	Glu	Ala	Ala	Arg	
			515			520					525					
gcc	ggc	gag	cat	ggc	aga	ggc	ttt	gcg	gtg	gtg	gct	gat	gag	gta	aga	1690
Ala	Gly	Glu	His	Gly	Arg	Gly	Phe	Ala	Val	Val	Ala	Asp	Glu	Val	Arg	
					535					540					545	

aag ctc gct gaa agg acg caa aaa tcg ctc agc gag att gaa gcc aat 1738
Lys Leu Ala Glu Arg Thr Gln Lys Ser Leu Ser Glu Ile Glu Ala Asn
550 555 560

atc aat att tta gtg caa agc att tca gac acg agc gaa agc att aaa 1786
Ile Asn Ile Leu Val Gln Ser Ile Ser Asp Thr Ser Glu Ser Ile Lys
565 570 575

aac cag gtt aaa gaa gtg gaa gaa atc aac gct tct att gaa gcc tta 1834
Asn Gln Val Lys Glu Val Glu Glu Ile Asn Ala Ser Ile Glu Ala Leu
580 585 590

aga tcg gtt act gag ggc aat cta aaa atc gct agc gat tct tta gaa 1882
Arg Ser Val Thr Glu Gly Asn Leu Lys Ile Ala Ser Asp Ser Leu Glu
595 600 605

atc agt caa gaa att gac aaa gtt tct aac gat att tta gaa gat gtg 1930
Ile Ser Gln Glu Ile Asp Lys Val Ser Asn Asp Ile Leu Glu Asp Val
610 615 620 625

aat aaa aag cag ttt taatgctcat tcatatttgc tgctcagtgg ataacctcta 1985
Asn Lys Lys Gln Phe
630

t 1986

<210> 460
<211> 630
<212> PRT
<213> Helicobacter pylori

<400> 460
Met Gln Asp Ser Leu His Phe Lys Val Asn Glu Val Gln Gly Val Leu
1 5 10 15
Glu Asn Thr Tyr Thr Ser Met Gly Ile Val Lys Glu Met Leu Pro Lys
20 25 30
Asp Thr Lys Arg Glu Ile Lys Ile Gly Leu Leu Lys Asn Phe Ile Leu
35 40 45
Ala Asn Ser His Val Ala Gly Val Ser Met Phe Phe Lys Gly Arg Glu
50 55 60
Asp Leu Arg Leu Thr Leu Leu Arg Asp Asn Asn Thr Ile Lys Leu Val
65 70 75 80
Glu Asn Pro Ser Leu Glu Asn Ser Pro Leu Ala Gln Lys Ala Met Lys
85 90 95
Asn Lys Glu Ile Ser Lys Ser Leu Gly Tyr Tyr Arg Lys Met Pro Asn
100 105 110
Gly Ala Glu Val Tyr Gly Val Asp Ile Leu Leu Pro Leu Leu Asn Glu
115 120 125
Asn Ala Gln Glu Val Val Gly Ala Leu Met Ile Phe Ile Ser Ile Asp
130 135 140
Ser Phe Ser Asn Glu Ile Thr Lys Asn Arg Ser Asp Leu Phe Leu Ile
145 150 155 160
Gly Thr Lys Gly Lys Val Leu Leu Ser Ala Asn Lys Ser Leu Gln Asp
165 170 175
Lys Pro Ile Ala Glu Ile Tyr Lys Ser Val Pro Lys Ala Thr Asn Glu
180 185 190
Val Met Ala Ile Leu Glu Asn Gly Ser Lys Ala Thr Leu Glu Tyr Leu
195 200 205
Asp Pro Phe Ser His Lys Glu Asn Phe Leu Ala Val Glu Thr Phe Lys

210		215		220
Met Leu Gly Lys Thr	Glu Ser Lys Asp Asn	Leu Asn Trp Met Ile Ala		
225	230	235	240	
Leu Ile Ile Glu Lys	Asp Lys Val Tyr Glu	Gln Val Gly Ser Val Arg		
	245	250	255	
Phe Val Val Ile Ile	Ala Ser Ala Ile Met	Val Leu Ala Leu Ile Ile		
	260	265	270	
Ala Ile Thr Leu Leu	Met Arg Ala Ile Val	Ser Ser Arg Leu Glu Ala		
	275	280	285	
Val Ser Ser Thr Leu	Ser His Phe Phe Lys	Leu Leu Asn Asn Gln Ala		
	290	295	300	
Asn Ser Ser Gly Ile	Lys Leu Ile Glu Ala	Lys Ser Asn Asp Glu Leu		
305	310	315	320	
Gly Arg Met Gln Thr	Ala Ile Asn Lys Asn	Ile Leu Gln Thr Gln Lys		
	325	330	335	
Ile Met Gln Glu Asp	Arg Gln Ala Val Gln	Asp Thr Ile Lys Val Val		
	340	345	350	
Ser Asp Val Lys Ala	Gly Asn Phe Ala Val	Arg Ile Thr Ala Glu Pro		
	355	360	365	
Ala Ser Pro Asp Leu	Lys Glu Leu Arg Asp	Ala Leu Asn Gly Ile Met		
	370	375	380	
Asp Tyr Leu Gln Glu	Ser Val Gly Thr His	Met Pro Ser Ile Phe Lys		
385	390	395	400	
Ile Phe Glu Ser Tyr	Ser Gly Leu Asp Phe	Arg Gly Arg Ile Gln Asn		
	405	410	415	
Ala Ser Gly Arg Val	Glu Leu Val Thr Asn	Ala Leu Gly Gln Glu Ile		
	420	425	430	
Gln Lys Met Leu Glu	Thr Ser Ser Asn Phe	Ala Lys Asp Leu Ala Asn		
	435	440	445	
Asp Ser Ala Asn Leu	Lys Glu Cys Val Gln	Asn Leu Glu Lys Ala Ser		
	450	455	460	
Asn Ser Gln His Lys	Ser Leu Met Glu Thr	Ser Lys Thr Ile Glu Asn		
465	470	475	480	
Ile Thr Thr Ser Ile	Gln Gly Val Ser Ser	Gln Ser Glu Ala Met Ile		
	485	490	495	
Glu Gln Gly Gln Asp	Ile Lys Ser Ile Val	Glu Ile Ile Arg Asp Ile		
	500	505	510	
Ala Asp Gln Thr Asn	Leu Leu Ala Leu Asn	Ala Ala Ile Glu Ala Ala		
	515	520	525	
Arg Ala Gly Glu His	Gly Arg Gly Phe Ala	Val Val Ala Asp Glu Val		
	530	535	540	
Arg Lys Leu Ala Glu	Arg Thr Gln Lys Ser	Leu Ser Glu Ile Glu Ala		
545	550	555	560	
Asn Ile Asn Ile Leu	Val Gln Ser Ile Ser	Asp Thr Ser Glu Ser Ile		
	565	570	575	
Lys Asn Gln Val Lys	Glu Val Glu Glu Ile	Asn Ala Ser Ile Glu Ala		
	580	585	590	
Leu Arg Ser Val Thr	Glu Gly Asn Leu Lys	Ile Ala Ser Asp Ser Leu		
	595	600	605	
Glu Ile Ser Gln Glu	Ile Asp Lys Val Ser	Asn Asp Ile Leu Glu Asp		
	610	615	620	
Val Asn Lys Lys Gln	Phe			
625	630			

<210> 461
 <211> 1758
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (8)...(1702)

<221> misc_feature
 <222> 375
 <223> n = A,T,C or G

<400> 461

gagataa	atg	atg	ttt	tct	tca	atg	ttt	gct	tcg	ttg	ggg	act	cgt	atc	49	
	Met	Met	Phe	Ser	Ser	Met	Phe	Ala	Ser	Leu	Gly	Thr	Arg	Ile		
	1				5					10						
atg	ctg	gtc	gtg	tta	gcc	gct	ctt	tta	ggg	tta	ggg	ggg	ctt	ttt	att	97
Met	Leu	Val	Val	Leu	Ala	Ala	Leu	Leu	Gly	Leu	Gly	Gly	Leu	Phe	Ile	
15					20				25					30		
ggg	ttt	gta	aag	gtt	atg	caa	aaa	gat	gtg	tta	gcg	caa	ctc	atg	gag	145
Gly	Phe	Val	Lys	Val	Met	Gln	Lys	Asp	Val	Leu	Ala	Gln	Leu	Met	Glu	
				35					40					45		
cat	tta	gaa	acc	ggg	caa	tac	aaa	aag	cgt	gaa	aaa	acg	ctc	gct	tac	193
His	Leu	Glu	Thr	Gly	Gln	Tyr	Lys	Lys	Arg	Glu	Lys	Thr	Leu	Ala	Tyr	
			50					55					60			
atg	aca	aaa	att	att	gaa	cag	ggc	att	cat	gag	tat	tac	aaa	aat	ttt	241
Met	Thr	Lys	Ile	Ile	Glu	Gln	Gly	Ile	His	Glu	Tyr	Tyr	Lys	Asn	Phe	
		65					70					75				
gac	aat	gct	act	gca	aga	aaa	atg	gcg	tta	gat	tat	ttc	aaa	cgc	atc	289
Asp	Asn	Ala	Thr	Ala	Arg	Lys	Met	Ala	Leu	Asp	Tyr	Phe	Lys	Arg	Ile	
	80					85					90					
aac	gac	gat	aag	ggc	atg	att	tat	atg	gtg	gtg	gtg	gat	aaa	aac	ggg	337
Asn	Asp	Asp	Lys	Gly	Met	Ile	Tyr	Met	Val	Val	Val	Asp	Lys	Asn	Gly	
95					100				105						110	
gtg	gta	ttg	ttt	gat	ccg	gtc	aat	cct	aaa	acc	gta	gnc	caa	tca	ggg	385
Val	Val	Leu	Phe	Asp	Pro	Val	Asn	Pro	Lys	Thr	Val	Xaa	Gln	Ser	Gly	
				115					120					125		
ctt	gac	gct	cag	agc	gtt	gat	ggg	gtg	tat	tat	gtt	agg	ggg	tat	ttg	433
Leu	Asp	Ala	Gln	Ser	Val	Asp	Gly	Val	Tyr	Tyr	Val	Arg	Gly	Tyr	Leu	
			130					135					140			
gag	gcg	gcc	aaa	aaa	ggg	gga	ggc	tac	act	tat	tat	aaa	atg	cct	aaa	481
Glu	Ala	Ala	Lys	Lys	Gly	Gly	Gly	Tyr	Thr	Tyr	Tyr	Lys	Met	Pro	Lys	
		145					150					155				
tac	gat	gga	ggc	gta	ccg	gag	aaa	aaa	ttc	gcc	tac	tcg	cat	tat	gat	529
Tyr	Asp	Gly	Gly	Val	Pro	Glu	Lys	Lys	Phe	Ala	Tyr	Ser	His	Tyr	Asp	
	160					165					170					
gaa	gtt	tct	caa	atg	gtg	atc	gca	acg	act	tcc	tat	tac	act	gac	att	577
Glu	Val	Ser	Gln	Met	Val	Ile	Ala	Thr	Thr	Ser	Tyr	Tyr	Thr	Asp	Ile	
175					180					185					190	
aac	aca	gaa	aat	aaa	gcg	atc	aaa	gaa	ggc	gtg	aat	aag	gtt	ttt	gat	625
Asn	Thr	Glu	Asn	Lys	Ala	Ile	Lys	Glu	Gly	Val	Asn	Lys	Val	Phe	Asp	

195										200					205					
gaa	aac	acc	acg	aaa	tta	ttc	ctt	tgg	ata	ctg	aca	gcg	acg	ata	gcg	673				
Glu	Asn	Thr	Thr	Lys	Leu	Phe	Leu	Trp	Ile	Leu	Thr	Ala	Thr	Ile	Ala					
210								215				220								
cta	gtg	gtt	ttg	acg	ctc	ata	tac	gct	aaa	tta	agg	atc	gtg	aaa	cgc	721				
Leu	Val	Val	Leu	Thr	Leu	Ile	Tyr	Ala	Lys	Leu	Arg	Ile	Val	Lys	Arg					
225												235								
att	gat	gaa	ctg	gtc	ctt	aaa	atc	aac	gct	ttt	agc	cgt	ggg	gat	aag	769				
Ile	Asp	Glu	Leu	Val	Leu	Lys	Ile	Asn	Ala	Phe	Ser	Arg	Gly	Asp	Lys					
240				245				250												
gat	ttg	aga	gcc	aaa	att	gat	gtg	ggt	gat	cgc	aac	gat	gaa	atc	tcg	817				
Asp	Leu	Arg	Ala	Lys	Ile	Asp	Val	Gly	Asp	Arg	Asn	Asp	Glu	Ile	Ser					
255				260				265				270								
caa	gtg	ggc	cgt	ggg	atc	aat	ttg	ttt	gtg	gaa	aac	gcc	cgc	ttg	att	865				
Gln	Val	Gly	Arg	Gly	Ile	Asn	Leu	Phe	Val	Glu	Asn	Ala	Arg	Leu	Ile					
				275				280				285								
atg	gaa	gag	att	aaa	ggg	att	tcc	acc	ctc	aat	aaa	act	tca	atg	gat	913				
Met	Glu	Glu	Ile	Lys	Gly	Ile	Ser	Thr	Leu	Asn	Lys	Thr	Ser	Met	Asp					
				290				295				300								
aaa	tta	gtc	caa	atc	acg	caa	gaa	acc	caa	aag	agc	atg	aaa	gat	tcc	961				
Lys	Leu	Val	Gln	Ile	Thr	Gln	Glu	Thr	Gln	Lys	Ser	Met	Lys	Asp	Ser					
305								310				315								
tca	acc	acc	cta	aat	tcc	gtg	aaa	aat	aaa	gcc	act	gat	ata	gcg	agc	1009				
Ser	Thr	Thr	Leu	Asn	Ser	Val	Lys	Asn	Lys	Ala	Thr	Asp	Ile	Ala	Ser					
320				325								330								
atg	atg	aat	gct	tcc	ata	gag	caa	tct	caa	ggg	tta	agg	aag	cgt	ttg	1057				
Met	Met	Asn	Ala	Ser	Ile	Glu	Gln	Ser	Gln	Gly	Leu	Arg	Lys	Arg	Leu					
335				340				345				350								
att	gaa	acg	caa	ggg	ctg	gtc	aaa	gag	agc	aag	gat	gcg	atc	ggg	gat	1105				
Ile	Glu	Thr	Gln	Gly	Leu	Val	Lys	Glu	Ser	Lys	Asp	Ala	Ile	Gly	Asp					
				355				360				365								
tta	ttt	tct	caa	atc	aca	gag	agc	gcg	cac	act	gaa	gag	gaa	ctc	tct	1153				
Leu	Phe	Ser	Gln	Ile	Thr	Glu	Ser	Ala	His	Thr	Glu	Glu	Glu	Leu	Ser					
370								375				380								
agc	aaa	gtg	gag	cag	cta	agc	cgt	aac	gct	gat	gat	gtc	aaa	tcc	att	1201				
Ser	Lys	Val	Glu	Gln	Leu	Ser	Arg	Asn	Ala	Asp	Asp	Val	Lys	Ser	Ile					
385								390				395								
ctg	gat	att	atc	aat	gat	att	gcc	gat	caa	acg	aat	tta	tta	gcc	cta	1249				
Leu	Asp	Ile	Ile	Asn	Asp	Ile	Ala	Asp	Gln	Thr	Asn	Leu	Leu	Ala	Leu					
400				405								410								
aac	gct	gct	att	gaa	gcc	gca	agg	gct	ggc	gag	cat	ggc	aga	ggc	ttt	1297				
Asn	Ala	Ala	Ile	Glu	Ala	Ala	Arg	Ala	Gly	Glu	His	Gly	Arg	Gly	Phe					
415				420				425				430								
gcg	gtg	gtg	gct	gat	gaa	ggt	agg	aat	tta	gcc	ggg	cgc	act	caa	aag	1345				

Ala Val Val Ala Asp Glu Val Arg Asn Leu Ala Gly Arg Thr Gln Lys	
435 440 445	
tct tta gcc gaa atc aat tcc act atc atg gtg att gtc caa gaa atc	1393
Ser Leu Ala Glu Ile Asn Ser Thr Ile Met Val Ile Val Gln Glu Ile	
450 455 460	
aat gcc gtg agt tcg caa atg aat ctc aat tcg caa aaa atg gag cgt	1441
Asn Ala Val Ser Ser Gln Met Asn Leu Asn Ser Gln Lys Met Glu Arg	
465 470 475	
ttg agc gat atg agt aaa agc gtg caa gaa act tac gaa aaa atg agt	1489
Leu Ser Asp Met Ser Lys Ser Val Gln Glu Thr Tyr Glu Lys Met Ser	
480 485 490	
tct aat tta agc tca gtc gtg tca gac agc aat caa agc atg gac gat	1537
Ser Asn Leu Ser Ser Val Val Ser Asp Ser Asn Gln Ser Met Asp Asp	
495 500 505 510	
tac gcc aaa tcc gga cac caa att gaa gtt atg gta agc gat ttt gca	1585
Tyr Ala Lys Ser Gly His Gln Ile Glu Val Met Val Ser Asp Phe Ala	
515 520 525	
gag gtg gaa aaa gtg gct tct aag act tta gcg gat tct tca gat att	1633
Glu Val Glu Lys Val Ala Ser Lys Thr Leu Ala Asp Ser Ser Asp Ile	
530 535 540	
tta aac atc gct acg cat gtg agt gga acg acc atg aat tta gac aaa	1681
Leu Asn Ile Ala Thr His Val Ser Gly Thr Thr Met Asn Leu Asp Lys	
545 550 555	
caa gtg aat ttg ttt aaa act taatcagggg gagtttatta aaaaagggtt	1732
Gln Val Asn Leu Phe Lys Thr	
560 565	
ggattgttaa aagtttctgt gatcac	1758
<210> 462	
<211> 565	
<212> PRT	
<213> Helicobacter pylori	
<220>	
<221> VARIANT	
<222> 123	
<223> Xaa = Any Amino Acid	
<400> 462	
Met Met Phe Ser Ser Met Phe Ala Ser Leu Gly Thr Arg Ile Met Leu	
1 5 10 15	
Val Val Leu Ala Leu Leu Gly Leu Gly Gly Leu Phe Ile Gly Phe	
20 25 30	
Val Lys Val Met Gln Lys Asp Val Leu Ala Gln Leu Met Glu His Leu	
35 40 45	
Glu Thr Gly Gln Tyr Lys Lys Arg Glu Lys Thr Leu Ala Tyr Met Thr	
50 55 60	
Lys Ile Ile Glu Gln Gly Ile His Glu Tyr Tyr Lys Asn Phe Asp Asn	
65 70 75 80	
Ala Thr Ala Arg Lys Met Ala Leu Asp Tyr Phe Lys Arg Ile Asn Asp	

				85				90					95			
Asp	Lys	Gly	Met	Ile	Tyr	Met	Val	Val	Val	Asp	Lys	Asn	Gly	Val	Val	
			100					105					110			
Leu	Phe	Asp	Pro	Val	Asn	Pro	Lys	Thr	Val	Xaa	Gln	Ser	Gly	Leu	Asp	
		115					120					125				
Ala	Gln	Ser	Val	Asp	Gly	Val	Tyr	Tyr	Val	Arg	Gly	Tyr	Leu	Glu	Ala	
	130					135					140					
Ala	Lys	Lys	Gly	Gly	Gly	Tyr	Thr	Tyr	Tyr	Lys	Met	Pro	Lys	Tyr	Asp	
145					150					155					160	
Gly	Gly	Val	Pro	Glu	Lys	Lys	Phe	Ala	Tyr	Ser	His	Tyr	Asp	Glu	Val	
				165					170					175		
Ser	Gln	Met	Val	Ile	Ala	Thr	Thr	Ser	Tyr	Tyr	Thr	Asp	Ile	Asn	Thr	
		180						185					190			
Glu	Asn	Lys	Ala	Ile	Lys	Glu	Gly	Val	Asn	Lys	Val	Phe	Asp	Glu	Asn	
	195						200					205				
Thr	Thr	Lys	Leu	Phe	Leu	Trp	Ile	Leu	Thr	Ala	Thr	Ile	Ala	Leu	Val	
	210					215					220					
Val	Leu	Thr	Leu	Ile	Tyr	Ala	Lys	Leu	Arg	Ile	Val	Lys	Arg	Ile	Asp	
225					230					235					240	
Glu	Leu	Val	Leu	Lys	Ile	Asn	Ala	Phe	Ser	Arg	Gly	Asp	Lys	Asp	Leu	
				245					250					255		
Arg	Ala	Lys	Ile	Asp	Val	Gly	Asp	Arg	Asn	Asp	Glu	Ile	Ser	Gln	Val	
			260				265						270			
Gly	Arg	Gly	Ile	Asn	Leu	Phe	Val	Glu	Asn	Ala	Arg	Leu	Ile	Met	Glu	
	275						280					285				
Glu	Ile	Lys	Gly	Ile	Ser	Thr	Leu	Asn	Lys	Thr	Ser	Met	Asp	Lys	Leu	
	290					295					300					
Val	Gln	Ile	Thr	Gln	Glu	Thr	Gln	Lys	Ser	Met	Lys	Asp	Ser	Ser	Thr	
305					310					315					320	
Thr	Leu	Asn	Ser	Val	Lys	Asn	Lys	Ala	Thr	Asp	Ile	Ala	Ser	Met	Met	
				325					330					335		
Asn	Ala	Ser	Ile	Glu	Gln	Ser	Gln	Gly	Leu	Arg	Lys	Arg	Leu	Ile	Glu	
			340					345					350			
Thr	Gln	Gly	Leu	Val	Lys	Glu	Ser	Lys	Asp	Ala	Ile	Gly	Asp	Leu	Phe	
		355					360					365				
Ser	Gln	Ile	Thr	Glu	Ser	Ala	His	Thr	Glu	Glu	Glu	Leu	Ser	Ser	Lys	
	370					375				380						
Val	Glu	Gln	Leu	Ser	Arg	Asn	Ala	Asp	Asp	Val	Lys	Ser	Ile	Leu	Asp	
385					390					395					400	
Ile	Ile	Asn	Asp	Ile	Ala	Asp	Gln	Thr	Asn	Leu	Leu	Ala	Leu	Asn	Ala	
				405					410					415		
Ala	Ile	Glu	Ala	Ala	Arg	Ala	Gly	Glu	His	Gly	Arg	Gly	Phe	Ala	Val	
			420					425					430			
Val	Ala	Asp	Glu	Val	Arg	Asn	Leu	Ala	Gly	Arg	Thr	Gln	Lys	Ser	Leu	
		435					440					445				
Ala	Glu	Ile	Asn	Ser	Thr	Ile	Met	Val	Ile	Val	Gln	Glu	Ile	Asn	Ala	
	450					455					460					
Val	Ser	Ser	Gln	Met	Asn	Leu	Asn	Ser	Gln	Lys	Met	Glu	Arg	Leu	Ser	
465					470					475					480	
Asp	Met	Ser	Lys	Ser	Val	Gln	Glu	Thr	Tyr	Glu	Lys	Met	Ser	Ser	Asn	
				485					490					495		
Leu	Ser	Ser	Val	Val	Ser	Asp	Ser	Asn	Gln	Ser	Met	Asp	Asp	Tyr	Ala	
			500					505					510			
Lys	Ser	Gly	His	Gln	Ile	Glu	Val	Met	Val	Ser	Asp	Phe	Ala	Glu	Val	
		515					520					525				
Glu	Lys	Val	Ala	Ser	Lys	Thr	Leu	Ala	Asp	Ser	Ser	Asp	Ile	Leu	Asn	
	530					535					540					
Ile	Ala	Thr	His	Val	Ser	Gly	Thr	Thr	Met	Asn	Leu	Asp	Lys	Gln	Val	
545					550					555					560	

Asn Leu Phe Lys Thr
565

<210> 463
<211> 525
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (16)...(474)

```

<400> 463
ccttgagatt gctct atg gaa gca ttc atc atg ctc gct ata tca gtg gct 51
          Met Glu Ala Phe Ile Met Leu Ala Ile Ser Val Ala
            1             5             10

tta ttt ttc acg gaa ttt agg gtg gtt gag gaa tct ttc atg ctc ttt 99
Leu Phe Phe Thr Glu Phe Arg Val Val Glu Glu Ser Phe Met Leu Phe
          15             20             25

tgg gtt tct tgc gtg att tgg act aat tta tcc att gaa gtt tta ttg 147
Trp Val Ser Cys Val Ile Trp Thr Asn Leu Ser Ile Glu Val Leu Leu
          30             35             40

agg gtg gaa atc cct tta atc tct tcc ata atc aag cgg gcg ttt tcc 195
Arg Val Glu Ile Pro Leu Ile Ser Ser Ile Ile Lys Arg Ala Phe Ser
          45             50             55             60

aca aac aaa ttg atc cca cgg ccc act tgc gag att tca tcg ttg cga 243
Thr Asn Lys Leu Ile Pro Arg Pro Thr Cys Glu Ile Ser Ser Leu Arg
          65             70             75

tca ccc aca tca att ttg gct ctc aaa tcc tta tcc cca cgg cta aaa 291
Ser Pro Thr Ser Ile Leu Ala Leu Lys Ser Leu Ser Pro Arg Leu Lys
          80             85             90

gcg ttg att tta agg acc agt tca tca atg cgt ttc acg atc ctt aat 339
Ala Leu Ile Leu Arg Thr Ser Ser Ser Met Arg Phe Thr Ile Leu Asn
          95             100             105

tta gcg tat atg agc gtc aaa acc act agc gct atc gtc gct gtc agt 387
Leu Ala Tyr Met Ser Val Lys Thr Thr Ser Ala Ile Val Ala Val Ser
          110             115             120

atc caa agg aat aat ttc gtg gtg ttt tca tca aaa acc tta ttc acg 435
Ile Gln Arg Asn Asn Phe Val Val Phe Ser Ser Lys Thr Leu Phe Thr
          125             130             135             140

cct tct ttg atc gct tta ttt tct gtg tta atg tca gtg taataggaag 484
Pro Ser Leu Ile Ala Leu Phe Ser Val Leu Met Ser Val
          145             150

tcgttgcgat caccatttga gaaacttcat cataatgcga g 525

```

<210> 464
<211> 153
<212> PRT

<213> Helicobacter pylori

<400> 464

Met	Glu	Ala	Phe	Ile	Met	Leu	Ala	Ile	Ser	Val	Ala	Leu	Phe	Phe	Thr
1				5					10					15	
Glu	Phe	Arg	Val	Val	Glu	Glu	Ser	Phe	Met	Leu	Phe	Trp	Val	Ser	Cys
			20					25					30		
Val	Ile	Trp	Thr	Asn	Leu	Ser	Ile	Glu	Val	Leu	Leu	Arg	Val	Glu	Ile
		35					40					45			
Pro	Leu	Ile	Ser	Ser	Ile	Ile	Lys	Arg	Ala	Phe	Ser	Thr	Asn	Lys	Leu
	50					55					60				
Ile	Pro	Arg	Pro	Thr	Cys	Glu	Ile	Ser	Ser	Leu	Arg	Ser	Pro	Thr	Ser
65					70					75				80	
Ile	Leu	Ala	Leu	Lys	Ser	Leu	Ser	Pro	Arg	Leu	Lys	Ala	Leu	Ile	Leu
				85					90					95	
Arg	Thr	Ser	Ser	Ser	Met	Arg	Phe	Thr	Ile	Leu	Asn	Leu	Ala	Tyr	Met
			100					105						110	
Ser	Val	Lys	Thr	Thr	Ser	Ala	Ile	Val	Ala	Val	Ser	Ile	Gln	Arg	Asn
		115					120					125			
Asn	Phe	Val	Val	Phe	Ser	Ser	Lys	Thr	Leu	Phe	Thr	Pro	Ser	Leu	Ile
	130					135					140				
Ala	Leu	Phe	Ser	Val	Leu	Met	Ser	Val							
145					150										

<210> 465

<211> 1209

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (25)...(1164)

<400> 465

aaattcaata	aaaaaggaaa	aacc	atg	cgc	atg	caa	acc	aaa	tta	atc	cat				51
			Met	Arg	Met	Gln	Thr	Lys	Leu	Ile	His				
			1					5							
ggg ggc att agt gag gac gca aca acg ggg gcg gtg agc gtg cct att															99
Gly Gly Ile Ser Glu Asp Ala Thr Thr Gly Ala Val Ser Val Pro Ile															
10				15				20						25	
tat caa act tcc acc tac cgc caa gac gcc ata ggc cgc cat aag ggc															147
Tyr Gln Thr Ser Thr Tyr Arg Gln Asp Ala Ile Gly Arg His Lys Gly															
			30					35					40		
tat gaa tac tct cgc tca ggc aac ccc acg cgc ttt gct tta gaa gaa															195
Tyr Glu Tyr Ser Arg Ser Gly Asn Pro Thr Arg Phe Ala Leu Glu Glu															
			45					50					55		
ctc atc gct gat tta gaa ggg ggg gtt aag ggg ttt gct ttt gcc tct															243
Leu Ile Ala Asp Leu Glu Gly Gly Val Lys Gly Phe Ala Phe Ala Ser															
			60					65					70		
gga tta gct gga atc cac gcc gtt ttt tcc ctc ttg caa tca ggc gat															291
Gly Leu Ala Gly Ile His Ala Val Phe Ser Leu Leu Gln Ser Gly Asp															
			75					80					85		

cat	gtg	tta	ttg	ggc	gat	gat	gtt	tat	ggg	ggg	act	ttc	cgc	ttg	ttt	339
His	Val	Leu	Leu	Gly	Asp	Asp	Val	Tyr	Gly	Gly	Thr	Phe	Arg	Leu	Phe	
90					95				100						105	
aat	caa	gtg	ctt	gtc	aaa	aac	ggg	ctt	tct	tgc	acc	att	ata	gac	act	387
Asn	Gln	Val	Leu	Val	Lys	Asn	Gly	Leu	Ser	Cys	Thr	Ile	Ile	Asp	Thr	
				110					115					120		
agc	gat	ata	tcc	caa	att	aaa	aag	gct	atc	aag	ccc	aac	acc	aaa	gcc	435
Ser	Asp	Ile	Ser	Gln	Ile	Lys	Lys	Ala	Ile	Lys	Pro	Asn	Thr	Lys	Ala	
			125					130					135			
ctt	tat	tta	gaa	acc	cct	agt	aac	ccc	ttg	ctt	aaa	atc	acg	gat	tta	483
Leu	Tyr	Leu	Glu	Thr	Pro	Ser	Asn	Pro	Leu	Leu	Lys	Ile	Thr	Asp	Leu	
		140					145					150				
gcg	caa	tgc	gct	agt	gtc	gct	aaa	gat	cat	ggc	ttg	ctc	act	atc	gtg	531
Ala	Gln	Cys	Ala	Ser	Val	Ala	Lys	Asp	His	Gly	Leu	Leu	Thr	Ile	Val	
	155					160					165					
gat	aac	acc	ttt	gcc	acc	ccc	tat	tat	caa	aac	ccg	ctt	ctt	ttg	gga	579
Asp	Asn	Thr	Phe	Ala	Thr	Pro	Tyr	Tyr	Gln	Asn	Pro	Leu	Leu	Leu	Gly	
170					175					180					185	
gcg	gac	att	gtg	gca	cat	agc	ggc	acc	aaa	tac	tta	ggc	ggg	cat	agc	627
Ala	Asp	Ile	Val	Ala	His	Ser	Gly	Thr	Lys	Tyr	Leu	Gly	Gly	His	Ser	
				190					195					200		
gat	gtg	gtc	gcc	ggg	ctt	gta	acc	act	aat	aat	gaa	gcg	cta	gcc	caa	675
Asp	Val	Val	Ala	Gly	Leu	Val	Thr	Thr	Asn	Asn	Glu	Ala	Leu	Ala	Gln	
			205					210					215			
gag	atc	gct	ttt	ttc	caa	aac	gct	atc	ggc	ggg	gtt	tta	ggc	cct	caa	723
Glu	Ile	Ala	Phe	Phe	Gln	Asn	Ala	Ile	Gly	Gly	Val	Leu	Gly	Pro	Gln	
		220					225					230				
gac	agc	tgg	ctg	ttg	caa	aga	ggg	att	aaa	acg	ctg	gga	ttg	cgc	atg	771
Asp	Ser	Trp	Leu	Leu	Gln	Arg	Gly	Ile	Lys	Thr	Leu	Gly	Leu	Arg	Met	
	235					240					245					
gaa	gcc	cat	caa	aaa	aac	gct	ctt	tgt	gtg	gct	gag	ttt	tta	gaa	aaa	819
Glu	Ala	His	Gln	Lys	Asn	Ala	Leu	Cys	Val	Ala	Glu	Phe	Leu	Glu	Lys	
250					255				260						265	
cac	cct	aaa	gtg	gaa	agg	gtt	tat	tac	ccg	ggc	ctt	ccc	act	cac	cct	867
His	Pro	Lys	Val	Glu	Arg	Val	Tyr	Tyr	Pro	Gly	Leu	Pro	Thr	His	Pro	
				270					275					280		
aat	tac	gaa	cta	gct	aaa	aaa	cag	atg	cgt	ggc	ttt	agc	ggg	atg	ctc	915
Asn	Tyr	Glu	Leu	Ala	Lys	Lys	Gln	Met	Arg	Gly	Phe	Ser	Gly	Met	Leu	
			285					290					295			
tct	ttc	act	ctc	aaa	aat	gat	agc	gag	gcg	gtt	gct	ttt	gta	gaa	agc	963
Ser	Phe	Thr	Leu	Lys	Asn	Asp	Ser	Glu	Ala	Val	Ala	Phe	Val	Glu	Ser	
		300					305					310				
ctt	aaa	cta	ttc	att	tta	ggc	gag	agt	ttg	ggc	ggg	gtg	gaa	agt	ttg	1011
Leu	Lys	Leu	Phe	Ile	Leu	Gly	Glu	Ser	Leu	Gly	Gly	Val	Glu	Ser	Leu	
	315					320					325					

gtg ggg att ccg gca ttt atg acc cat gcg tgc atc cct aaa acg caa	1059
Val Gly Ile Pro Ala Phe Met Thr His Ala Cys Ile Pro Lys Thr Gln	
330 335 340 345	

cga gaa gct gct ggg att aga gat ggc ctg gtg cgc ttg tct gta ggg	1107
Arg Glu Ala Ala Gly Ile Arg Asp Gly Leu Val Arg Leu Ser Val Gly	
350 355 360	

att gag cat gaa cag gat ttg tta gaa gat tta gag caa gcg ttc gct	1155
Ile Glu His Glu Gln Asp Leu Leu Glu Asp Leu Glu Gln Ala Phe Ala	
365 370 375	

aaa ata ggc taaagttttca ttacaattta tgaataaagg agttaaaaaac	1204
Lys Ile Gly	
380	

atgaa	1209
-------	------

<210> 466

<211> 380

<212> PRT

<213> Helicobacter pylori

<400> 466

Met Arg Met Gln Thr Lys Leu Ile His Gly Gly Ile Ser Glu Asp Ala	
1 5 10 15	
Thr Thr Gly Ala Val Ser Val Pro Ile Tyr Gln Thr Ser Thr Tyr Arg	
20 25 30	
Gln Asp Ala Ile Gly Arg His Lys Gly Tyr Glu Tyr Ser Arg Ser Gly	
35 40 45	
Asn Pro Thr Arg Phe Ala Leu Glu Glu Leu Ile Ala Asp Leu Glu Gly	
50 55 60	
Gly Val Lys Gly Phe Ala Phe Ala Ser Gly Leu Ala Gly Ile His Ala	
65 70 75 80	
Val Phe Ser Leu Leu Gln Ser Gly Asp His Val Leu Leu Gly Asp Asp	
85 90 95	
Val Tyr Gly Gly Thr Phe Arg Leu Phe Asn Gln Val Leu Val Lys Asn	
100 105 110	
Gly Leu Ser Cys Thr Ile Ile Asp Thr Ser Asp Ile Ser Gln Ile Lys	
115 120 125	
Lys Ala Ile Lys Pro Asn Thr Lys Ala Leu Tyr Leu Glu Thr Pro Ser	
130 135 140	
Asn Pro Leu Leu Lys Ile Thr Asp Leu Ala Gln Cys Ala Ser Val Ala	
145 150 155 160	
Lys Asp His Gly Leu Leu Thr Ile Val Asp Asn Thr Phe Ala Thr Pro	
165 170 175	
Tyr Tyr Gln Asn Pro Leu Leu Leu Gly Ala Asp Ile Val Ala His Ser	
180 185 190	
Gly Thr Lys Tyr Leu Gly Gly His Ser Asp Val Val Ala Gly Leu Val	
195 200 205	
Thr Thr Asn Asn Glu Ala Leu Ala Gln Glu Ile Ala Phe Phe Gln Asn	
210 215 220	
Ala Ile Gly Gly Val Leu Gly Pro Gln Asp Ser Trp Leu Leu Gln Arg	
225 230 235 240	
Gly Ile Lys Thr Leu Gly Leu Arg Met Glu Ala His Gln Lys Asn Ala	
245 250 255	
Leu Cys Val Ala Glu Phe Leu Glu Lys His Pro Lys Val Glu Arg Val	
260 265 270	

Tyr	Tyr	Pro	Gly	Leu	Pro	Thr	His	Pro	Asn	Tyr	Glu	Leu	Ala	Lys	Lys
		275					280					285			
Gln	Met	Arg	Gly	Phe	Ser	Gly	Met	Leu	Ser	Phe	Thr	Leu	Lys	Asn	Asp
	290					295					300				
Ser	Glu	Ala	Val	Ala	Phe	Val	Glu	Ser	Leu	Lys	Leu	Phe	Ile	Leu	Gly
305					310					315					320
Glu	Ser	Leu	Gly	Gly	Val	Glu	Ser	Leu	Val	Gly	Ile	Pro	Ala	Phe	Met
			325						330					335	
Thr	His	Ala	Cys	Ile	Pro	Lys	Thr	Gln	Arg	Glu	Ala	Ala	Gly	Ile	Arg
		340						345					350		
Asp	Gly	Leu	Val	Arg	Leu	Ser	Val	Gly	Ile	Glu	His	Glu	Gln	Asp	Leu
	355						360					365			
Leu	Glu	Asp	Leu	Glu	Gln	Ala	Phe	Ala	Lys	Ile	Gly				
	370					375					380				

<210> 467
 <211> 912
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (46)...(873)

<400> 467
 attattaact ttttatgcta taatgcgagg gttctttcat caaga atg gtg att gac 57
 Met Val Ile Asp
 1

gag att ttt caa ata atg atg tta aga aga att aaa gta ggt tct aat 105
 Glu Ile Phe Gln Ile Met Met Leu Arg Arg Ile Lys Val Gly Ser Asn
 5 10 15 20

ttg aat aaa aaa gag agt ttg tta gat gcg ttt gtt aaa acc tat ctg 153
 Leu Asn Lys Lys Glu Ser Leu Leu Asp Ala Phe Val Lys Thr Tyr Leu
 25 30 35

cag att tta gaa ccc att agt tct aaa cgc tta aaa gag ttg gcg gac 201
 Gln Ile Leu Glu Pro Ile Ser Ser Lys Arg Leu Lys Glu Leu Ala Asp
 40 45 50

ttg aaa ata tct tgc gcg acg atc agg aat tat ttt caa atc ctt tct 249
 Leu Lys Ile Ser Cys Ala Thr Ile Arg Asn Tyr Phe Gln Ile Leu Ser
 55 60 65

aaa gag ggc atg ctt tat caa gcc cat tct agt ggc gct aga ttg ccc 297
 Lys Glu Gly Met Leu Tyr Gln Ala His Ser Ser Gly Ala Arg Leu Pro
 70 75 80

act ttt aag gcg ttt gaa aac tat tgg caa aag tcg ttg cgc ttt gaa 345
 Thr Phe Lys Ala Phe Glu Asn Tyr Trp Gln Lys Ser Leu Arg Phe Glu
 85 90 95 100

act tta aag gtg aat gaa aaa cgc cta aaa agc gcg agt gaa aat ttt 393
 Thr Leu Lys Val Asn Glu Lys Arg Leu Lys Ser Ala Ser Glu Asn Phe
 105 110 115

ggg ctt ttc acg ctg tta aaa aaa ccc agt ttg gag cgt tta gaa aga 441

Gly	Leu	Phe	Thr	Leu	Leu	Lys	Lys	Pro	Ser	Leu	Glu	Arg	Leu	Glu	Arg		
			120					125					130				
gtc	att	gag	tgc	gaa	aaa	cgc	ttt	ttg	att	ttg	gac	ttt	ttg	gcg	ttt	489	
Val	Ile	Glu	Cys	Glu	Lys	Arg	Phe	Leu	Ile	Leu	Asp	Phe	Leu	Ala	Phe		
		135					140					145					
tct	tgc	gca	ctg	ggc	tac	agc	ggt	aaa	atg	gaa	aag	ttt	tta	tta	gag	537	
Ser	Cys	Ala	Leu	Gly	Tyr	Ser	Val	Lys	Met	Glu	Lys	Phe	Leu	Leu	Glu		
	150					155					160						
ctt	gtg	ggc	aga	agc	ggt	aaa	gaa	gtg	cgc	tca	atc	gct	gct	tct	ttc	585	
Leu	Val	Gly	Arg	Ser	Val	Lys	Glu	Val	Arg	Ser	Ile	Ala	Ala	Ser	Phe		
165					170					175					180		
aat	gcg	ttg	agt	ttg	gcc	agg	caa	tta	gag	cgt	ttg	gag	tat	tcc	aac	633	
Asn	Ala	Leu	Ser	Leu	Ala	Arg	Gln	Leu	Glu	Arg	Leu	Glu	Tyr	Ser	Asn		
				185					190					195			
aca	caa	atc	aca	cgc	ttt	aat	ctg	atg	ggg	tta	aaa	acg	ctt	tta	aac	681	
Thr	Gln	Ile	Thr	Arg	Phe	Asn	Leu	Met	Gly	Leu	Lys	Thr	Leu	Leu	Asn		
			200					205					210				
agc	cct	tta	ttt	ttt	gac	att	tta	ggg	ggt	aag	ggt	tta	gag	cgt	ttg	729	
Ser	Pro	Leu	Phe	Phe	Asp	Ile	Leu	Gly	Gly	Lys	Val	Leu	Glu	Arg	Leu		
		215					220					225					
agt	aag	ggt	ttg	cat	ttt	ata	gag	cct	gat	tgc	atg	cta	gta	aca	cgc	777	
Ser	Lys	Gly	Leu	His	Phe	Ile	Glu	Pro	Asp	Cys	Met	Leu	Val	Thr	Arg		
		230				235					240						
cct	gta	gaa	ttt	caa	aac	aag	cgg	atg	caa	ctg	ctt	tgc	gtg	ggg	aaa	825	
Pro	Val	Glu	Phe	Gln	Asn	Lys	Arg	Met	Gln	Leu	Cys	Val	Gly	Lys			
245					250					255				260			
cta	gaa	tgc	gat	tat	gaa	ggg	ttt	ttt	caa	acg	att	tct	gag	gag	gaa	873	
Leu	Glu	Cys	Asp	Tyr	Glu	Gly	Phe	Phe	Gln	Thr	Ile	Ser	Glu	Glu	Glu		
				265					270					275			
taatgaaaga tgaacacaac caagaacacg atcatttaa																912	

<210> 468

<211> 276

<212> PRT

<213> Helicobacter pylori

<400> 468

Met	Val	Ile	Asp	Glu	Ile	Phe	Gln	Ile	Met	Met	Leu	Arg	Arg	Ile	Lys		
1				5				10						15			
Val	Gly	Ser	Asn	Leu	Asn	Lys	Lys	Glu	Ser	Leu	Leu	Asp	Ala	Phe	Val		
			20					25					30				
Lys	Thr	Tyr	Leu	Gln	Ile	Leu	Glu	Pro	Ile	Ser	Ser	Lys	Arg	Leu	Lys		
		35				40						45					
Glu	Leu	Ala	Asp	Leu	Lys	Ile	Ser	Cys	Ala	Thr	Ile	Arg	Asn	Tyr	Phe		
		50				55					60						
Gln	Ile	Leu	Ser	Lys	Glu	Gly	Met	Leu	Tyr	Gln	Ala	His	Ser	Ser	Gly		
65					70				75						80		
Ala	Arg	Leu	Pro	Thr	Phe	Lys	Ala	Phe	Glu	Asn	Tyr	Trp	Gln	Lys	Ser		
				85					90					95			

Leu	Arg	Phe	Glu	Thr	Leu	Lys	Val	Asn	Glu	Lys	Arg	Leu	Lys	Ser	Ala
			100					105					110		
Ser	Glu	Asn	Phe	Gly	Leu	Phe	Thr	Leu	Leu	Lys	Lys	Pro	Ser	Leu	Glu
		115					120					125			
Arg	Leu	Glu	Arg	Val	Ile	Glu	Cys	Glu	Lys	Arg	Phe	Leu	Ile	Leu	Asp
	130					135					140				
Phe	Leu	Ala	Phe	Ser	Cys	Ala	Leu	Gly	Tyr	Ser	Val	Lys	Met	Glu	Lys
145					150					155				160	
Phe	Leu	Leu	Glu	Leu	Val	Gly	Arg	Ser	Val	Lys	Glu	Val	Arg	Ser	Ile
			165					170						175	
Ala	Ala	Ser	Phe	Asn	Ala	Leu	Ser	Leu	Ala	Arg	Gln	Leu	Glu	Arg	Leu
			180					185					190		
Glu	Tyr	Ser	Asn	Thr	Gln	Ile	Thr	Arg	Phe	Asn	Leu	Met	Gly	Leu	Lys
	195						200					205			
Thr	Leu	Leu	Asn	Ser	Pro	Leu	Phe	Phe	Asp	Ile	Leu	Gly	Gly	Lys	Val
	210				215						220				
Leu	Glu	Arg	Leu	Ser	Lys	Gly	Leu	His	Phe	Ile	Glu	Pro	Asp	Cys	Met
225					230				235					240	
Leu	Val	Thr	Arg	Pro	Val	Glu	Phe	Gln	Asn	Lys	Arg	Met	Gln	Leu	Leu
				245					250					255	
Cys	Val	Gly	Lys	Leu	Glu	Cys	Asp	Tyr	Glu	Gly	Phe	Phe	Gln	Thr	Ile
		260						265					270		
Ser	Glu	Glu	Glu												
		275													

<210> 469
 <211> 720
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (50)...(685)

<400> 469
 agctcttttac tattttatta tctatctttt attaaaaaaaaa cttgttatc atg ata aac 58
 Met Ile Asn
 1

atg aac aca cac aca aga ggc att gac agc aat ctg att cat tcg ctc 106
 Met Asn Thr His Thr Arg Gly Ile Asp Ser Asn Leu Ile His Ser Leu
 5 10 15

caa agc att tca tta tcc atg ttt aga aag ggt ttt ttt ggg ctt tat 154
 Gln Ser Ile Ser Leu Ser Met Phe Arg Lys Gly Phe Phe Gly Leu Tyr
 20 25 30 35

caa ggc tct att tca gca cgc att ggc gca aat caa ttt gtg atc aac 202
 Gln Gly Ser Ile Ser Ala Arg Ile Gly Ala Asn Gln Phe Val Ile Asn
 40 45 50

aaa aga aac gct gtt ttt gat caa ttg aat gaa aac acc tta ctg gtt 250
 Lys Arg Asn Ala Val Phe Asp Gln Leu Asn Glu Asn Thr Leu Leu Val
 55 60 65

ttg cat gac aaa ata gat tac cgc tgg aaa gaa gcg agc ttg gat tcg 298
 Leu His Asp Lys Ile Asp Tyr Arg Trp Lys Glu Ala Ser Leu Asp Ser
 70 75 80

ccc att cat gcg agc gtg tat agg gag ttt ttg gac gct aaa ttc atc	346
Pro Ile His Ala Ser Val Tyr Arg Glu Phe Leu Asp Ala Lys Phe Ile	
85 90 95	
gct tac gcg cgc cct cct tat agt ttg gcg tat tcc ttg cgc cac aac	394
Ala Tyr Ala Arg Pro Pro Tyr Ser Leu Ala Tyr Ser Leu Arg His Asn	
100 105 110 115	
cga ttg ctc cct aga gat tat tta ggg tat cgt tct ttg ggc gaa gaa	442
Arg Leu Leu Pro Arg Asp Tyr Leu Gly Tyr Arg Ser Leu Gly Glu Glu	
120 125 130	
att tcc att ttt aac ccc aaa gac tat gac agc tgg caa gaa aga gcg	490
Ile Ser Ile Phe Asn Pro Lys Asp Tyr Asp Ser Trp Gln Glu Arg Ala	
135 140 145	
gat aca gaa att tta cgc caa ctg caa gag agc aaa aaa tat ttt gtt	538
Asp Thr Glu Ile Leu Arg Gln Leu Gln Glu Ser Lys Lys Tyr Phe Val	
150 155 160	
ttc att aag ggg tgt ggg att ttt gcc tac cac aga gag ctt tct aaa	586
Phe Ile Lys Gly Cys Gly Ile Phe Ala Tyr His Arg Glu Leu Ser Lys	
165 170 175	
ctc atg gaa gtt ttt gat ttg att gaa aac tca tgc aag gtt tta cga	634
Leu Met Glu Val Phe Asp Leu Ile Glu Asn Ser Cys Lys Val Leu Arg	
180 185 190 195	
ttg ggc gat tta atg gat tat tgc tat aat gat gat cca cga ttg agc	682
Leu Gly Asp Leu Met Asp Tyr Cys Tyr Asn Asp Asp Pro Arg Leu Ser	
200 205 210	
gtg taaaaagcta aaaaggataa aacatgacca tcaac	720
Val	

<210> 470

<211> 212

<212> PRT

<213> *Helicobacter pylori*

<400> 470

Met Ile Asn Met Asn Thr His Thr Arg Gly Ile Asp Ser Asn Leu Ile	
1 5 10 15	
His Ser Leu Gln Ser Ile Ser Leu Ser Met Phe Arg Lys Gly Phe Phe	
20 25 30	
Gly Leu Tyr Gln Gly Ser Ile Ser Ala Arg Ile Gly Ala Asn Gln Phe	
35 40 45	
Val Ile Asn Lys Arg Asn Ala Val Phe Asp Gln Leu Asn Glu Asn Thr	
50 55 60	
Leu Leu Val Leu His Asp Lys Ile Asp Tyr Arg Trp Lys Glu Ala Ser	
65 70 75 80	
Leu Asp Ser Pro Ile His Ala Ser Val Tyr Arg Glu Phe Leu Asp Ala	
85 90 95	
Lys Phe Ile Ala Tyr Ala Arg Pro Pro Tyr Ser Leu Ala Tyr Ser Leu	
100 105 110	
Arg His Asn Arg Leu Leu Pro Arg Asp Tyr Leu Gly Tyr Arg Ser Leu	

Gly	Lys	Thr	Glu	Leu	Ile	His	Tyr	Ile	Lys	Ser	Cys	Leu	Ala	Ser	Leu		
				125					130					135			
ttt	acc	gat	aga	gcg	att	agc	tat	agg	gcg	agt	cgt	ggg	ttt	gat	cat	546	
Phe	Thr	Asp	Arg	Ala	Ile	Ser	Tyr	Arg	Ala	Ser	Arg	Gly	Phe	Asp	His		
			140					145					150				
tta	aaa	gtc	gcg	ctc	agc	gtg	ggg	gtg	caa	aaa	atg	gtg	cga	gcg	gat	594	
Leu	Lys	Val	Ala	Leu	Ser	Val	Gly	Val	Gln	Lys	Met	Val	Arg	Ala	Asp		
		155					160					165					
aaa	ggc	agc	gcg	ggc	gtg	atg	ttt	tct	att	gac	acc	gaa	acc	ggg	ttt	642	
Lys	Gly	Ser	Ala	Gly	Val	Met	Phe	Ser	Ile	Asp	Thr	Glu	Thr	Gly	Phe		
	170					175				180							
aaa	gac	gcg	gtg	ttt	atc	act	tca	gcg	tgg	ggg	tta	ggc	gaa	aat	gtg	690	
Lys	Asp	Ala	Val	Phe	Ile	Thr	Ser	Ala	Trp	Gly	Leu	Gly	Glu	Asn	Val		
	185				190				195						200		
gtg	ggg	ggc	acg	ata	aac	cct	gat	gaa	ttt	tat	gtg	ttt	aag	ccc	act	738	
Val	Gly	Gly	Thr	Ile	Asn	Pro	Asp	Glu	Phe	Tyr	Val	Phe	Lys	Pro	Thr		
			205					210					215				
tta	gag	caa	aac	aaa	cgc	ccc	att	atc	aaa	cgc	caa	ctc	ggc	aat	aaa	786	
Leu	Glu	Gln	Asn	Lys	Arg	Pro	Ile	Ile	Lys	Arg	Gln	Leu	Gly	Asn	Lys		
			220				225					230					
acg	caa	aaa	atg	gtc	tat	gcc	cca	agg	ggg	agc	gaa	cac	ccc	acc	aga	834	
Thr	Gln	Lys	Met	Val	Tyr	Ala	Pro	Arg	Gly	Ser	Glu	His	Pro	Thr	Arg		
		235				240					245						
aac	att	aaa	acc	acc	aaa	aaa	gaa	tgg	caa	tcc	ttt	tca	ttg	agc	gat	882	
Asn	Ile	Lys	Thr	Thr	Lys	Lys	Glu	Trp	Gln	Ser	Phe	Ser	Leu	Ser	Asp		
	250					255				260							
gaa	gac	gtg	ctg	att	tta	gcc	aaa	tac	gcc	att	gaa	att	gaa	aaa	cac	930	
Glu	Asp	Val	Leu	Ile	Leu	Ala	Lys	Tyr	Ala	Ile	Glu	Ile	Glu	Lys	His		
	265			270				275							280		
tac	tct	aaa	gaa	gcc	aaa	caa	tac	cgc	cct	atg	gat	ata	gaa	tgg	gct	978	
Tyr	Ser	Lys	Glu	Ala	Lys	Gln	Tyr	Arg	Pro	Met	Asp	Ile	Glu	Trp	Ala		
			285					290					295				
aaa	gat	ggc	gag	agc	ggg	gaa	atc	ttt	atc	gtt	caa	gcg	cgc	cca	gaa	1026	
Lys	Asp	Gly	Glu	Ser	Gly	Glu	Ile	Phe	Ile	Val	Gln	Ala	Arg	Pro	Glu		
		300					305					310					
acc	gtt	caa	agc	caa	aaa	agt	aaa	gaa	gaa	agt	caa	gtc	ttt	gaa	aaa	1074	
Thr	Val	Gln	Ser	Gln	Lys	Ser	Lys	Glu	Glu	Ser	Gln	Val	Phe	Glu	Lys		
		315				320					325						
ttc	aaa	ttc	aaa	aac	cct	aac	gaa	aag	aaa	gag	att	atc	tta	caa	ggc	1122	
Phe	Lys	Phe	Lys	Asn	Pro	Asn	Glu	Lys	Lys	Glu	Ile	Ile	Leu	Gln	Gly		
	330				335					340							
aga	gcg	att	ggg	agt	aaa	att	ggc	tca	gga	aaa	gtg	cgc	atc	atc	aat	1170	
Arg	Ala	Ile	Gly	Ser	Lys	Ile	Gly	Ser	Gly	Lys	Val	Arg	Ile	Ile	Asn		
	345				350				355						360		

gat ttg gag cac atg aat tct ttt aaa gag ggc gaa att tta gtt acg	1218
Asp Leu Glu His Met Asn Ser Phe Lys Glu Gly Glu Ile Leu Val Thr	
365 370 375	
gat aac acc gat ccg gac tgg gag cct tgc atg aaa aaa gcg agc gcg	1266
Asp Asn Thr Asp Pro Asp Trp Glu Pro Cys Met Lys Lys Ala Ser Ala	
380 385 390	
gtt atc act aat cgt gga ggg cgc act tgc cat gcc gct att gtg gcg	1314
Val Ile Thr Asn Arg Gly Gly Arg Thr Cys His Ala Ala Ile Val Ala	
395 400 405	
aga gaa att ggc gtg cca gct atc gtt ggg gtg agc ggg gcg act gat	1362
Arg Glu Ile Gly Val Pro Ala Ile Val Gly Val Ser Gly Ala Thr Asp	
410 415 420	
agc ctt tat acc ggc atg gaa atc acg gtt tct tgc gct gag ggc gaa	1410
Ser Leu Tyr Thr Gly Met Glu Ile Thr Val Ser Cys Ala Glu Gly Glu	
425 430 435 440	
gag ggc tat gtg tat gcg ggc att tat gag cat gaa att gaa agg gtg	1458
Glu Gly Tyr Val Tyr Ala Gly Ile Tyr Glu His Glu Ile Glu Arg Val	
445 450 455	
gag ctt tct aac atg caa gaa act caa aca aaa att tac atc aat att	1506
Glu Leu Ser Asn Met Gln Glu Thr Gln Thr Lys Ile Tyr Ile Asn Ile	
460 465 470	
gga aac cct gaa aaa gcc ttt ggc ttt tct caa ctc cct aat cac ggc	1554
Gly Asn Pro Glu Lys Ala Phe Gly Phe Ser Gln Leu Pro Asn His Gly	
475 480 485	
gta ggg cta gcc agg atg gaa atg att att tta aat caa atc aaa gcc	1602
Val Gly Leu Ala Arg Met Glu Met Ile Ile Leu Asn Gln Ile Lys Ala	
490 495 500	
cac cct tta gct tta gtg gat ttg cac cac aaa aaa agc gtg aaa gaa	1650
His Pro Leu Ala Leu Val Asp Leu His His Lys Lys Ser Val Lys Glu	
505 510 515 520	
aaa aat gaa att gaa aac ctc atg gca ggc tat gct aac cct aaa gat	1698
Lys Asn Glu Ile Glu Asn Leu Met Ala Gly Tyr Ala Asn Pro Lys Asp	
525 530 535	
ttt ttt gtg aaa aaa atc gct gaa ggc att ggc atg atc agt gca gcg	1746
Phe Phe Val Lys Lys Ile Ala Glu Gly Ile Gly Met Ile Ser Ala Ala	
540 545 550	
ttt tac cct aaa cct gtc att gtg aga acg agc gat ttc aaa tcc aat	1794
Phe Tyr Pro Lys Pro Val Ile Val Arg Thr Ser Asp Phe Lys Ser Asn	
555 560 565	
gaa tac atg cgc atg ctt ggc ggc tct agc tat gag cct aat gaa gaa	1842
Glu Tyr Met Arg Met Leu Gly Gly Ser Ser Tyr Glu Pro Asn Glu Glu	
570 575 580	
aac ccc atg ctt ggc tat agg ggg gct agt cgg tat tat tca gag agc	1890
Asn Pro Met Leu Gly Tyr Arg Gly Ala Ser Arg Tyr Tyr Ser Glu Ser	
585 590 595 600	

tat aat gaa gcg ttt tcg tgg gag tgt gaa gcc tta gcg tta gtg agg	1938
Tyr Asn Glu Ala Phe Ser Trp Glu Cys Glu Ala Leu Ala Leu Val Arg	
605 610 615	
gaa gaa atg gga tta acc aac atg aaa gtg atg atc cct ttt ttg cga	1986
Glu Glu Met Gly Leu Thr Asn Met Lys Val Met Ile Pro Phe Leu Arg	
620 625 630	
acc att gaa gag ggt aaa aaa gtc cta gaa atc tta aga aaa aac aat	2034
Thr Ile Glu Glu Gly Lys Lys Val Leu Glu Ile Leu Arg Lys Asn Asn	
635 640 645	
tta gaa tcc ggt aaa aac ggg ctt gaa att tat atc atg tgc gaa ttg	2082
Leu Glu Ser Gly Lys Asn Gly Leu Glu Ile Tyr Ile Met Cys Glu Leu	
650 655 660	
ccg gtg aat gtc att ttg gct gat gat ttc ttg agc ttg ttt gat ggc	2130
Pro Val Asn Val Ile Leu Ala Asp Asp Phe Leu Ser Leu Phe Asp Gly	
665 670 675 680	
ttt tct att gga tca aac gat tta acc cag ctc act tta ggc gtg gat	2178
Phe Ser Ile Gly Ser Asn Asp Leu Thr Gln Leu Thr Leu Gly Val Asp	
685 690 695	
aga gac agc gaa ttg gtc agc cat gtc ttt gat gaa agg aat gaa gcg	2226
Arg Asp Ser Glu Leu Val Ser His Val Phe Asp Glu Arg Asn Glu Ala	
700 705 710	
atg cta aag atg ttt aaa aaa gcg att gaa gct tgc aaa agg cac aac	2274
Met Leu Lys Met Phe Lys Lys Ala Ile Glu Ala Cys Lys Arg His Asn	
715 720 725	
aaa tat tgc ggg att tgc ggg caa gcc cca agc gat tac cct gaa gta	2322
Lys Tyr Cys Gly Ile Cys Gly Gln Ala Pro Ser Asp Tyr Pro Glu Val	
730 735 740	
aca gag ttt tta gtc aaa gag ggc atc act tcc att tct tta aac cct	2370
Thr Glu Phe Leu Val Lys Glu Gly Ile Thr Ser Ile Ser Leu Asn Pro	
745 750 755 760	
gat agc gtg atc ccc act tgg aac gct gta gcc aag tta gaa aaa gaa	2418
Asp Ser Val Ile Pro Thr Trp Asn Ala Val Ala Lys Leu Glu Lys Glu	
765 770 775	
cta aaa gaa cat ggc tta act gaa cat tgataataaaa taaatcaatc	2465
Leu Lys Glu His Gly Leu Thr Glu His	
780 785	
taacttgagt ggatttttcg tattagtttc cat	2498
<210> 472	
<211> 785	
<212> PRT	
<213> Helicobacter pylori	
<400> 472	
Met Phe Gln Glu Leu Val Pro Ile Gly Ile Lys Val Pro Asp Gly Phe	
1 5 10 15	

Ala	Ile	Thr	Ser	Glu	Ala	Tyr	Trp	Tyr	Leu	Leu	Glu	Gln	Gly	Gly	Ala	
			20					25					30			
Lys	Gln	Lys	Ile	Ile	Glu	Leu	Leu	Glu	Asn	Val	Asp	Ala	Thr	Glu	Ile	
		35					40					45				
Asp	Val	Leu	Lys	Ile	Arg	Ser	Lys	Gln	Ile	Arg	Glu	Leu	Ile	Phe	Gly	
	50					55					60					
Thr	Pro	Phe	Pro	Ser	Asp	Leu	Arg	Asp	Glu	Ile	Phe	Gln	Ala	Tyr	Glu	
65					70					75					80	
Ile	Leu	Ser	Gln	Gln	Tyr	His	Met	Lys	Glu	Ala	Asp	Val	Ala	Val	Arg	
			85						90					95		
Ser	Ser	Ala	Thr	Ala	Glu	Asp	Leu	Pro	Asp	Ala	Ser	Phe	Ala	Gly	Gln	
		100						105					110			
Gln	Asp	Thr	Tyr	Leu	Asn	Ile	Lys	Gly	Lys	Thr	Glu	Leu	Ile	His	Tyr	
	115						120					125				
Ile	Lys	Ser	Cys	Leu	Ala	Ser	Leu	Phe	Thr	Asp	Arg	Ala	Ile	Ser	Tyr	
	130					135					140					
Arg	Ala	Ser	Arg	Gly	Phe	Asp	His	Leu	Lys	Val	Ala	Leu	Ser	Val	Gly	
145					150					155					160	
Val	Gln	Lys	Met	Val	Arg	Ala	Asp	Lys	Gly	Ser	Ala	Gly	Val	Met	Phe	
			165						170					175		
Ser	Ile	Asp	Thr	Glu	Thr	Gly	Phe	Lys	Asp	Ala	Val	Phe	Ile	Thr	Ser	
		180						185					190			
Ala	Trp	Gly	Leu	Gly	Glu	Asn	Val	Val	Gly	Gly	Thr	Ile	Asn	Pro	Asp	
	195						200					205				
Glu	Phe	Tyr	Val	Phe	Lys	Pro	Thr	Leu	Glu	Gln	Asn	Lys	Arg	Pro	Ile	
	210					215					220					
Ile	Lys	Arg	Gln	Leu	Gly	Asn	Lys	Thr	Gln	Lys	Met	Val	Tyr	Ala	Pro	
225					230					235					240	
Arg	Gly	Ser	Glu	His	Pro	Thr	Arg	Asn	Ile	Lys	Thr	Thr	Lys	Lys	Glu	
				245				250						255		
Trp	Gln	Ser	Phe	Ser	Leu	Ser	Asp	Glu	Asp	Val	Leu	Ile	Leu	Ala	Lys	
		260						265					270			
Tyr	Ala	Ile	Glu	Ile	Glu	Lys	His	Tyr	Ser	Lys	Glu	Ala	Lys	Gln	Tyr	
	275						280					285				
Arg	Pro	Met	Asp	Ile	Glu	Trp	Ala	Lys	Asp	Gly	Glu	Ser	Gly	Glu	Ile	
	290					295					300					
Phe	Ile	Val	Gln	Ala	Arg	Pro	Glu	Thr	Val	Gln	Ser	Gln	Lys	Ser	Lys	
305					310					315					320	
Glu	Glu	Ser	Gln	Val	Phe	Glu	Lys	Phe	Lys	Phe	Lys	Asn	Pro	Asn	Glu	
				325					330					335		
Lys	Lys	Glu	Ile	Ile	Leu	Gln	Gly	Arg	Ala	Ile	Gly	Ser	Lys	Ile	Gly	
		340						345					350			
Ser	Gly	Lys	Val	Arg	Ile	Ile	Asn	Asp	Leu	Glu	His	Met	Asn	Ser	Phe	
	355						360					365				
Lys	Glu	Gly	Glu	Ile	Leu	Val	Thr	Asp	Asn	Thr	Asp	Pro	Asp	Trp	Glu	
	370					375					380					
Pro	Cys	Met	Lys	Lys	Ala	Ser	Ala	Val	Ile	Thr	Asn	Arg	Gly	Gly	Arg	
385					390					395					400	
Thr	Cys	His	Ala	Ala	Ile	Val	Ala	Arg	Glu	Ile	Gly	Val	Pro	Ala	Ile	
				405					410					415		
Val	Gly	Val	Ser	Gly	Ala	Thr	Asp	Ser	Leu	Tyr	Thr	Gly	Met	Glu	Ile	
			420					425					430			
Thr	Val	Ser	Cys	Ala	Glu	Gly	Glu	Glu	Gly	Tyr	Val	Tyr	Ala	Gly	Ile	
	435						440					445				
Tyr	Glu	His	Glu	Ile	Glu	Arg	Val	Glu	Leu	Ser	Asn	Met	Gln	Glu	Thr	
	450					455					460					
Gln	Thr	Lys	Ile	Tyr	Ile	Asn	Ile	Gly	Asn	Pro	Glu	Lys	Ala	Phe	Gly	
465					470					475					480	
Phe	Ser	Gln	Leu	Pro	Asn	His	Gly	Val	Gly	Leu	Ala	Arg	Met	Glu	Met	

				485					490					495			
Ile	Ile	Leu	Asn	Gln	Ile	Lys	Ala	His	Pro	Leu	Ala	Leu	Val	Asp	Leu		
			500					505					510				
His	His	Lys	Lys	Ser	Val	Lys	Glu	Lys	Asn	Glu	Ile	Glu	Asn	Leu	Met		
		515					520					525					
Ala	Gly	Tyr	Ala	Asn	Pro	Lys	Asp	Phe	Phe	Val	Lys	Lys	Ile	Ala	Glu		
	530					535					540						
Gly	Ile	Gly	Met	Ile	Ser	Ala	Ala	Phe	Tyr	Pro	Lys	Pro	Val	Ile	Val		
545					550					555					560		
Arg	Thr	Ser	Asp	Phe	Lys	Ser	Asn	Glu	Tyr	Met	Arg	Met	Leu	Gly	Gly		
			565						570					575			
Ser	Ser	Tyr	Glu	Pro	Asn	Glu	Glu	Asn	Pro	Met	Leu	Gly	Tyr	Arg	Gly		
			580					585					590				
Ala	Ser	Arg	Tyr	Tyr	Ser	Glu	Ser	Tyr	Asn	Glu	Ala	Phe	Ser	Trp	Glu		
		595					600					605					
Cys	Glu	Ala	Leu	Ala	Leu	Val	Arg	Glu	Glu	Met	Gly	Leu	Thr	Asn	Met		
	610					615					620						
Lys	Val	Met	Ile	Pro	Phe	Leu	Arg	Thr	Ile	Glu	Glu	Gly	Lys	Lys	Val		
625					630					635					640		
Leu	Glu	Ile	Leu	Arg	Lys	Asn	Asn	Leu	Glu	Ser	Gly	Lys	Asn	Gly	Leu		
			645						650					655			
Glu	Ile	Tyr	Ile	Met	Cys	Glu	Leu	Pro	Val	Asn	Val	Ile	Leu	Ala	Asp		
			660					665					670				
Asp	Phe	Leu	Ser	Leu	Phe	Asp	Gly	Phe	Ser	Ile	Gly	Ser	Asn	Asp	Leu		
		675					680					685					
Thr	Gln	Leu	Thr	Leu	Gly	Val	Asp	Arg	Asp	Ser	Glu	Leu	Val	Ser	His		
	690				695						700						
Val	Phe	Asp	Glu	Arg	Asn	Glu	Ala	Met	Leu	Lys	Met	Phe	Lys	Lys	Ala		
705					710					715					720		
Ile	Glu	Ala	Cys	Lys	Arg	His	Asn	Lys	Tyr	Cys	Gly	Ile	Cys	Gly	Gln		
			725						730					735			
Ala	Pro	Ser	Asp	Tyr	Pro	Glu	Val	Thr	Glu	Phe	Leu	Val	Lys	Glu	Gly		
			740					745					750				
Ile	Thr	Ser	Ile	Ser	Leu	Asn	Pro	Asp	Ser	Val	Ile	Pro	Thr	Trp	Asn		
		755					760					765					
Ala	Val	Ala	Lys	Leu	Glu	Lys	Glu	Leu	Lys	Glu	His	Gly	Leu	Thr	Glu		
	770					775					780						
His																	
785																	

<210> 473
 <211> 565
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (61)...(483)

<400> 473
 gttatcttta atcaatcaga tgatagaatt tatcttttat ttttgaattg ggagcatttg 60
 atg aaa aaa tta gcg gtt tct tta tta ttt aca ggg act ttt ttg ggg 108
 Met Lys Lys Leu Ala Val Ser Leu Leu Phe Thr Gly Thr Phe Leu Gly
 1 5 10 15
 ctt ttt ttg aat gcg agc gat ttt aag agc atg gat gac aag caa cta 156
 Leu Phe Leu Asn Ala Ser Asp Phe Lys Ser Met Asp Asp Lys Gln Leu
 20 25 30

tta gag caa gca ggg aaa gtt gct cct agc gaa gtc cct gag ttt cgc	204
Leu Glu Gln Ala Gly Lys Val Ala Pro Ser Glu Val Pro Glu Phe Arg	
35 40 45	
gcg gaa gtc aat aag cga tta gca gtg atg aaa gaa gaa gat cgt aaa	252
Ala Glu Val Asn Lys Arg Leu Ala Val Met Lys Glu Glu Asp Arg Lys	
50 55 60	
aat tat aaa gcg gat ttt aag aaa gcg atg gat aag aat tta gct tct	300
Asn Tyr Lys Ala Asp Phe Lys Lys Ala Met Asp Lys Asn Leu Ala Ser	
65 70 75 80	
tta agc caa gaa gat cgc aac aag cgt aaa aaa gaa att ctt gaa gcg	348
Leu Ser Gln Glu Asp Arg Asn Lys Arg Lys Lys Glu Ile Leu Glu Ala	
85 90 95	
att gct aac aaa aag aaa aca atg acc atg aaa gaa tat cgt gaa gaa	396
Ile Ala Asn Lys Lys Lys Thr Met Thr Met Lys Glu Tyr Arg Glu Glu	
100 105 110	
ggg ttg gat ttg cat gat tgc gca tgc gaa ggc cct ttt cat gat cat	444
Gly Leu Asp Leu His Asp Cys Ala Cys Glu Gly Pro Phe His Asp His	
115 120 125	
gag aga aaa aaa ggg aaa aaa cca agc cat cat aag cat tagcgcttag	493
Glu Arg Lys Lys Gly Lys Lys Pro Ser His His Lys His	
130 135 140	
ggtgtgctaa ctttttttga tttttgtgaa accacgccgt aagtccttag cttttggctg	553
tggggattaa gg	565

<210> 474

<211> 141

<212> PRT

<213> Helicobacter pylori

<400> 474

Met Lys Lys Leu Ala Val Ser Leu Leu Phe Thr Gly Thr Phe Leu Gly	
1 5 10 15	
Leu Phe Leu Asn Ala Ser Asp Phe Lys Ser Met Asp Asp Lys Gln Leu	
20 25 30	
Leu Glu Gln Ala Gly Lys Val Ala Pro Ser Glu Val Pro Glu Phe Arg	
35 40 45	
Ala Glu Val Asn Lys Arg Leu Ala Val Met Lys Glu Glu Asp Arg Lys	
50 55 60	
Asn Tyr Lys Ala Asp Phe Lys Lys Ala Met Asp Lys Asn Leu Ala Ser	
65 70 75 80	
Leu Ser Gln Glu Asp Arg Asn Lys Arg Lys Lys Glu Ile Leu Glu Ala	
85 90 95	
Ile Ala Asn Lys Lys Lys Thr Met Thr Met Lys Glu Tyr Arg Glu Glu	
100 105 110	
Gly Leu Asp Leu His Asp Cys Ala Cys Glu Gly Pro Phe His Asp His	
115 120 125	
Glu Arg Lys Lys Gly Lys Lys Pro Ser His His Lys His	
130 135 140	

<210> 475

```
<211> 558
<212> DNA
<213> Helicobacter pylori
```

<400> 475

aaa tta gaa gta ggg caa tta gcc cct gat ttt aga ttg aaa aac agc 104
Lys Leu Glu Val Gly Gln Leu Ala Pro Asp Phe Arg Leu Lys Asn Ser
5 10 15

ctg tat ttc tac cct aaa gac aac acc ccc gga tgc act cta gaa gcc 200
Leu Tyr Phe Tyr Pro Lys Asp Asn Thr Pro Gly Cys Thr Leu Glu Ala
35 40 45 50

gtc gta ggc ata agc cct gat aac gcg caa tcg cat caa aaa ttt atc 296
Val Val Gly Ile Ser Pro Asp Asn Ala Gln Ser His Gln Lys Phe Ile
70 75 80

gcc gcc aat ctt tac aaa gct tat ggc aaa cgc atg ctt tat ggg aag 392
Ala Ala Asn Leu Tyr Lys Ala Tyr Gly Lys Arg Met Leu Tyr Gly Lys
100 105 110

ggt tta gaa aaa tgt ttc tac aat gtc aaa gcg aaa ggc cat gct caa 488
Val Leu Glu Lys Cys Phe Tyr Asn Val Lys Ala Lys Gly His Ala Gln
135 140 145

aatttgaqat tttttaqcca tt 558

<400> 476

Met	Glu	Lys	Leu	Glu	Val	Gly	Gln	Leu	Ala	Pro	Asp	Phe	Arg	Leu	Lys
1				5					10					15	
Asn	Ser	Asp	Gly	Val	Glu	Ile	Ser	Leu	Lys	Asp	Leu	Leu	His	Lys	Lys
			20					25					30		
Val	Val	Leu	Tyr	Phe	Tyr	Pro	Lys	Asp	Asn	Thr	Pro	Gly	Cys	Thr	Leu
		35					40					45			
Glu	Ala	Lys	Asp	Phe	Ser	Ala	Leu	Phe	Ser	Glu	Phe	Glu	Lys	Lys	Asn
	50					55					60				
Ala	Val	Val	Val	Gly	Ile	Ser	Pro	Asp	Asn	Ala	Gln	Ser	His	Gln	Lys
65					70					75					80
Phe	Ile	Ser	Gln	Cys	Ser	Leu	Asn	Val	Ile	Leu	Leu	Cys	Asp	Glu	Asp
			85					90						95	
Lys	Lys	Ala	Ala	Asn	Leu	Tyr	Lys	Ala	Tyr	Gly	Lys	Arg	Met	Leu	Tyr
			100					105					110		
Gly	Lys	Glu	His	Leu	Gly	Ile	Ile	Arg	Ser	Thr	Phe	Ile	Ile	Asn	Thr
		115					120					125			
Gln	Gly	Val	Leu	Glu	Lys	Cys	Phe	Tyr	Asn	Val	Lys	Ala	Lys	Gly	His
	130					135					140				
Ala	Gln	Lys	Val	Leu	Glu	Ser	Leu								
145					150										

<210> 477

<211> 700

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (19)...(651)

<400> 477

acttagaagg	ggtgattt	atg	agt	aaa	gag	ctt	att	tta	aag	cgc	att	aaa		51
		Met	Ser	Lys	Glu	Leu	Ile	Leu	Lys	Arg	Ile	Lys		
		1				5					10			
gaa gcc aga gcc aag cat gcc att cag gga gcg aac cct att tat agg														99
Glu Ala Arg Ala Lys His Ala Ile Gln Gly Ala Asn Pro Ile Tyr Arg														
	15					20					25			
aat atc att aaa gtg gag ttt gag gac ttg gtg gaa gaa tac aag cat														147
Asn Ile Ile Lys Val Glu Phe Glu Asp Leu Val Glu Glu Tyr Lys His														
	30					35					40			
ttc caa gtg ttg aat aaa gct gaa gtc att gaa agc gct aaa gaa aat														195
Phe Gln Val Leu Asn Lys Ala Glu Val Ile Glu Ser Ala Lys Glu Asn														
	45					50					55			
tta gag caa gcc att tta aag gct tta gaa aat ttt aaa agc aaa aaa														243
Leu Glu Gln Ala Ile Leu Lys Ala Leu Glu Asn Phe Lys Ser Lys Lys														
	60				65				70					75
atc tta cac tcc aca gat ttg aat ttg aat ttt gaa gcg ttt aag gat														291
Ile Leu His Ser Thr Asp Leu Asn Leu Asn Phe Glu Ala Phe Lys Asp														
			80					85					90	
ttt act tta cag cct tat gat aaa gaa att gaa gcg atg cgt gaa gag														339
Phe Thr Leu Gln Pro Tyr Asp Lys Glu Ile Glu Ala Met Arg Glu Glu														

95					100					105						
ttg	ttt	gag	att	gat	acg	gct	tta	ttg	cat	ggg	gtt	tgt	ggg	att	tca	387
Leu	Phe	Glu	Ile	Asp	Thr	Ala	Leu	Leu	His	Gly	Val	Cys	Gly	Ile	Ser	
		110					115					120				
agc	ttg	ggc	atg	att	ggg	gcg	gtc	tct	tcg	cat	gca	agc	ccg	cga	ttg	435
Ser	Leu	Gly	Met	Ile	Gly	Ala	Val	Ser	Ser	His	Ala	Ser	Pro	Arg	Leu	
	125					130					135					
ctt	tcg	ctc	atc	acc	ctt	aat	tgc	atc	atc	tta	ttg	aaa	aaa	gaa	tcc	483
Leu	Ser	Leu	Ile	Thr	Leu	Asn	Cys	Ile	Ile	Leu	Leu	Lys	Lys	Glu	Ser	
140					145					150					155	
att	gtg	cgc	aat	ttg	agt	gaa	ggc	atg	caa	gct	tta	aaa	aac	caa	agc	531
Ile	Val	Arg	Asn	Leu	Ser	Glu	Gly	Met	Gln	Ala	Leu	Lys	Asn	Gln	Ser	
			160						165					170		
caa	aac	ggt	gca	tta	ccc	aca	aac	atg	ctc	ctt	att	ggc	ggg	cct	agc	579
Gln	Asn	Gly	Ala	Leu	Pro	Thr	Asn	Met	Leu	Leu	Ile	Gly	Gly	Pro	Ser	
		175						180					185			
cgg	aca	gct	gac	att	gaa	tta	aaa	acc	gtt	ttt	ggg	gtg	cat	ggg	cct	627
Arg	Thr	Ala	Asp	Ile	Glu	Leu	Lys	Thr	Val	Phe	Gly	Val	His	Gly	Pro	
		190					195				200					
caa	aaa	gtc	gct	atc	att	ctc	tac	taaaggataa	gaatggaaaa	attagaagta						681
Gln	Lys	Val	Ala	Ile	Ile	Leu	Tyr									
	205					210										

gggcaattag cccctgatt 700

<210> 478

<211> 211

<212> PRT

<213> Helicobacter pylori

<400> 478

Met	Ser	Lys	Glu	Leu	Ile	Leu	Lys	Arg	Ile	Lys	Glu	Ala	Arg	Ala	Lys	
1				5					10					15		
His	Ala	Ile	Gln	Gly	Ala	Asn	Pro	Ile	Tyr	Arg	Asn	Ile	Ile	Lys	Val	
		20						25					30			
Glu	Phe	Glu	Asp	Leu	Val	Glu	Glu	Tyr	Lys	His	Phe	Gln	Val	Leu	Asn	
	35					40						45				
Lys	Ala	Glu	Val	Ile	Glu	Ser	Ala	Lys	Glu	Asn	Leu	Glu	Gln	Ala	Ile	
	50					55					60					
Leu	Lys	Ala	Leu	Glu	Asn	Phe	Lys	Ser	Lys	Lys	Ile	Leu	His	Ser	Thr	
65					70				75					80		
Asp	Leu	Asn	Leu	Asn	Phe	Glu	Ala	Phe	Lys	Asp	Phe	Thr	Leu	Gln	Pro	
		85						90					95			
Tyr	Asp	Lys	Glu	Ile	Glu	Ala	Met	Arg	Glu	Glu	Leu	Phe	Glu	Ile	Asp	
		100					105						110			
Thr	Ala	Leu	Leu	His	Gly	Val	Cys	Gly	Ile	Ser	Ser	Leu	Gly	Met	Ile	
	115					120						125				
Gly	Ala	Val	Ser	Ser	His	Ala	Ser	Pro	Arg	Leu	Leu	Ser	Leu	Ile	Thr	
	130					135					140					
Leu	Asn	Cys	Ile	Ile	Leu	Leu	Lys	Lys	Glu	Ser	Ile	Val	Arg	Asn	Leu	
145					150				155					160		
Ser	Glu	Gly	Met	Gln	Ala	Leu	Lys	Asn	Gln	Ser	Gln	Asn	Gly	Ala	Leu	

				165					170					175			
Pro	Thr	Asn	Met	Leu	Leu	Ile	Gly	Gly	Pro	Ser	Arg	Thr	Ala	Asp	Ile		
			180					185					190				
Glu	Leu	Lys	Thr	Val	Phe	Gly	Val	His	Gly	Pro	Gln	Lys	Val	Ala	Ile		
		195					200					205					
Ile	Leu	Tyr															
	210																

<210> 479
 <211> 571
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (52)...(531)

<400> 479 tattccaata acgactaccc tattatatttg cctagcgggtt catgcacagg g atg atg <div style="text-align: right; margin-right: 50px;">Met Met</div> <div style="text-align: right; margin-right: 50px;">1</div>															57
cgg cat gat tat ttg gaa ttg ttt gaa ggg cat gcg gaa ttc aac atg Arg His Asp Tyr Leu Glu Leu Phe Glu Gly His Ala Glu Phe Asn Met <div style="text-align: right; margin-right: 50px;">5</div> <div style="text-align: right; margin-right: 50px;">10</div> <div style="text-align: right; margin-right: 50px;">15</div>															105
gtt aaa gat ttt tgc tct agg gtg tat gaa ttg agc gaa ttt ttg gat Val Lys Asp Phe Cys Ser Arg Val Tyr Glu Leu Ser Glu Phe Leu Asp <div style="text-align: right; margin-right: 50px;">20</div> <div style="text-align: right; margin-right: 50px;">25</div> <div style="text-align: right; margin-right: 50px;">30</div>															153
aaa aaa ttg caa gtc aaa tat gaa gat aag ggc gaa ccc ctt aaa atc Lys Lys Leu Gln Val Lys Tyr Glu Asp Lys Gly Glu Pro Leu Lys Ile <div style="text-align: right; margin-right: 50px;">35</div> <div style="text-align: right; margin-right: 50px;">40</div> <div style="text-align: right; margin-right: 50px;">45</div> <div style="text-align: right; margin-right: 50px;">50</div>															201
aca tgg cat tct aat tgc cat gcc tta agg gtg gct aaa gtg att gac Thr Trp His Ser Asn Cys His Ala Leu Arg Val Ala Lys Val Ile Asp <div style="text-align: right; margin-right: 50px;">55</div> <div style="text-align: right; margin-right: 50px;">60</div> <div style="text-align: right; margin-right: 50px;">65</div>															249
tcg gcg aaa aac ctc atc aga cag ctt aaa aat gtg gaa ctc att gaa Ser Ala Lys Asn Leu Ile Arg Gln Leu Lys Asn Val Glu Leu Ile Glu <div style="text-align: right; margin-right: 50px;">70</div> <div style="text-align: right; margin-right: 50px;">75</div> <div style="text-align: right; margin-right: 50px;">80</div>															297
ttg gaa aaa gaa gaa gaa tgc tgc ggg ttt ggg ggg act ttt tcg gtt Leu Glu Lys Glu Glu Glu Cys Cys Gly Phe Gly Gly Thr Phe Ser Val <div style="text-align: right; margin-right: 50px;">85</div> <div style="text-align: right; margin-right: 50px;">90</div> <div style="text-align: right; margin-right: 50px;">95</div>															345
aaa gag cct gaa att tca gcg gtt atg gtt aaa gaa aag att aaa aac Lys Glu Pro Glu Ile Ser Ala Val Met Val Lys Glu Lys Ile Lys Asn <div style="text-align: right; margin-right: 50px;">100</div> <div style="text-align: right; margin-right: 50px;">105</div> <div style="text-align: right; margin-right: 50px;">110</div>															393
ata gaa agc cgt caa gtg gat gtg att gtt tca gcg gat gct ggg tgt Ile Glu Ser Arg Gln Val Asp Val Ile Val Ser Ala Asp Ala Gly Cys <div style="text-align: right; margin-right: 50px;">115</div> <div style="text-align: right; margin-right: 50px;">120</div> <div style="text-align: right; margin-right: 50px;">125</div> <div style="text-align: right; margin-right: 50px;">130</div>															441
ttg atg aat atc agc acc gct atg caa aaa atg ggc tct ttg aca aaa Leu Met Asn Ile Ser Thr Ala Met Gln Lys Met Gly Ser Leu Thr Lys <div style="text-align: right; margin-right: 50px;">135</div> <div style="text-align: right; margin-right: 50px;">140</div> <div style="text-align: right; margin-right: 50px;">145</div>															489

ccc atg cat ttt tat gac ttt tta gcc tca aga ctt ggg ctt 531
 Pro Met His Phe Tyr Asp Phe Leu Ala Ser Arg Leu Gly Leu
 150 155 160

taacattaaa gaattatttt aaggaatgat catggaaaaa 571

<210> 480
 <211> 160
 <212> PRT
 <213> Helicobacter pylori

<400> 480
 Met Met Arg His Asp Tyr Leu Glu Leu Phe Glu Gly His Ala Glu Phe
 1 5 10 15
 Asn Met Val Lys Asp Phe Cys Ser Arg Val Tyr Glu Leu Ser Glu Phe
 20 25 30
 Leu Asp Lys Lys Leu Gln Val Lys Tyr Glu Asp Lys Gly Glu Pro Leu
 35 40 45
 Lys Ile Thr Trp His Ser Asn Cys His Ala Leu Arg Val Ala Lys Val
 50 55 60
 Ile Asp Ser Ala Lys Asn Leu Ile Arg Gln Leu Lys Asn Val Glu Leu
 65 70 75 80
 Ile Glu Leu Glu Lys Glu Glu Glu Cys Cys Gly Phe Gly Gly Thr Phe
 85 90 95
 Ser Val Lys Glu Pro Glu Ile Ser Ala Val Met Val Lys Glu Lys Ile
 100 105 110
 Lys Asn Ile Glu Ser Arg Gln Val Asp Val Ile Val Ser Ala Asp Ala
 115 120 125
 Gly Cys Leu Met Asn Ile Ser Thr Ala Met Gln Lys Met Gly Ser Leu
 130 135 140
 Thr Lys Pro Met His Phe Tyr Asp Phe Leu Ala Ser Arg Leu Gly Leu
 145 150 155 160

<210> 481
 <211> 759
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (70)...(714)

<400> 481
 aacctgcaaa cccaccttaa aaggctcaaa agaagtgagt ttgtgggcca aaaaaaggaa 60
 ttagagggc atg ggg agg ttt tct tta aaa gaa att tta atg ctc agc ctt 111
 Met Gly Arg Phe Ser Leu Lys Glu Ile Leu Met Leu Ser Leu
 1 5 10

 acc tta ttg gct tta ctg ggt tgg att ttt ggc aaa cct tta ggc ttg 159
 Thr Leu Leu Ala Leu Leu Gly Trp Ile Phe Gly Lys Pro Leu Gly Leu
 15 20 25 30

 cat gcg agt gcg acg gct ttg att gtc atg gtt tta atg gcg ttt tgt 207
 His Ala Ser Ala Thr Ala Leu Ile Val Met Val Leu Met Ala Phe Cys
 35 40 45

 aag att gta agc tat gaa gac atc att aaa aac aag agc gcg ttc aat 255
 Lys Ile Val Ser Tyr Glu Asp Ile Ile Lys Asn Lys Ser Ala Phe Asn

50					55					60					
att ttt tta ttg ctt gga tgc ctg ctc acg atg gct ggc ggg ctt aaa	303														
Ile Phe Leu Leu Leu Gly Ser Leu Leu Thr Met Ala Gly Gly Leu Lys															
65 70 75															
aat gta ggg ttt tta aat ttt atc ggc aat gcg gct caa aat ttt tta	351														
Asn Val Gly Phe Leu Asn Phe Ile Gly Asn Ala Ala Gln Asn Phe Leu															
80 85 90															
gag cat gct cac ttg gat ccg tta ata gcg gtc ttg ttt att gta gcc	399														
Glu His Ala His Leu Asp Pro Leu Ile Ala Val Leu Phe Ile Val Ala															
95 100 105 110															
ctc ttt tat ctg tgc cat tat ttt ttc gca agc atc acc gct cat gtg	447														
Leu Phe Tyr Leu Ser His Tyr Phe Phe Ala Ser Ile Thr Ala His Val															
115 120 125															
agc gcg tta ttc gcg ctt ttt gta ggg att ggt tgc cac att caa ggg	495														
Ser Ala Leu Phe Ala Leu Phe Val Gly Ile Gly Ser His Ile Gln Gly															
130 135 140															
gtc aat ttg caa gaa ttg agc ttg ttt tta atg ttt tct tta ggg att	543														
Val Asn Leu Gln Glu Leu Ser Leu Phe Leu Met Phe Ser Leu Gly Ile															
145 150 155															
atg ggg att tta acg ccc tat ggc aca ggc cca tcc acc att tat tac	591														
Met Gly Ile Leu Thr Pro Tyr Gly Thr Gly Pro Ser Thr Ile Tyr Tyr															
160 165 170															
ggg agc ggg tat att caa agc aag gat ttt tgg aaa tgg ggg ttt att	639														
Gly Ser Gly Tyr Ile Gln Ser Lys Asp Phe Trp Lys Trp Gly Phe Ile															
175 180 185 190															
ttt ggc ttt ttg tat tta atc gtg ttt tta agc gtg tgc aca cct tgg	687														
Phe Gly Phe Leu Tyr Leu Ile Val Phe Leu Ser Val Cys Thr Pro Trp															
195 200 205															
gtc aaa ttc atc gct tat agg tgg ttg tagctggaaa ctttacacaa	734														
Val Lys Phe Ile Ala Tyr Arg Trp Leu															
210 215															
cgccctttta aaatggtatg aagaa	759														
<210> 482															
<211> 215															
<212> PRT															
<213> Helicobacter pylori															
<400> 482															
Met Gly Arg Phe Ser Leu Lys Glu Ile Leu Met Leu Ser Leu Thr Leu															
1 5 10 15															
Leu Ala Leu Leu Gly Trp Ile Phe Gly Lys Pro Leu Gly Leu His Ala															
20 25 30															
Ser Ala Thr Ala Leu Ile Val Met Val Leu Met Ala Phe Cys Lys Ile															
35 40 45															
Val Ser Tyr Glu Asp Ile Ile Lys Asn Lys Ser Ala Phe Asn Ile Phe															
50 55 60															
Leu Leu Leu Gly Ser Leu Leu Thr Met Ala Gly Gly Leu Lys Asn Val															

65					70					75					80
Gly	Phe	Leu	Asn	Phe	Ile	Gly	Asn	Ala	Ala	Gln	Asn	Phe	Leu	Glu	His
				85					90					95	
Ala	His	Leu	Asp	Pro	Leu	Ile	Ala	Val	Leu	Phe	Ile	Val	Ala	Leu	Phe
			100					105					110		
Tyr	Leu	Ser	His	Tyr	Phe	Phe	Ala	Ser	Ile	Thr	Ala	His	Val	Ser	Ala
		115					120					125			
Leu	Phe	Ala	Leu	Phe	Val	Gly	Ile	Gly	Ser	His	Ile	Gln	Gly	Val	Asn
	130					135					140				
Leu	Gln	Glu	Leu	Ser	Leu	Phe	Leu	Met	Phe	Ser	Leu	Gly	Ile	Met	Gly
145					150				155					160	
Ile	Leu	Thr	Pro	Tyr	Gly	Thr	Gly	Pro	Ser	Thr	Ile	Tyr	Tyr	Gly	Ser
			165					170						175	
Gly	Tyr	Ile	Gln	Ser	Lys	Asp	Phe	Trp	Lys	Trp	Gly	Phe	Ile	Phe	Gly
		180					185					190			
Phe	Leu	Tyr	Leu	Ile	Val	Phe	Leu	Ser	Val	Cys	Thr	Pro	Trp	Val	Lys
	195						200					205			
Phe	Ile	Ala	Tyr	Arg	Trp	Leu									
	210					215									

<210> 483
 <211> 357
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (37) ... (309)

<400> 483	
aaggggggat ttatatcggg aaagagttgt ttaagc atg gct agt ggc ctt ttt	54
Met Ala Ser Gly Leu Phe	
1 5	
gaa aac gat gga atc aaa gac aac aaa gcg cga gat ttt ttc tat agc	102
Glu Asn Asp Gly Ile Lys Asp Asn Lys Ala Arg Asp Phe Phe Tyr Ser	
10 15 20	
cat agc tcc cta att gtc ttt ttc ctt tta ctg ctt ggg ttt ggg tat	150
His Ser Ser Leu Ile Val Phe Phe Leu Leu Leu Leu Gly Phe Gly Tyr	
25 30 35	
tat tta ggg aag ttg ctt ttt ggg ggc tct tct tta gaa gtt tat ttg	198
Tyr Leu Gly Lys Leu Leu Phe Gly Gly Ser Ser Leu Glu Val Tyr Leu	
40 45 50	
gat tta aga gac aag cat gaa cga ttg cag caa gaa atc acc gaa ttg	246
Asp Leu Arg Asp Lys His Glu Arg Leu Gln Gln Glu Ile Thr Glu Leu	
55 60 65 70	
caa agc aag aat gtg cgc ttg caa aag cgt ttg ttt gag ttg aag gaa	294
Gln Ser Lys Asn Val Arg Leu Gln Lys Arg Leu Phe Glu Leu Lys Glu	
75 80 85	
tta cgg cct aga gat tagatttaag gaaaatggta gtgttaaaaa agatgatagg	349
Leu Arg Pro Arg Asp	
90	

tttggtgg

357

<210> 484

<211> 91

<212> PRT

<213> Helicobacter pylori

<400> 484

Met	Ala	Ser	Gly	Leu	Phe	Glu	Asn	Asp	Gly	Ile	Lys	Asp	Asn	Lys	Ala
1				5					10					15	
Arg	Asp	Phe	Phe	Tyr	Ser	His	Ser	Ser	Leu	Ile	Val	Phe	Phe	Leu	Leu
			20					25					30		
Leu	Leu	Gly	Phe	Gly	Tyr	Tyr	Leu	Gly	Lys	Leu	Leu	Phe	Gly	Gly	Ser
		35					40					45			
Ser	Leu	Glu	Val	Tyr	Leu	Asp	Leu	Arg	Asp	Lys	His	Glu	Arg	Leu	Gln
	50				55						60				
Gln	Glu	Ile	Thr	Glu	Leu	Gln	Ser	Lys	Asn	Val	Arg	Leu	Gln	Lys	Arg
65				70					75						80
Leu	Phe	Glu	Leu	Lys	Glu	Leu	Arg	Pro	Arg	Asp					
			85						90						

<210> 485

<211> 678

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)...(675)

<400> 485

atg	ata	gaa	ggt	tta	atg	ata	gaa	gat	gat	ata	gaa	tta	gcc	gag	ttt	48
Met	Ile	Glu	Val	Leu	Met	Ile	Glu	Asp	Asp	Ile	Glu	Leu	Ala	Glu	Phe	
1				5					10					15		
ttg	agc	gag	ttt	ttg	ctc	caa	cat	ggc	att	cat	gta	acc	aat	tac	gat	96
Leu	Ser	Glu	Phe	Leu	Leu	Gln	His	Gly	Ile	His	Val	Thr	Asn	Tyr	Asp	
			20					25					30			
gag	cca	tat	acc	ggc	att	agt	gcg	gct	aac	aca	caa	aat	tat	gat	ttg	144
Glu	Pro	Tyr	Thr	Gly	Ile	Ser	Ala	Ala	Asn	Thr	Gln	Asn	Tyr	Asp	Leu	
			35				40					45				
ttg	ttg	ttg	gat	ttg	act	ttg	cct	aat	tta	gac	ggg	ctt	gaa	gtg	tgt	192
Leu	Leu	Leu	Asp	Leu	Thr	Leu	Pro	Asn	Leu	Asp	Gly	Leu	Glu	Val	Cys	
			50			55					60					
agg	cgc	atc	tcc	aaa	caa	aaa	cat	atc	cct	att	att	att	tct	tca	gcg	240
Arg	Arg	Ile	Ser	Lys	Gln	Lys	His	Ile	Pro	Ile	Ile	Ile	Ser	Ser	Ala	
65				70					75						80	
aga	agt	gat	gtg	gaa	gat	aag	att	aaa	gca	cta	gat	tat	ggg	gct	gat	288
Arg	Ser	Asp	Val	Glu	Asp	Lys	Ile	Lys	Ala	Leu	Asp	Tyr	Gly	Ala	Asp	
			85						90					95		
gat	tac	ctc	cct	aaa	ccc	tat	gat	cct	aaa	gaa	tta	tta	gct	cgc	atc	336
Asp	Tyr	Leu	Pro	Lys	Pro	Tyr	Asp	Pro	Lys	Glu	Leu	Leu	Ala	Arg	Ile	
			100					105					110			

caa tcg cta ctc agg cgt tct cat aaa aaa gaa gaa gtg agt gag cca	384
Gln Ser Leu Leu Arg Arg Ser His Lys Lys Glu Glu Val Ser Glu Pro	
115 120 125	
ggc gat gcg aat atc ttt agg gtg gat aag gat agc cga gaa gtg tat	432
Gly Asp Ala Asn Ile Phe Arg Val Asp Lys Asp Ser Arg Glu Val Tyr	
130 135 140	
atg cat gaa aaa aag ctg gac tta act agg gct gaa tat gaa atc ctt	480
Met His Glu Lys Lys Leu Asp Leu Thr Arg Ala Glu Tyr Glu Ile Leu	
145 150 155 160	
tcg ctt ctc att agc aaa aaa ggt tat gtg ttt agc cgt gaa agc att	528
Ser Leu Leu Ile Ser Lys Lys Gly Tyr Val Phe Ser Arg Glu Ser Ile	
165 170 175	
gcg att gag agc gag agc atc aac cct gaa agc tct aat aaa agc att	576
Ala Ile Glu Ser Glu Ser Ile Asn Pro Glu Ser Ser Asn Lys Ser Ile	
180 185 190	
gat gtg atc att ggc cgt ttg cga tct aag att gaa aaa aat cct aaa	624
Asp Val Ile Ile Gly Arg Leu Arg Ser Lys Ile Glu Lys Asn Pro Lys	
195 200 205	
caa ccg caa tac atc atc tct gtt aga ggg att ggt tat aaa tta gaa	672
Gln Pro Gln Tyr Ile Ile Ser Val Arg Gly Ile Gly Tyr Lys Leu Glu	
210 215 220	
tac tga	678
Tyr	
225	

<210> 486
 <211> 225
 <212> PRT
 <213> Helicobacter pylori

<400> 486

Met Ile Glu Val Leu Met Ile Glu Asp Asp Ile Glu Leu Ala Glu Phe	
1 5 10 15	
Leu Ser Glu Phe Leu Leu Gln His Gly Ile His Val Thr Asn Tyr Asp	
20 25 30	
Glu Pro Tyr Thr Gly Ile Ser Ala Ala Asn Thr Gln Asn Tyr Asp Leu	
35 40 45	
Leu Leu Leu Asp Leu Thr Leu Pro Asn Leu Asp Gly Leu Glu Val Cys	
50 55 60	
Arg Arg Ile Ser Lys Gln Lys His Ile Pro Ile Ile Ser Ser Ala	
65 70 75 80	
Arg Ser Asp Val Glu Asp Lys Ile Lys Ala Leu Asp Tyr Gly Ala Asp	
85 90 95	
Asp Tyr Leu Pro Lys Pro Tyr Asp Pro Lys Glu Leu Leu Ala Arg Ile	
100 105 110	
Gln Ser Leu Leu Arg Arg Ser His Lys Lys Glu Glu Val Ser Glu Pro	
115 120 125	
Gly Asp Ala Asn Ile Phe Arg Val Asp Lys Asp Ser Arg Glu Val Tyr	
130 135 140	
Met His Glu Lys Lys Leu Asp Leu Thr Arg Ala Glu Tyr Glu Ile Leu	

145		150		155		160									
Ser	Leu	Leu	Ile	Ser	Lys	Lys	Gly	Tyr	Val	Phe	Ser	Arg	Glu	Ser	Ile
				165					170					175	
Ala	Ile	Glu	Ser	Glu	Ser	Ile	Asn	Pro	Glu	Ser	Ser	Asn	Lys	Ser	Ile
				180					185					190	
Asp	Val	Ile	Ile	Gly	Arg	Leu	Arg	Ser	Lys	Ile	Glu	Lys	Asn	Pro	Lys
		195					200					205			
Gln	Pro	Gln	Tyr	Ile	Ile	Ser	Val	Arg	Gly	Ile	Gly	Tyr	Lys	Leu	Glu
	210					215					220				
Tyr															
225															

<210> 487
 <211> 1134
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (72) ... (1082)

<400> 487
 aagtctatgc cacgatcaat gggtttccctt tcaattcaca gctcaaactt ttagaagaac 60
 atattgataa a atg gca gaa tta gag ccg gac gct ttt att atc gct gcg 110
 Met Ala Glu Leu Glu Pro Asp Ala Phe Ile Ile Ala Ala
 1 5 10

cct ggt gtg gtg aaa ctc gct tta aaa atc gcc ccg cat atc cct atc 158
 Pro Gly Val Val Lys Leu Ala Leu Lys Ile Ala Pro His Ile Pro Ile
 15 20 25

cat tta tcc acg caa gcg aat gtc tta aat ttg cta gat gca caa gtg 206
 His Leu Ser Thr Gln Ala Asn Val Leu Asn Leu Leu Asp Ala Gln Val
 30 35 40 45

ttt tat gat tta ggg gtt aaa cgc atc gtg tgc gcg agg gaa ttg agc 254
 Phe Tyr Asp Leu Gly Val Lys Arg Ile Val Cys Ala Arg Glu Leu Ser
 50 55 60

ctg aat gat gcg att gag att aaa aaa gcc tta cct aat tta gaa tta 302
 Leu Asn Asp Ala Ile Glu Ile Lys Lys Ala Leu Pro Asn Leu Glu Leu
 65 70 75

gaa atc ttt gtg cat ggg agc atg tgc ttt gcc ttt tca ggg cgc tgc 350
 Glu Ile Phe Val His Gly Ser Met Cys Phe Ala Phe Ser Gly Arg Cys
 80 85 90

ttg att tcg gcc tta caa aag ggg cgc gtg cct aat aga ggg agt tgc 398
 Leu Ile Ser Ala Leu Gln Lys Gly Arg Val Pro Asn Arg Gly Ser Cys
 95 100 105

gcg aat gat tgc cgg ttt gat tat gaa tat tac gtg aaa aac cct gat 446
 Ala Asn Asp Cys Arg Phe Asp Tyr Glu Tyr Tyr Val Lys Asn Pro Asp
 110 115 120 125

aat ggc gtg atg atg aga ctg gtt gaa gaa gag ggc gta ggc acg cat 494
 Asn Gly Val Met Met Arg Leu Val Glu Glu Glu Gly Val Gly Thr His
 130 135 140

att ttt aac gct aag gat ttg aac ctc tct ggc cat atc gct gaa att	542
Ile Phe Asn Ala Lys Asp Leu Asn Leu Ser Gly His Ile Ala Glu Ile	
145 150 155	
tta agt tcc aac gcc att agc gcg ctt aag att gaa ggg cgc acc aag	590
Leu Ser Ser Asn Ala Ile Ser Ala Leu Lys Ile Glu Gly Arg Thr Lys	
160 165 170	
tcc agt tac tac gcc gcg caa acc acg cgc atc tat cgt tta gcg gtt	638
Ser Ser Tyr Tyr Ala Ala Gln Thr Thr Arg Ile Tyr Arg Leu Ala Val	
175 180 185	
gat gat ttt tac cat aac acc tta aag ccg agt ttt tat gcc agc gaa	686
Asp Asp Phe Tyr His Asn Thr Leu Lys Pro Ser Phe Tyr Ala Ser Glu	
190 195 200 205	
ttg aac acg ctt aaa aac agg ggt ttt acg gac ggc tat ttg atg cga	734
Leu Asn Thr Leu Lys Asn Arg Gly Phe Thr Asp Gly Tyr Leu Met Arg	
210 215 220	
agg cct ttt gaa agg ttg gat act caa aac cac caa aca gcc att agc	782
Arg Pro Phe Glu Arg Leu Asp Thr Gln Asn His Gln Thr Ala Ile Ser	
225 230 235	
gaa ggg gat ttt caa gtc aat ggc gaa ata acc gaa gac ggg cgt ttt	830
Glu Gly Asp Phe Gln Val Asn Gly Glu Ile Thr Glu Asp Gly Arg Phe	
240 245 250	
ttt gca tgc aaa ttc acc act acc act aac acc gct tat gaa atc atc	878
Phe Ala Cys Lys Phe Thr Thr Thr Thr Asn Thr Ala Tyr Glu Ile Ile	
255 260 265	
gct ccc aaa aat gcg gct atc acg ccc ata gtc aat gaa att ggc aag	926
Ala Pro Lys Asn Ala Ala Ile Thr Pro Ile Val Asn Glu Ile Gly Lys	
270 275 280 285	
att tac acc ttt gaa aaa cgc tct tat tta gtg ctg tat aaa atc ctt	974
Ile Tyr Thr Phe Glu Lys Arg Ser Tyr Leu Val Leu Tyr Lys Ile Leu	
290 295 300	
tta gaa aat aac acc gag cta gaa act atc cat agc ggg aac gtg aat	1022
Leu Glu Asn Asn Thr Glu Leu Glu Thr Ile His Ser Gly Asn Val Asn	
305 310 315	
tta gtg cga ctg ccc gca ccc tta ccg gct ttt agt ttt tta cgc acc	1070
Leu Val Arg Leu Pro Ala Pro Leu Pro Ala Phe Ser Phe Leu Arg Thr	
320 325 330	
caa gtc aga gtc taaaaatggc gtttagagat taggtattga aaatgattaa	1122
Gln Val Arg Val	
335	
gagaaacgca tg	1134
<210> 486	
<211> 337	
<212> PRT	
<213> Helicobacter pylori	

<400> 488

Met	Ala	Glu	Leu	Glu	Pro	Asp	Ala	Phe	Ile	Ile	Ala	Ala	Pro	Gly	Val
1				5					10					15	
Val	Lys	Leu	Ala	Leu	Lys	Ile	Ala	Pro	His	Ile	Pro	Ile	His	Leu	Ser
			20					25					30		
Thr	Gln	Ala	Asn	Val	Leu	Asn	Leu	Leu	Asp	Ala	Gln	Val	Phe	Tyr	Asp
		35					40					45			
Leu	Gly	Val	Lys	Arg	Ile	Val	Cys	Ala	Arg	Glu	Leu	Ser	Leu	Asn	Asp
	50					55					60				
Ala	Ile	Glu	Ile	Lys	Lys	Ala	Leu	Pro	Asn	Leu	Glu	Leu	Glu	Ile	Phe
65					70					75					80
Val	His	Gly	Ser	Met	Cys	Phe	Ala	Phe	Ser	Gly	Arg	Cys	Leu	Ile	Ser
				85					90					95	
Ala	Leu	Gln	Lys	Gly	Arg	Val	Pro	Asn	Arg	Gly	Ser	Cys	Ala	Asn	Asp
			100					105					110		
Cys	Arg	Phe	Asp	Tyr	Glu	Tyr	Tyr	Val	Lys	Asn	Pro	Asp	Asn	Gly	Val
		115						120				125			
Met	Met	Arg	Leu	Val	Glu	Glu	Glu	Gly	Val	Gly	Thr	His	Ile	Phe	Asn
	130					135					140				
Ala	Lys	Asp	Leu	Asn	Leu	Ser	Gly	His	Ile	Ala	Glu	Ile	Leu	Ser	Ser
145					150					155					160
Asn	Ala	Ile	Ser	Ala	Leu	Lys	Ile	Glu	Gly	Arg	Thr	Lys	Ser	Ser	Tyr
				165					170					175	
Tyr	Ala	Ala	Gln	Thr	Thr	Arg	Ile	Tyr	Arg	Leu	Ala	Val	Asp	Asp	Phe
			180					185					190		
Tyr	His	Asn	Thr	Leu	Lys	Pro	Ser	Phe	Tyr	Ala	Ser	Glu	Leu	Asn	Thr
		195					200					205			
Leu	Lys	Asn	Arg	Gly	Phe	Thr	Asp	Gly	Tyr	Leu	Met	Arg	Arg	Pro	Phe
	210					215					220				
Glu	Arg	Leu	Asp	Thr	Gln	Asn	His	Gln	Thr	Ala	Ile	Ser	Glu	Gly	Asp
225					230					235					240
Phe	Gln	Val	Asn	Gly	Glu	Ile	Thr	Glu	Asp	Gly	Arg	Phe	Phe	Ala	Cys
				245					250					255	
Lys	Phe	Thr	Thr	Thr	Thr	Asn	Thr	Ala	Tyr	Glu	Ile	Ile	Ala	Pro	Lys
			260					265					270		
Asn	Ala	Ala	Ile	Thr	Pro	Ile	Val	Asn	Glu	Ile	Gly	Lys	Ile	Tyr	Thr
		275					280					285			
Phe	Glu	Lys	Arg	Ser	Tyr	Leu	Val	Leu	Tyr	Lys	Ile	Leu	Leu	Glu	Asn
	290					295					300				
Asn	Thr	Glu	Leu	Glu	Thr	Ile	His	Ser	Gly	Asn	Val	Asn	Leu	Val	Arg
305					310					315					320
Leu	Pro	Ala	Pro	Leu	Pro	Ala	Phe	Ser	Phe	Leu	Arg	Thr	Gln	Val	Arg
				325					330					335	

Val

<210> 489

<211> 1123

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (19)...(1038)

<400> 489

attaaggaga	aataagaa	atg	tta	caa	ccc	cct	aaa	att	gtc	gct	gaa	ttg	51
		Met	Leu	Gln	Pro	Pro	Lys	Ile	Val	Ala	Glu	Leu	

					1						5						10	
agc	gct	aat	cat	aac	cag	gat	tta	aac	cta	gcc	aaa	gaa	agc	ctt	cat	99		
Ser	Ala	Asn	His	Asn	Gln	Asp	Leu	Asn	Leu	Ala	Lys	Glu	Ser	Leu	His			
					15						20						25	
gcc	att	aag	gaa	agc	ggg	gcg	gat	ttt	gtc	aag	ctc	caa	acc	tac	acg	147		
Ala	Ile	Lys	Glu	Ser	Gly	Ala	Asp	Phe	Val	Lys	Leu	Gln	Thr	Tyr	Thr			
					30						35						40	
cca	agc	tgc	atg	act	tta	aac	tct	aaa	gaa	gat	cct	ttc	atc	att	caa	195		
Pro	Ser	Cys	Met	Thr	Leu	Asn	Ser	Lys	Glu	Asp	Pro	Phe	Ile	Ile	Gln			
					45						50						55	
ggc	act	tta	tgg	gat	aaa	gaa	aat	ttg	tat	gaa	ttg	tat	caa	aag	gct	243		
Gly	Thr	Leu	Trp	Asp	Lys	Glu	Asn	Leu	Tyr	Glu	Leu	Tyr	Gln	Lys	Ala			
					60						65						70	
tct	acc	ccc	cta	gaa	tgg	cat	gct	gaa	ttg	ttt	gag	ttg	gct	aga	aag	291		
Ser	Thr	Pro	Leu	Glu	Trp	His	Ala	Glu	Leu	Phe	Glu	Leu	Ala	Arg	Lys			
					80						85						90	
ctt	gat	tta	ggc	att	ttt	agc	tcg	cct	ttt	agt	tca	caa	gct	tta	gag	339		
Leu	Asp	Leu	Gly	Ile	Phe	Ser	Ser	Pro	Phe	Ser	Ser	Gln	Ala	Leu	Glu			
					95						100						105	
ctt	tta	gag	agc	cta	aat	tgc	ccc	atg	tat	aaa	atc	gct	agt	ttt	gaa	387		
Leu	Leu	Glu	Ser	Leu	Asn	Cys	Pro	Met	Tyr	Lys	Ile	Ala	Ser	Phe	Glu			
					110						115						120	
atc	gtt	gat	ttg	gac	ttg	att	gaa	aag	gcc	gct	cgc	aca	caa	aag	ccc	435		
Ile	Val	Asp	Leu	Asp	Leu	Ile	Glu	Lys	Ala	Ala	Arg	Thr	Gln	Lys	Pro			
					125						130						135	
att	atc	ctt	tct	agc	ggg	atc	gct	aca	cac	acc	gaa	ttg	caa	gac	gct	483		
Ile	Ile	Leu	Ser	Ser	Gly	Ile	Ala	Thr	His	Thr	Glu	Leu	Gln	Asp	Ala			
					140						145						150	
atc	tca	ttg	tgc	aga	aga	gtg	aat	aat	ttt	gac	atc	acc	ctt	tta	aaa	531		
Ile	Ser	Leu	Cys	Arg	Arg	Val	Asn	Asn	Phe	Asp	Ile	Thr	Leu	Leu	Lys			
					160						165						170	
tgc	gtg	agc	gct	tat	ccc	agt	aaa	ata	gaa	gac	gct	aac	ttg	ttg	agc	579		
Cys	Val	Ser	Ala	Tyr	Pro	Ser	Lys	Ile	Glu	Asp	Ala	Asn	Leu	Leu	Ser			
					175						180						185	
atg	gtt	aaa	tta	ggc	gaa	atc	ttt	ggc	gtt	aaa	ttt	ggc	ttg	agc	gat	627		
Met	Val	Lys	Leu	Gly	Glu	Ile	Phe	Gly	Val	Lys	Phe	Gly	Leu	Ser	Asp			
					190						195						200	
cac	acg	att	ggc	tct	ctt	tgc	ccc	att	tta	gcc	acc	act	tta	gga	gcg	675		
His	Thr	Ile	Gly	Ser	Leu	Cys	Pro	Ile	Leu	Ala	Thr	Thr	Leu	Gly	Ala			
					205						210						215	
agc	atg	ata	gaa	aag	cat	ttc	att	tta	aac	aaa	tcc	tta	caa	acc	cca	723		
Ser	Met	Ile	Glu	Lys	His	Phe	Ile	Leu	Asn	Lys	Ser	Leu	Gln	Thr	Pro			
					220						225						230	
gac	agc	gct	ttt	agc	atg	gat	ttt	aac	gga	ttt	aaa	agc	atg	gtt	gaa	771		

Asp	Ser	Ala	Phe	Ser	Met	Asp	Phe	Asn	Gly	Phe	Lys	Ser	Met	Val	Glu		
				240					245					250			
gcc	atc	aag	caa	agc	gtt	tta	gcc	tta	ggc	gaa	gaa	gag	cca	aga	atc	819	
Ala	Ile	Lys	Gln	Ser	Val	Leu	Ala	Leu	Gly	Glu	Glu	Glu	Pro	Arg	Ile		
			255					260					265				
aat	cca	aag	act	tta	gaa	aag	cga	aga	ttt	ttt	gca	cgc	tct	tta	ttt	867	
Asn	Pro	Lys	Thr	Leu	Glu	Lys	Arg	Arg	Phe	Phe	Ala	Arg	Ser	Leu	Phe		
		270					275					280					
gtt	att	aag	gat	att	caa	aaa	ggc	gaa	gca	ttg	act	gaa	aac	aat	atc	915	
Val	Ile	Lys	Asp	Ile	Gln	Lys	Gly	Glu	Ala	Leu	Thr	Glu	Asn	Asn	Ile		
	285					290					295						
aaa	gcc	tta	cgc	ccc	aac	ctt	ggc	tta	cac	cct	aaa	ttt	tat	aaa	gaa	963	
Lys	Ala	Leu	Arg	Pro	Asn	Leu	Gly	Leu	His	Pro	Lys	Phe	Tyr	Lys	Glu		
300					305				310						315		
att	tta	ggc	caa	aaa	gca	tca	aaa	ttc	tta	aaa	gcc	aac	acc	ccc	tta	1011	
Ile	Leu	Gly	Gln	Lys	Ala	Ser	Lys	Phe	Leu	Lys	Ala	Asn	Thr	Pro	Leu		
			320					325						330			
agc	gct	gat	gat	ata	gaa	cgc	tca	ttg	taggttcggt	ttgatcaaaa						1058	
Ser	Ala	Asp	Asp	Ile	Glu	Arg	Ser	Leu									
		335					340										
aatgggggttt	ttaattttgt	tttatgggttt	tagatttgat	tttaaactca	ttttctttat	1118											
tttaa						1123											

<210> 490
 <211> 340
 <212> PRT
 <213> Helicobacter pylori

<400> 490

Met	Leu	Gln	Pro	Pro	Lys	Ile	Val	Ala	Glu	Leu	Ser	Ala	Asn	His	Asn		
1				5					10					15			
Gln	Asp	Leu	Asn	Leu	Ala	Lys	Glu	Ser	Leu	His	Ala	Ile	Lys	Glu	Ser		
		20						25					30				
Gly	Ala	Asp	Phe	Val	Lys	Leu	Gln	Thr	Tyr	Thr	Pro	Ser	Cys	Met	Thr		
	35					40						45					
Leu	Asn	Ser	Lys	Glu	Asp	Pro	Phe	Ile	Ile	Gln	Gly	Thr	Leu	Trp	Asp		
	50				55					60							
Lys	Glu	Asn	Leu	Tyr	Glu	Leu	Tyr	Gln	Lys	Ala	Ser	Thr	Pro	Leu	Glu		
65				70					75					80			
Trp	His	Ala	Glu	Leu	Phe	Glu	Leu	Ala	Arg	Lys	Leu	Asp	Leu	Gly	Ile		
		85						90					95				
Phe	Ser	Ser	Pro	Phe	Ser	Ser	Gln	Ala	Leu	Glu	Leu	Leu	Glu	Ser	Leu		
		100						105					110				
Asn	Cys	Pro	Met	Tyr	Lys	Ile	Ala	Ser	Phe	Glu	Ile	Val	Asp	Leu	Asp		
	115					120						125					
Leu	Ile	Glu	Lys	Ala	Ala	Arg	Thr	Gln	Lys	Pro	Ile	Ile	Leu	Ser	Ser		
	130					135					140						
Gly	Ile	Ala	Thr	His	Thr	Glu	Leu	Gln	Asp	Ala	Ile	Ser	Leu	Cys	Arg		
145				150					155					160			
Arg	Val	Asn	Asn	Phe	Asp	Ile	Thr	Leu	Leu	Lys	Cys	Val	Ser	Ala	Tyr		
		165						170						175			
Pro	Ser	Lys	Ile	Glu	Asp	Ala	Asn	Leu	Leu	Ser	Met	Val	Lys	Leu	Gly		

90	95	100	
cac tac gaa gca agc acg gac aaa acc tac gag aaa ctc aaa gat gaa His Tyr Glu Ala Ser Thr Asp Lys Thr Tyr Glu Lys Leu Lys Asp Glu 105 110 115 120			390
cta aaa aaa atc aaa aaa agc aaa ttg aaa agt ttc atc caa tcc tat Leu Lys Lys Ile Lys Lys Ser Lys Leu Lys Ser Phe Ile Gln Ser Tyr 125 130 135			438
gtc agc gat ttg aaa aat ttc tat cag gct ttt ctt gat cta ttg agc Val Ser Asp Leu Lys Asn Phe Tyr Gln Ala Phe Leu Asp Leu Leu Ser 140 145 150			486
gag att gac acc aac cca acc acc ttt aag gtc atg ctc atc aac aag Glu Ile Asp Thr Asn Pro Thr Thr Phe Lys Val Met Leu Ile Asn Lys 155 160 165			534
atc gac tcg tct ttt ttc aat tcg ctc atc cgc ctg aaa atc aac aac Ile Asp Ser Ser Phe Phe Asn Ser Leu Ile Arg Leu Lys Ile Asn Asn 170 175 180			582
gaa cta gac gat gaa acg ctg aaa ctc ttt gcc aaa acc gat att gtg Glu Leu Asp Asp Glu Thr Leu Lys Leu Phe Ala Lys Thr Asp Ile Val 185 190 195 200			630
ctt ttc aaa gct act aga gat agg cca gga acg gac aac ctg att aat Leu Phe Lys Ala Thr Arg Asp Arg Pro Gly Thr Asp Asn Leu Ile Asn 205 210 215			678
gcg tat ctt aaa aag ggc aaa gag gga ttg aag agc gag atg att gct Ala Tyr Leu Lys Lys Gly Lys Glu Gly Leu Lys Ser Glu Met Ile Ala 220 225 230			726
caa tgc aga aat gat ata ggg ctg gct ttt tgg cag tct gta aac aac Gln Cys Arg Asn Asp Ile Gly Leu Ala Phe Trp Gln Ser Val Asn Asn 235 240 245			774
gca tcc aac tca tca tgc ttc cac tat atc ttc ttt gaa aag aac tgc Ala Ser Asn Ser Ser Cys Phe His Tyr Ile Phe Phe Glu Lys Asn Cys 250 255 260			822
cag gag atg ggt ctt gcc gat ctc aaa aaa ttg atc cct agg aag caa Gln Glu Met Gly Leu Ala Asp Leu Lys Lys Leu Ile Pro Arg Lys Gln 265 270 275 280			870
ttc tcc caa gaa aaa gaa cac atc atc ccc atc aat tta tta aaa cag Phe Ser Gln Glu Lys Glu His Ile Ile Pro Ile Asn Leu Leu Lys Gln 285 290 295			918
gaa tcc aac aat aag atc aga gat ctt ggt ttt gaa gac aaa aaa gat Glu Ser Asn Asn Lys Ile Arg Asp Leu Gly Phe Glu Asp Lys Lys Asp 300 305 310			966
ctt gaa gac tac att gac aca tac ggc aac ctc atc tcc ctg gaa aaa Leu Glu Asp Tyr Ile Asp Thr Tyr Gly Asn Leu Ile Ser Leu Glu Lys 315 320 325			1014
tcg ctc aat cgt aag gca agc gat aag gat ctg tat gga aaa gat gaa			1062

Ser Leu Asn Arg Lys Ala Ser Asp Lys Asp Leu Tyr Gly Lys Asp Glu
 330 335 340
 atc tat aaa agt agt gag atc cct ttc aac agg cgc ttt gat aca aaa 1110
 Ile Tyr Lys Ser Ser Glu Ile Pro Phe Asn Arg Arg Phe Asp Thr Lys
 345 350 355 360
 aac ttc aat aag aag gca ttg gta aaa aga aat gaa gaa atg cga gaa 1158
 Asn Phe Asn Lys Lys Ala Leu Val Lys Arg Asn Glu Glu Met Arg Glu
 365 370 375
 tgg ctg atc gac acc ttt ttt aag gat ttc gcc gcc cac taaagagagt 1207
 Trp Leu Ile Asp Thr Phe Phe Lys Asp Phe Ala Ala His
 380 385
 gagattaaaa gagagtgatc gcactca 1234
 <210> 492
 <211> 389
 <212> PRT
 <213> Helicobacter pylori

<400> 492
 Met Val Leu Met Arg Phe Glu Glu Pro Asp Pro Gly Arg Ala Ile Arg
 1 5 10 15
 Thr Phe Gln Ser Val Asn Asp Arg Gly Val Pro Leu Leu Leu Asp
 20 25 30
 Lys Leu Lys Ser Leu Leu Ile Tyr Tyr Ser Asn Ile Phe Cys Asp Gly
 35 40 45
 Lys Arg Gly Leu Asp Gln Phe Ile Ile Asp His Phe Gly Glu Ile Phe
 50 55 60
 Lys Ile Phe Ala Lys Ile Lys Lys Ser Asp His Ile Ser Ser Val Gly
 65 70 75 80
 Gly Phe Asp Glu Gly Asp Ile Phe Arg Tyr His Ala Gly Ser Gln Lys
 85 90 95
 Phe Asp Gly Ile Glu Phe Leu Gly His Tyr Glu Ala Ser Thr Asp Lys
 100 105 110
 Thr Tyr Glu Lys Leu Lys Asp Glu Leu Lys Lys Ile Lys Lys Ser Lys
 115 120 125
 Leu Lys Ser Phe Ile Gln Ser Tyr Val Ser Asp Leu Lys Asn Phe Tyr
 130 135 140
 Gln Ala Phe Leu Asp Leu Leu Ser Glu Ile Asp Thr Asn Pro Thr Thr
 145 150 155 160
 Phe Lys Val Met Leu Ile Asn Lys Ile Asp Ser Ser Phe Phe Asn Ser
 165 170 175
 Leu Ile Arg Leu Lys Ile Asn Asn Glu Leu Asp Asp Glu Thr Leu Lys
 180 185 190
 Leu Phe Ala Lys Thr Asp Ile Val Leu Phe Lys Ala Thr Arg Asp Arg
 195 200 205
 Pro Gly Thr Asp Asn Leu Ile Asn Ala Tyr Leu Lys Lys Gly Lys Glu
 210 215 220
 Gly Leu Lys Ser Glu Met Ile Ala Gln Cys Arg Asn Asp Ile Gly Leu
 225 230 235 240
 Ala Phe Trp Gln Ser Val Asn Asn Ala Ser Asn Ser Ser Cys Phe His
 245 250 255
 Tyr Ile Phe Phe Glu Lys Asn Cys Gln Glu Met Gly Leu Ala Asp Leu
 260 265 270
 Lys Lys Leu Ile Pro Arg Lys Gln Phe Ser Gln Glu Lys Glu His Ile
 275 280 285

Ile Pro Ile Asn Leu Leu Lys Gln Glu Ser Asn Asn Lys Ile Arg Asp
 290 295 300
 Leu Gly Phe Glu Asp Lys Lys Asp Leu Glu Asp Tyr Ile Asp Thr Tyr
 305 310 315 320
 Gly Asn Leu Ile Ser Leu Glu Lys Ser Leu Asn Arg Lys Ala Ser Asp
 325 330 335
 Lys Asp Leu Tyr Gly Lys Asp Glu Ile Tyr Lys Ser Ser Glu Ile Pro
 340 345 350
 Phe Asn Arg Arg Phe Asp Thr Lys Asn Phe Asn Lys Lys Ala Leu Val
 355 360 365
 Lys Arg Asn Glu Glu Met Arg Glu Trp Leu Ile Asp Thr Phe Phe Lys
 370 375 380
 Asp Phe Ala Ala His
 385

<210> 493
 <211> 889
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (16)...(840)

<400> 493
 ttataaagga aaatc atg gga ttt tta aaa ggt aaa aaa ggg ctt att gta 51
 Met Gly Phe Leu Lys Gly Lys Lys Gly Leu Ile Val
 1 5 10
 ggg gtg gcg aac aat aaa tcc atc gct tat ggg atc gct caa tct tgt 99
 Gly Val Ala Asn Asn Lys Ser Ile Ala Tyr Gly Ile Ala Gln Ser Cys
 15 20 25
 ttc aat caa ggg gct act ttg gct ttc act tat ttg aat gag agt tta 147
 Phe Asn Gln Gly Ala Thr Leu Ala Phe Thr Tyr Leu Asn Glu Ser Leu
 30 35 40
 gaa aag cgc gta agg cct atc gcg cag gaa ttg aat agc ccc tat gtg 195
 Glu Lys Arg Val Arg Pro Ile Ala Gln Glu Leu Asn Ser Pro Tyr Val
 45 50 55 60
 tat gaa ttg gat gtg agc aaa gaa gag cat ttc aag tcg cta tac aat 243
 Tyr Glu Leu Asp Val Ser Lys Glu Glu His Phe Lys Ser Leu Tyr Asn
 65 70 75
 agc gtt aaa aag gat tta ggc tca ttg gat ttt att gtt cat agc gtg 291
 Ser Val Lys Lys Asp Leu Gly Ser Leu Asp Phe Ile Val His Ser Val
 80 85 90
 gcc ttt gcc cct aaa gag gct tta gag ggg agc ttg ttg gaa act tct 339
 Ala Phe Ala Pro Lys Glu Ala Leu Glu Gly Ser Leu Leu Glu Thr Ser
 95 100 105
 aaa agc gcg ttt aac acc gct atg gaa att tct gtt tat tct tta ata 387
 Lys Ser Ala Phe Asn Thr Ala Met Glu Ile Ser Val Tyr Ser Leu Ile
 110 115 120
 gag ctg aca aac acc cta aaa cct tta ttg aat aac gga gcg tct gtt 435

[illegible]

Lys Glu Ala Leu Glu Gly Ser Leu Leu Glu Thr Ser Lys Ser Ala Phe
 100 105 110
 Asn Thr Ala Met Glu Ile Ser Val Tyr Ser Leu Ile Glu Leu Thr Asn
 115 120 125
 Thr Leu Lys Pro Leu Leu Asn Asn Gly Ala Ser Val Leu Thr Leu Ser
 130 135 140
 Tyr Leu Gly Ser Thr Lys Tyr Met Ala His Tyr Asn Val Met Gly Leu
 145 150 155 160
 Ala Lys Ala Ala Leu Glu Ser Ala Val Arg Tyr Leu Ala Val Asp Leu
 165 170 175
 Gly Lys His His Ile Arg Val Asn Ala Leu Ser Ala Gly Pro Ile Arg
 180 185 190
 Thr Leu Ala Ser Ser Gly Ile Ala Asp Phe Arg Met Ile Leu Lys Trp
 195 200 205
 Asn Glu Ile Asn Ala Pro Leu Arg Lys Asn Val Ser Leu Glu Glu Val
 210 215 220
 Gly Asn Ala Gly Met Tyr Leu Leu Ser Ser Leu Ser Ser Gly Val Ser
 225 230 235 240
 Gly Glu Val His Phe Val Asp Ala Gly Tyr His Val Met Gly Met Gly
 245 250 255
 Ala Val Glu Glu Lys Asp Asn Lys Ala Thr Leu Leu Trp Asp Leu His
 260 265 270
 Lys Glu Gln
 275

<210> 495
 <211> 1760
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (33) ... (1688)

<400> 495
 tggagggttag taatttttaa gggtaaaata aa atg gaa aat cat tcg cat gcc 53
 Met Glu Asn His Ser His Ala
 1 5

 aat acg cat acc gat acg cgc acc gat gat aaa agc act aag atc gtg 101
 Asn Thr His Thr Asp Thr Arg Thr Asp Asp Lys Ser Thr Lys Ile Val
 10 15 20

 cgc ttg ttg ggg tta ata ggg gga gcg tta atc gcg ctt gtt atc tac 149
 Arg Leu Leu Gly Leu Ile Gly Gly Ala Leu Ile Ala Leu Val Ile Tyr
 25 30 35

 tat gcg ctc aat tct caa atg cct cat att gta gaa gaa atc ccc aag 197
 Tyr Ala Leu Asn Ser Gln Met Pro His Ile Val Glu Glu Ile Pro Lys
 40 45 50 55

 ctc agt tct ttg aat tat aag gcg atg cct gtt gtg gca ggg gtg gct 245
 Leu Ser Ser Leu Asn Tyr Lys Ala Met Pro Val Val Ala Gly Val Ala
 60 65 70

 gtt tta atg ggg ata tgg tgg atg act gaa gcc att gac ttg ccc gca 293
 Val Leu Met Gly Ile Trp Trp Met Thr Glu Ala Ile Asp Leu Pro Ala
 75 80 85

acc gcg ctt tta cct ttg gtg ctt ttt agc gtc ttt agc gtg gat caa	341
Thr Ala Leu Leu Pro Leu Val Leu Phe Ser Val Phe Ser Val Asp Gln	
90 95 100	
ttc gct agc gtc agc tct tct tac gca tgc ccg atc atc ttt ctt ttt	389
Phe Ala Ser Val Ser Ser Ser Tyr Ala Ser Pro Ile Ile Phe Leu Phe	
105 110 115	
atg gga ggg ttt att tta gcc cta agc atg caa aaa tgg aat ttg cac	437
Met Gly Gly Phe Ile Leu Ala Leu Ser Met Gln Lys Trp Asn Leu His	
120 125 130 135	
acg cgc atc gct tta agc att att tta tta gta ggc aca agc cct agg	485
Thr Arg Ile Ala Leu Ser Ile Ile Leu Leu Val Gly Thr Ser Pro Arg	
140 145 150	
agg ttg att tta ggt ttc atg atg gct aca ggc ttt ctg tct atg tgg	533
Arg Leu Ile Leu Gly Phe Met Met Ala Thr Gly Phe Leu Ser Met Trp	
155 160 165	
gtg agc aat acc gca acg gcg gtg atg atg ctc cct gtt ggc atg agc	581
Val Ser Asn Thr Ala Thr Ala Val Met Met Leu Pro Val Gly Met Ser	
170 175 180	
gtt ttg caa tta gtc gct aaa ctg gtg ggc aaa gaa gac gcc tct aat	629
Val Leu Gln Leu Val Ala Lys Leu Val Gly Lys Glu Asp Ala Ser Asn	
185 190 195	
tca tgg cat caa aaa gaa gaa atc acc aaa gcg cat ggg ggt att atg	677
Ser Trp His Gln Lys Glu Glu Ile Thr Lys Ala His Gly Gly Ile Met	
200 205 210 215	
agt aat atc gtg cat aag ggt aaa gat att act caa gtc att caa gaa	725
Ser Asn Ile Val His Lys Gly Lys Asp Ile Thr Gln Val Ile Gln Glu	
220 225 230	
aag act act atc tat cgc acg aat ttc agt att tgc ttg atg ctt ggc	773
Lys Thr Thr Ile Tyr Arg Thr Asn Phe Ser Ile Cys Leu Met Leu Gly	
235 240 245	
atc gct tat gcg gct tct att ggc tct tta ggc act ttg att ggc acg	821
Ile Ala Tyr Ala Ala Ser Ile Gly Ser Leu Gly Thr Leu Ile Gly Thr	
250 255 260	
ccg cct aac gct tta ttg gcc ggc tat atg aaa acc gct ttc aat att	869
Pro Pro Asn Ala Leu Leu Ala Gly Tyr Met Lys Thr Ala Phe Asn Ile	
265 270 275	
gaa att gat ttc gct cag tgg atg gtg ttt ggg acg ccg tta gcc ttt	917
Glu Ile Asp Phe Ala Gln Trp Met Val Phe Gly Thr Pro Leu Ala Phe	
280 285 290 295	
atc atg ctc att tta gcg tgg ctc ttg ctc act tat gtg att ttc cct	965
Ile Met Leu Ile Leu Ala Trp Leu Leu Leu Thr Tyr Val Ile Phe Pro	
300 305 310	
tta aag att aaa gaa atc cca ggg ggt aag gaa gtc att agg gta gag	1013
Leu Lys Ile Lys Glu Ile Pro Gly Gly Lys Glu Val Ile Arg Val Glu	

315	320	325	
tta aaa aaa tta ggc cgt ttg agt cag gcg gaa atc tct gtg ggg att Leu Lys Lys Leu Gly Arg Leu Ser Gln Ala Glu Ile Ser Val Gly Ile 330 335 340			1061
att ttt att tta gcg tct tta ggg tgg att ttt tta ggc gta atg tta Ile Phe Ile Leu Ala Ser Leu Gly Trp Ile Phe Leu Gly Val Met Leu 345 350 355			1109
aaa tct tgg ggc gtt aag ata gat aaa att gat tca gtg atc gct atg Lys Ser Trp Gly Val Lys Ile Asp Lys Ile Asp Ser Val Ile Ala Met 360 365 370 375			1157
ggg gtt tct gcg ctt tta ttc att ttg ccc gct aac cat cag ggc gat Gly Val Ser Ala Leu Leu Phe Ile Leu Pro Ala Asn His Gln Gly Asp 380 385 390			1205
agg ctc att gat tgg ggt gtt gct aaa aaa ctc cct tgg gat gtg ttg Arg Leu Ile Asp Trp Gly Val Ala Lys Lys Leu Pro Trp Asp Val Leu 395 400 405			1253
ctt tta ttt ggc ggc ggg tta gcc ttg agc gcg caa ttt tct aaa acc Leu Leu Phe Gly Gly Gly Leu Ala Leu Ser Ala Gln Phe Ser Lys Thr 410 415 420			1301
ggg ttg agt ttg tgg atc ggg cat tta gtc tct ggc ttt tcg cat tta Gly Leu Ser Leu Trp Ile Gly His Leu Val Ser Gly Phe Ser His Leu 425 430 435			1349
ccg att tta ttc atc att gtc atg gtt act tta atg gtc att ttc tta Pro Ile Leu Phe Ile Ile Val Met Val Thr Leu Met Val Ile Phe Leu 440 445 450 455			1397
acc gaa atc act tct aac acc gcc acc gct gcc gca ttt tta ccg gtg Thr Glu Ile Thr Ser Asn Thr Ala Thr Ala Ala Ala Phe Leu Pro Val 460 465 470			1445
att gga ggg gtt gcg atg ggc atg ggt tat gaa aac cat cag agc ttg Ile Gly Gly Val Ala Met Gly Met Gly Tyr Glu Asn His Gln Ser Leu 475 480 485			1493
tta ttg acc att cct gta gcc ttg agt gcg act tgc gcg ttc atg ctc Leu Leu Thr Ile Pro Val Ala Leu Ser Ala Thr Cys Ala Phe Met Leu 490 495 500			1541
cct gtg gtc acc cca ccg aat gca ata gct tat ggc tct ggg tat gtt Pro Val Val Thr Pro Pro Asn Ala Ile Ala Tyr Gly Ser Gly Tyr Val 505 510 515			1589
aaa ata acg gac atg att aaa gcc ggt ttg tgg ctt aat ctg gta gga Lys Ile Thr Asp Met Ile Lys Ala Gly Leu Trp Leu Asn Leu Val Gly 520 525 530 535			1637
gtt gtt ttg att agc acg ttt agc tat ttt ttg gtt tcg tta ata ttt Val Val Leu Ile Ser Thr Phe Ser Tyr Phe Leu Val Ser Leu Ile Phe 540 545 550			1685
aat tgattaagga aaaaagtga agaagagtta tttaaagaaa aatctcgta			1738

Asn

cattacaggg tttgttttaa tc

1760

<210> 496

<211> 552

<212> PRT

<213> *Helicobacter pylori*

<400> 496

Met	Glu	Asn	His	Ser	His	Ala	Asn	Thr	His	Thr	Asp	Thr	Arg	Thr	Asp
1				5					10					15	
Asp	Lys	Ser	Thr	Lys	Ile	Val	Arg	Leu	Leu	Gly	Leu	Ile	Gly	Gly	Ala
			20					25					30		
Leu	Ile	Ala	Leu	Val	Ile	Tyr	Tyr	Ala	Leu	Asn	Ser	Gln	Met	Pro	His
		35					40					45			
Ile	Val	Glu	Glu	Ile	Pro	Lys	Leu	Ser	Ser	Leu	Asn	Tyr	Lys	Ala	Met
	50					55					60				
Pro	Val	Val	Ala	Gly	Val	Ala	Val	Leu	Met	Gly	Ile	Trp	Trp	Met	Thr
65				70						75					80
Glu	Ala	Ile	Asp	Leu	Pro	Ala	Thr	Ala	Leu	Leu	Pro	Leu	Val	Leu	Phe
			85					90						95	
Ser	Val	Phe	Ser	Val	Asp	Gln	Phe	Ala	Ser	Val	Ser	Ser	Ser	Tyr	Ala
			100					105						110	
Ser	Pro	Ile	Ile	Phe	Leu	Phe	Met	Gly	Gly	Phe	Ile	Leu	Ala	Leu	Ser
		115					120					125			
Met	Gln	Lys	Trp	Asn	Leu	His	Thr	Arg	Ile	Ala	Leu	Ser	Ile	Ile	Leu
	130					135					140				
Leu	Val	Gly	Thr	Ser	Pro	Arg	Arg	Leu	Ile	Leu	Gly	Phe	Met	Met	Ala
145					150					155					160
Thr	Gly	Phe	Leu	Ser	Met	Trp	Val	Ser	Asn	Thr	Ala	Thr	Ala	Val	Met
				165					170					175	
Met	Leu	Pro	Val	Gly	Met	Ser	Val	Leu	Gln	Leu	Val	Ala	Lys	Leu	Val
			180					185					190		
Gly	Lys	Glu	Asp	Ala	Ser	Asn	Ser	Trp	His	Gln	Lys	Glu	Glu	Ile	Thr
		195					200					205			
Lys	Ala	His	Gly	Gly	Ile	Met	Ser	Asn	Ile	Val	His	Lys	Gly	Lys	Asp
	210					215					220				
Ile	Thr	Gln	Val	Ile	Gln	Glu	Lys	Thr	Thr	Ile	Tyr	Arg	Thr	Asn	Phe
225					230					235					240
Ser	Ile	Cys	Leu	Met	Leu	Gly	Ile	Ala	Tyr	Ala	Ala	Ser	Ile	Gly	Ser
				245					250					255	
Leu	Gly	Thr	Leu	Ile	Gly	Thr	Pro	Pro	Asn	Ala	Leu	Leu	Ala	Gly	Tyr
			260					265					270		
Met	Lys	Thr	Ala	Phe	Asn	Ile	Glu	Ile	Asp	Phe	Ala	Gln	Trp	Met	Val
		275					280					285			
Phe	Gly	Thr	Pro	Leu	Ala	Phe	Ile	Met	Leu	Ile	Leu	Ala	Trp	Leu	Leu
	290					295					300				
Leu	Thr	Tyr	Val	Ile	Phe	Pro	Leu	Lys	Ile	Lys	Glu	Ile	Pro	Gly	Gly
305					310					315					320
Lys	Glu	Val	Ile	Arg	Val	Glu	Leu	Lys	Lys	Leu	Gly	Arg	Leu	Ser	Gln
				325					330					335	
Ala	Glu	Ile	Ser	Val	Gly	Ile	Ile	Phe	Ile	Leu	Ala	Ser	Leu	Gly	Trp
			340					345					350		
Ile	Phe	Leu	Gly	Val	Met	Leu	Lys	Ser	Trp	Gly	Val	Lys	Ile	Asp	Lys
	355						360					365			
Ile	Asp	Ser	Val	Ile	Ala	Met	Gly	Val	Ser	Ala	Leu	Leu	Phe	Ile	Leu
	370					375					380				

Pro	Ala	Asn	His	Gln	Gly	Asp	Arg	Leu	Ile	Asp	Trp	Gly	Val	Ala	Lys
385					390					395					400
Lys	Leu	Pro	Trp	Asp	Val	Leu	Leu	Leu	Phe	Gly	Gly	Gly	Leu	Ala	Leu
				405					410					415	
Ser	Ala	Gln	Phe	Ser	Lys	Thr	Gly	Leu	Ser	Leu	Trp	Ile	Gly	His	Leu
		420					425						430		
Val	Ser	Gly	Phe	Ser	His	Leu	Pro	Ile	Leu	Phe	Ile	Ile	Val	Met	Val
	435					440						445			
Thr	Leu	Met	Val	Ile	Phe	Leu	Thr	Glu	Ile	Thr	Ser	Asn	Thr	Ala	Thr
450					455					460					
Ala	Ala	Ala	Phe	Leu	Pro	Val	Ile	Gly	Gly	Val	Ala	Met	Gly	Met	Gly
465				470					475						480
Tyr	Glu	Asn	His	Gln	Ser	Leu	Leu	Leu	Thr	Ile	Pro	Val	Ala	Leu	Ser
		485						490						495	
Ala	Thr	Cys	Ala	Phe	Met	Leu	Pro	Val	Val	Thr	Pro	Pro	Asn	Ala	Ile
		500					505						510		
Ala	Tyr	Gly	Ser	Gly	Tyr	Val	Lys	Ile	Thr	Asp	Met	Ile	Lys	Ala	Gly
	515					520						525			
Leu	Trp	Leu	Asn	Leu	Val	Gly	Val	Val	Leu	Ile	Ser	Thr	Phe	Ser	Tyr
	530				535						540				
Phe	Leu	Val	Ser	Leu	Ile	Phe	Asn								
545					550										

<210> 497

<211> 661

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (53)...(592)

<400> 497

gggtggcggcg tattttaacg ggcgtcctat agaatgcgct cttattagcg cc atg gtc 58
Met Val
1

atg	gct	agt	gtt	atc	gct	tat	caa	aaa	gcg	cac	cat	agc	gaa	gcc	att	106
Met	Ala	Ser	Val	Ile	Ala	Tyr	Gln	Lys	Ala	His	His	Ser	Glu	Ala	Ile	
		5					10					15				

tta	ccc	ttt	ttg	tat	ccg	ggc	gtt	ggg	ttt	ttt	gcg	ctt	ttt	ggg	gtt	154
Leu	Pro	Phe	Leu	Tyr	Pro	Gly	Val	Gly	Phe	Phe	Ala	Leu	Phe	Gly	Val	
	20					25					30					

tat	aag	gat	ttt	ggt	gca	gta	gcg	atc	att	tgg	ctt	tta	gtc	gtg	gtg	202
Tyr	Lys	Asp	Phe	Gly	Ala	Val	Ala	Ile	Ile	Trp	Leu	Leu	Val	Val	Val	
	35				40					45					50	

gtt	gca	agc	gat	gtg	ggg	gcg	ttt	ttt	gga	ggc	aag	ctt	tta	ggc	aaa	250
Val	Ala	Ser	Asp	Val	Gly	Ala	Phe	Phe	Gly	Gly	Lys	Leu	Leu	Gly	Lys	
				55					60					65		

acc	cct	ttc	acg	ccc	act	tcg	ccg	aat	aaa	acc	tta	gag	ggc	gcg	ttg	298
Thr	Pro	Phe	Thr	Pro	Thr	Ser	Pro	Asn	Lys	Thr	Leu	Glu	Gly	Ala	Leu	
			70					75					80			

att	ggc	gtg	gtt	ttg	gcg	agc	gtt	tta	gga	tcg	ttt	gtg	ggc	atg	ggg	346
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Ile	Gly	Val	Val	Leu	Ala	Ser	Val	Leu	Gly	Ser	Phe	Val	Gly	Met	Gly		
		85					90					95					
aaa	ttg	agc	gga	ggc	ttt	ttt	atg	gcg	ctc	ttt	ttt	agt	ttt	tta	atc	394	
Lys	Leu	Ser	Gly	Gly	Phe	Phe	Met	Ala	Leu	Phe	Phe	Ser	Phe	Leu	Ile		
	100					105					110						
gct	ctt	gtg	gcg	gtg	ttt	ggg	gat	ttg	tat	gaa	agc	tat	ttg	aaa	aga	442	
Ala	Leu	Val	Ala	Val	Phe	Gly	Asp	Leu	Tyr	Glu	Ser	Tyr	Leu	Lys	Arg		
115					120					125					130		
aag	gtc	ggc	atc	aaa	gat	agc	ggc	aag	att	tta	ccc	ggg	cat	ggg	ggc	490	
Lys	Val	Gly	Ile	Lys	Asp	Ser	Gly	Lys	Ile	Leu	Pro	Gly	His	Gly	Gly		
			135					140						145			
gtt	tta	gac	cgg	ttg	gat	tcc	atg	ctt	ttt	ggg	gct	tta	ggc	ttg	cat	538	
Val	Leu	Asp	Arg	Leu	Asp	Ser	Met	Leu	Phe	Gly	Ala	Leu	ggc	ttg	cat		
		150					155						160				
gcg	ctg	ttg	tat	ttt	tta	gaa	att	tgg	aaa	gaa	acg	gcg	gtg	ttt	tta	586	
Ala	Leu	Leu	Tyr	Phe	Leu	Glu	Ile	Trp	Lys	Glu	Thr	Ala	Val	Phe	Leu		
	165					170					175						
ggg	gat	tgaatgggttg	ttttaggaag	caccggctct	attgggaaaa	acgccctaaa	642										
Gly	Asp																
	180																
aatcgcaaaa	aaatttggc															661	

<210> 498
 <211> 180
 <212> PRT
 <213> Helicobacter pylori

Met	Val	Met	Ala	Ser	Val	Ile	Ala	Tyr	Gln	Lys	Ala	His	His	Ser	Glu		
1				5					10					15			
Ala	Ile	Leu	Pro	Phe	Leu	Tyr	Pro	Gly	Val	Gly	Phe	Phe	Ala	Leu	Phe		
		20						25					30				
Gly	Val	Tyr	Lys	Asp	Phe	Gly	Ala	Val	Ala	Ile	Ile	Trp	Leu	Leu	Val		
	35					40						45					
Val	Val	Val	Ala	Ser	Asp	Val	Gly	Ala	Phe	Phe	Gly	Gly	Lys	Leu	Leu		
	50				55						60						
Gly	Lys	Thr	Pro	Phe	Thr	Pro	Thr	Ser	Pro	Asn	Lys	Thr	Leu	Glu	Gly		
65					70				75					80			
Ala	Leu	Ile	Gly	Val	Val	Leu	Ala	Ser	Val	Leu	Gly	Ser	Phe	Val	Gly		
			85					90					95				
Met	Gly	Lys	Leu	Ser	Gly	Gly	Phe	Phe	Met	Ala	Leu	Phe	Phe	Ser	Phe		
		100					105						110				
Leu	Ile	Ala	Leu	Val	Ala	Val	Phe	Gly	Asp	Leu	Tyr	Glu	Ser	Tyr	Leu		
	115					120						125					
Lys	Arg	Lys	Val	Gly	Ile	Lys	Asp	Ser	Gly	Lys	Ile	Leu	Pro	Gly	His		
	130					135					140						
Gly	Gly	Val	Leu	Asp	Arg	Leu	Asp	Ser	Met	Leu	Phe	Gly	Ala	Leu	Gly		
145					150				155						160		
Leu	His	Ala	Leu	Leu	Tyr	Phe	Leu	Glu	Ile	Trp	Lys	Glu	Thr	Ala	Val		
			165					170						175			
Phe	Leu	Gly	Asp														
		180															

<210> 499
 <211> 1157
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (12)...(1115)

<400> 499
 taggggattg a atg gtt gtt tta gga agc acc ggc tct att ggg aaa aac 50
 Met Val Val Leu Gly Ser Thr Gly Ser Ile Gly Lys Asn
 1 5 10

gcc cta aaa atc gca aaa aaa ttt ggc ata gaa ata gag gcc tta agc 98
 Ala Leu Lys Ile Ala Lys Lys Phe Gly Ile Glu Ile Glu Ala Leu Ser
 15 20 25

tgt ggg aaa aat atc gct tta atc aat gaa caa atc caa gtt ttc aaa 146
 Cys Gly Lys Asn Ile Ala Leu Ile Asn Glu Gln Ile Gln Val Phe Lys
 30 35 40 45

ccc aag aaa gtg gcg att tta gat cct agc gat ttg aat gat tta gag 194
 Pro Lys Lys Val Ala Ile Leu Asp Pro Ser Asp Leu Asn Asp Leu Glu
 50 55 60

cct ttg ggt gcg gaa gtg ttt gtg ggg tta gag ggc att gat gcg atg 242
 Pro Leu Gly Ala Glu Val Phe Val Gly Leu Glu Gly Ile Asp Ala Met
 65 70 75

ata gaa gag tgc acc tca aat tta gtc ctt aac gcc att gtg ggc gtg 290
 Ile Glu Glu Cys Thr Ser Asn Leu Val Leu Asn Ala Ile Val Gly Val
 80 85 90

gca gga ttg aaa gcg agc ttt aaa agc tta caa agg aat aaa aaa ctg 338
 Ala Gly Leu Lys Ala Ser Phe Lys Ser Leu Gln Arg Asn Lys Lys Leu
 95 100 105

gcc cta gcg aat aaa gaa agc tta gtg agc gcg ggg cat tta tta gac 386
 Ala Leu Ala Asn Lys Glu Ser Leu Val Ser Ala Gly His Leu Leu Asp
 110 115 120 125

att tca caa atc acg ccc att gat agc gag cat ttt ggt ttg tgg gcg 434
 Ile Ser Gln Ile Thr Pro Ile Asp Ser Glu His Phe Gly Leu Trp Ala
 130 135 140

ttg ttg caa aac aag act tta aag cct aaa tcc tta atc att agc gcg 482
 Leu Leu Gln Asn Lys Thr Leu Lys Pro Lys Ser Leu Ile Ile Ser Ala
 145 150 155

agt ggg ggg gct ttc agg gac acg cct tta gaa ttt att cct att caa 530
 Ser Gly Gly Ala Phe Arg Asp Thr Pro Leu Glu Phe Ile Pro Ile Gln
 160 165 170

aac gcg caa aat gcg ctc aag cac cct aat tgg agc atg gga tct aaa 578
 Asn Ala Gln Asn Ala Leu Lys His Pro Asn Trp Ser Met Gly Ser Lys
 175 180 185

atc acc att gat tca gcg agc atg gtc aat aag ctt ttt gaa atc cta	626
Ile Thr Ile Asp Ser Ala Ser Met Val Asn Lys Leu Phe Glu Ile Leu	
190 195 200 205	
gaa act tat tgg ctt ttt ggc gcg tct tta aag att gat gcg ctg att	674
Glu Thr Tyr Trp Leu Phe Gly Ala Ser Leu Lys Ile Asp Ala Leu Ile	
210 215 220	
gaa agg agt tct atc gtg cat gct ttg gtg gag ttt gaa gac aac tct	722
Glu Arg Ser Ser Ile Val His Ala Leu Val Glu Phe Glu Asp Asn Ser	
225 230 235	
atc atc gcg cat tta gcg agc gca gat atg caa tta ccc ata agc tat	770
Ile Ile Ala His Leu Ala Ser Ala Asp Met Gln Leu Pro Ile Ser Tyr	
240 245 250	
gcg atc gat ccg aag ttg gcc tct ttg agc gcg tct atc aag ccc tta	818
Ala Ile Asp Pro Lys Leu Ala Ser Leu Ser Ala Ser Ile Lys Pro Leu	
255 260 265	
gat cta tac gct tta agc gcg att aaa ttt gaa ccc att agc atg gag	866
Asp Leu Tyr Ala Leu Ser Ala Ile Lys Phe Glu Pro Ile Ser Met Glu	
270 275 280 285	
cgc tac act ttg tgg tgt tat aaa gac tta ctg cta gaa aac cct aag	914
Arg Tyr Thr Leu Trp Cys Tyr Lys Asp Leu Leu Glu Asn Pro Lys	
290 295 300	
ctt ggc gtg gtg ctg aat gcg agc aat gaa gtg gcg atg gag aag ttt	962
Leu Gly Val Val Leu Asn Ala Ser Asn Glu Val Ala Met Glu Lys Phe	
305 310 315	
tta aac aaa gag atc gct ttt ggt ggc ctt atc caa acc att tct caa	1010
Leu Asn Lys Glu Ile Ala Phe Gly Gly Leu Ile Gln Thr Ile Ser Gln	
320 325 330	
gcc tta gaa tca tac gat aaa atg cct ttc aag ctc tct agt tta gaa	1058
Ala Leu Glu Ser Tyr Asp Lys Met Pro Phe Lys Leu Ser Ser Leu Glu	
335 340 345	
gaa gtg ctg gaa tta gac aaa gaa gtt agg gag cgt ttt aaa aat gta	1106
Glu Val Leu Glu Leu Asp Lys Glu Val Arg Glu Arg Phe Lys Asn Val	
350 355 360 365	
gcg gga gtg tagtataata agattttgct tctaatagcg ttttatttca	1155
Ala Gly Val	
at	1157
<210> 500	
<211> 368	
<212> PRT	
<213> Helicobacter pylori	
<400> 500	
Met Val Val Leu Gly Ser Thr Gly Ser Ile Gly Lys Asn Ala Leu Lys	
1 5 10 15	
Ile Ala Lys Lys Phe Gly Ile Glu Ile Glu Ala Leu Ser Cys Gly Lys	

ctc tgg gac gca tat tct aaa gaa gtt caa agg cgc atg gac aac ccc	99
Leu Trp Asp Ala Tyr Ser Lys Glu Val Gln Arg Arg Met Asp Asn Pro	
15 20 25	
acg cat tta ggg gtc atc acc gaa gag cag gct aaa gcc aaa aac gct	147
Thr His Leu Gly Val Ile Thr Glu Glu Gln Ala Lys Ala Lys Asn Ala	
30 35 40	
aag ctc att gtg gcg gat tat ggc gca gag gca tgc ggt gat gcg gtg	195
Lys Leu Ile Val Ala Asp Tyr Gly Ala Glu Ala Cys Gly Asp Ala Val	
45 50 55	
agg ttg tat tgg ctt gta gat gaa agc acg gat aga att gtt gac gcg	243
Arg Leu Tyr Trp Leu Val Asp Glu Ser Thr Asp Arg Ile Val Asp Ala	
60 65 70	
aag ttt aaa agc ttt ggt tgc gga aca gcg atc gca agc tca gac atg	291
Lys Phe Lys Ser Phe Gly Cys Gly Thr Ala Ile Ala Ser Ser Asp Met	
75 80 85 90	
atg gta gag ttg tgc ttg aat aaa aga gtc caa gat gcg gta aaa atc	339
Met Val Glu Leu Cys Leu Asn Lys Arg Val Gln Asp Ala Val Lys Ile	
95 100 105	
acg aat tta gat gtg gaa aga ggc ttg aga gac gat ccg gac acg ccg	387
Thr Asn Leu Asp Val Glu Arg Gly Leu Arg Asp Asp Pro Asp Thr Pro	
110 115 120	
gcg gtg cct ggg caa aaa atg cac tgc tcg gtg atg gcg tat gat gtg	435
Ala Val Pro Gly Gln Lys Met His Cys Ser Val Met Ala Tyr Asp Val	
125 130 135	
atc aaa aaa gct gcc ggc atg tat ttg ggg aaa aac gct gaa gat ttt	483
Ile Lys Lys Ala Ala Gly Met Tyr Leu Gly Lys Asn Ala Glu Asp Phe	
140 145 150	
gaa gaa gaa atc atc gtg tgc gag tgc gct agg gtg agt tta ggt acg	531
Glu Glu Glu Ile Ile Val Cys Glu Cys Ala Arg Val Ser Leu Gly Thr	
155 160 165 170	
att aaa gaa gtg att aag ctc aat gat tta aaa agc gtt gaa gaa atc	579
Ile Lys Glu Val Ile Lys Leu Asn Asp Leu Lys Ser Val Glu Glu Ile	
175 180 185	
act aac tac acc aaa gcc ggt gct ttt tgt aaa agc tgt gtg agg cct	627
Thr Asn Tyr Thr Lys Ala Gly Ala Phe Cys Lys Ser Cys Val Arg Pro	
190 195 200	
gga ggg cat gaa aaa agg gat tat tac ttg gtg gat att ctt aaa gaa	675
Gly Gly His Glu Lys Arg Asp Tyr Tyr Leu Val Asp Ile Leu Lys Glu	
205 210 215	
gtg cgc gaa gaa atg gaa gct gaa aaa ctt aaa gcg acc gct aat aaa	723
Val Arg Glu Glu Met Glu Ala Glu Lys Leu Lys Ala Thr Ala Asn Lys	
220 225 230	
tcc caa agc gga gaa ttg gct ttc agg gaa atg act atg gtt caa aag	771
Ser Gln Ser Gly Glu Leu Ala Phe Arg Glu Met Thr Met Val Gln Lys	
235 240 245 250	

att aaa gcg gtg gat aaa gtc att gat gaa aat atc cgc ccg atg ctt 819
 Ile Lys Ala Val Asp Lys Val Ile Asp Glu Asn Ile Arg Pro Met Leu
 255 260 265

 atg atg gat gga ggg gat tta gag att tta gac att aaa gaa agc gat 867
 Met Met Asp Gly Gly Asp Leu Glu Ile Leu Asp Ile Lys Glu Ser Asp
 270 275 280

 gat tac att gat gtg tat atc cgc tac atg ggg gca tgt gat ggg tgc 915
 Asp Tyr Ile Asp Val Tyr Ile Arg Tyr Met Gly Ala Cys Asp Gly Cys
 285 290 295

 atg agc gcg act acc ggg act tta ttt gcc att gaa aac gct ttg cag 963
 Met Ser Ala Thr Thr Gly Thr Leu Phe Ala Ile Glu Asn Ala Leu Gln
 300 305 310

 gaa tta ttg gat cgc agt atc agg gtg tta ccg att tgaacttttt 1009
 Glu Leu Leu Asp Arg Ser Ile Arg Val Leu Pro Ile
 315 320 325

 agggggtgga ggcctt 1025

<210> 502
 <211> 326
 <212> PRT
 <213> Helicobacter pylori

<400> 502
 Met Ala Lys His Asp Leu Val Gly Ser Val Leu Trp Asp Ala Tyr Ser
 1 5 10 15
 Lys Glu Val Gln Arg Arg Met Asp Asn Pro Thr His Leu Gly Val Ile
 20 25 30
 Thr Glu Glu Gln Ala Lys Ala Lys Asn Ala Lys Leu Ile Val Ala Asp
 35 40 45
 Tyr Gly Ala Glu Ala Cys Gly Asp Ala Val Arg Leu Tyr Trp Leu Val
 50 55 60
 Asp Glu Ser Thr Asp Arg Ile Val Asp Ala Lys Phe Lys Ser Phe Gly
 65 70 75 80
 Cys Gly Thr Ala Ile Ala Ser Ser Asp Met Met Val Glu Leu Cys Leu
 85 90 95
 Asn Lys Arg Val Gln Asp Ala Val Lys Ile Thr Asn Leu Asp Val Glu
 100 105 110
 Arg Gly Leu Arg Asp Asp Pro Asp Thr Pro Ala Val Pro Gly Gln Lys
 115 120 125
 Met His Cys Ser Val Met Ala Tyr Asp Val Ile Lys Lys Ala Ala Gly
 130 135 140
 Met Tyr Leu Gly Lys Asn Ala Glu Asp Phe Glu Glu Glu Ile Ile Val
 145 150 155 160
 Cys Glu Cys Ala Arg Val Ser Leu Gly Thr Ile Lys Glu Val Ile Lys
 165 170 175
 Leu Asn Asp Leu Lys Ser Val Glu Glu Ile Thr Asn Tyr Thr Lys Ala
 180 185 190
 Gly Ala Phe Cys Lys Ser Cys Val Arg Pro Gly Gly His Glu Lys Arg
 195 200 205
 Asp Tyr Tyr Leu Val Asp Ile Leu Lys Glu Val Arg Glu Glu Met Glu
 210 215 220
 Ala Glu Lys Leu Lys Ala Thr Ala Asn Lys Ser Gln Ser Gly Glu Leu
 225 230 235 240

Ala Phe Arg Glu Met Thr Met Val Gln Lys Ile Lys Ala Val Asp Lys
245 250 255
Val Ile Asp Glu Asn Ile Arg Pro Met Leu Met Met Asp Gly Gly Asp
260 265 270
Leu Glu Ile Leu Asp Ile Lys Glu Ser Asp Asp Tyr Ile Asp Val Tyr
275 280 285
Ile Arg Tyr Met Gly Ala Cys Asp Gly Cys Met Ser Ala Thr Thr Gly
290 295 300
Thr Leu Phe Ala Ile Glu Asn Ala Leu Gln Glu Leu Leu Asp Arg Ser
305 310 315 320
Ile Arg Val Leu Pro Ile
325

<210> 503
<211> 414
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (19)...(375)

<400> 503
tagagcttga ttttttta atg tta ata atg gat tgg aaa tta aaa gtg gtg 51
Met Leu Ile Met Asp Trp Lys Leu Lys Val Val
1 5 10
aaa gaa atc atc acc att acc gcc aca acc gcc aca atg ggg atc tta 99
Lys Glu Ile Ile Thr Ile Thr Ala Thr Thr Ala Thr Met Gly Ile Leu
15 20 25
acc aca tat tca tta aac act aat atg agc acc att aaa gaa aag ccg 147
Thr Thr Tyr Ser Leu Asn Thr Asn Met Ser Thr Ile Lys Glu Lys Pro
30 35 40
gca aaa aaa gta gaa agc ctt gtt tta gcc ccg gat ttt gcg tta atg 195
Ala Lys Lys Val Glu Ser Leu Val Leu Ala Pro Asp Phe Ala Leu Met
45 50 55
ata gac tgc ccc act aaa gcg cac cct gtc att ccc ccc aaa agc cct 243
Ile Asp Cys Pro Thr Lys Ala His Pro Val Ile Pro Pro Lys Ser Pro
60 65 70 75
gag atg ata ttc ccc aag cct tgc gct tta gtt tct tta ttt tta tcg 291
Glu Met Ile Phe Pro Lys Pro Cys Ala Leu Val Ser Leu Phe Leu Ser
80 85 90
ctc acg ccg tct ttt aaa atc aca tct aaa gtt tta gcc gtc aat aag 339
Leu Thr Pro Ser Phe Lys Ile Thr Ser Lys Val Leu Ala Val Asn Lys
95 100 105
ctt tct atc gtt ccc act agt gct aaa gaa aga gcg taaggcaaca 385
Leu Ser Ile Val Pro Thr Ser Ala Lys Glu Arg Ala
110 115
actctatcat tattttaaaa tccaaattt 414

<210> 504

<211> 119
 <212> PRT
 <213> Helicobacter pylori

<400> 504
 Met Leu Ile Met Asp Trp Lys Leu Lys Val Val Lys Glu Ile Ile Thr
 1 5 10 15
 Ile Thr Ala Thr Ala Thr Met Gly Ile Leu Thr Thr Tyr Ser Leu
 20 25 30
 Asn Thr Asn Met Ser Thr Ile Lys Glu Lys Pro Ala Lys Lys Val Glu
 35 40 45
 Ser Leu Val Leu Ala Pro Asp Phe Ala Leu Met Ile Asp Cys Pro Thr
 50 55 60
 Lys Ala His Pro Val Ile Pro Pro Lys Ser Pro Glu Met Ile Phe Pro
 65 70 75 80
 Lys Pro Cys Ala Leu Val Ser Leu Phe Leu Ser Leu Thr Pro Ser Phe
 85 90 95
 Lys Ile Thr Ser Lys Val Leu Ala Val Asn Lys Leu Ser Ile Val Pro
 100 105 110
 Thr Ser Ala Lys Glu Arg Ala
 115

<210> 505
 <211> 686
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (16)...(660)

<400> 505
 tataagggttg ctctc atg aaa aaa ccc tat agg aag att tct gat tat gcg 51
 Met Lys Lys Pro Tyr Arg Lys Ile Ser Asp Tyr Ala
 1 5 10
 atc gtg ggt ggt ttg agc gcg tta gtg atg gtg agc att gtg ggg tgt 99
 Ile Val Gly Gly Leu Ser Ala Leu Val Met Val Ser Ile Val Gly Cys
 15 20 25
 aag agc aat gct gat gac aaa cca aaa gag caa agc tct tta agt caa 147
 Lys Ser Asn Ala Asp Asp Lys Pro Lys Glu Gln Ser Ser Leu Ser Gln
 30 35 40
 agc gtt caa aaa ggc gcg ttt gtg att tta gaa gag caa aag gat aaa 195
 Ser Val Gln Lys Gly Ala Phe Val Ile Leu Glu Glu Gln Lys Asp Lys
 45 50 55 60
 tct tac aag gtt gtt gaa gaa tac ccc agc tca aga acc cac att ata 243
 Ser Tyr Lys Val Val Glu Glu Tyr Pro Ser Ser Arg Thr His Ile Ile
 65 70 75
 gtg cgc gat ttg caa ggc aat gaa cgc gtg tta agc aat gaa gag att 291
 Val Arg Asp Leu Gln Gly Asn Glu Arg Val Leu Ser Asn Glu Glu Ile
 80 85 90
 caa aag ctc atc aaa gaa gaa gaa gct aaa att gat aac ggc acg agc 339
 Gln Lys Leu Ile Lys Glu Glu Glu Ala Lys Ile Asp Asn Gly Thr Ser

95	100	105	
aag ctt gtc cag cct aat aat gga ggg agt aat gaa ggc tca ggc ttt			387
Lys Leu Val Gln Pro Asn Asn Gly Gly Ser Asn Glu Gly Ser Gly Phe			
110	115	120	
ggc ttg ggg agc gcg att tta ggg agc gcg gcg ggg gcg att tta ggg			435
Gly Leu Gly Ser Ala Ile Leu Gly Ser Ala Ala Gly Ala Ile Leu Gly			
125	130	135	140
agt tat att ggt aat aag ctt ttc aat aac cct aat tac cag caa aac			483
Ser Tyr Ile Gly Asn Lys Leu Phe Asn Asn Pro Asn Tyr Gln Gln Asn			
145	150	155	
gcc caa cgg acc tac aaa tcc cca caa gct tac caa cgc tct caa aat			531
Ala Gln Arg Thr Tyr Lys Ser Pro Gln Ala Tyr Gln Arg Ser Gln Asn			
160	165	170	
tcc ttt tct aaa agt gcg ccc agt gct tca agc atg ggc gga gcg agt			579
Ser Phe Ser Lys Ser Ala Pro Ser Ala Ser Ser Met Gly Gly Ala Ser			
175	180	185	
aag gga cag agc ggg ttt ttt ggc tct agt agg cct act agt tca ccg			627
Lys Gly Gln Ser Gly Phe Phe Gly Ser Ser Arg Pro Thr Ser Ser Pro			
190	195	200	
gcg gta agc tct ggg aca agg ggc ttt aac tca taattttaatt gattcaaggc			680
Ala Val Ser Ser Gly Thr Arg Gly Phe Asn Ser			
205	210	215	
taaaaa			686

<210> 506
 <211> 215
 <212> PRT
 <213> *Helicobacter pylori*

<400> 506

Met	Lys	Lys	Pro	Tyr	Arg	Lys	Ile	Ser	Asp	Tyr	Ala	Ile	Val	Gly	Gly
1				5					10					15	
Leu	Ser	Ala	Leu	Val	Met	Val	Ser	Ile	Val	Gly	Cys	Lys	Ser	Asn	Ala
			20					25					30		
Asp	Asp	Lys	Pro	Lys	Glu	Gln	Ser	Ser	Leu	Ser	Gln	Ser	Val	Gln	Lys
		35					40					45			
Gly	Ala	Phe	Val	Ile	Leu	Glu	Glu	Gln	Lys	Asp	Lys	Ser	Tyr	Lys	Val
	50				55					60					
Val	Glu	Glu	Tyr	Pro	Ser	Ser	Arg	Thr	His	Ile	Ile	Val	Arg	Asp	Leu
	65				70				75					80	
Gln	Gly	Asn	Glu	Arg	Val	Leu	Ser	Asn	Glu	Glu	Ile	Gln	Lys	Leu	Ile
			85					90					95		
Lys	Glu	Glu	Glu	Ala	Lys	Ile	Asp	Asn	Gly	Thr	Ser	Lys	Leu	Val	Gln
			100				105						110		
Pro	Asn	Asn	Gly	Gly	Ser	Asn	Glu	Gly	Ser	Gly	Phe	Gly	Leu	Gly	Ser
			115				120					125			
Ala	Ile	Leu	Gly	Ser	Ala	Ala	Gly	Ala	Ile	Leu	Gly	Ser	Tyr	Ile	Gly
	130				135					140					
Asn	Lys	Leu	Phe	Asn	Asn	Pro	Asn	Tyr	Gln	Gln	Asn	Ala	Gln	Arg	Thr
	145			150					155					160	
Tyr	Lys	Ser	Pro	Gln	Ala	Tyr	Gln	Arg	Ser	Gln	Asn	Ser	Phe	Ser	Lys

				165					170				175				
Ser	Ala	Pro	Ser	Ala	Ser	Ser	Met	Gly	Gly	Ala	Ser	Lys	Gly	Gln	Ser		
			180					185					190				
Gly	Phe	Phe	Gly	Ser	Ser	Arg	Pro	Thr	Ser	Ser	Pro	Ala	Val	Ser	Ser		
		195					200					205					
Gly	Thr	Arg	Gly	Phe	Asn	Ser											
	210					215											

<210> 507
 <211> 1407
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (16)...(1362)

<400> 507
 ttataggact tttta atg gag tta gaa act cat ttg tca aaa tat ttc acc 51
 Met Glu Leu Glu Thr His Leu Ser Lys Tyr Phe Thr
 1 5 10

cta gcc ttt acg cat aaa agc atg agc tta gaa atg cga gaa aaa ctc 99
 Leu Ala Phe Thr His Lys Ser Met Ser Leu Glu Met Arg Glu Lys Leu
 15 20 25

gct att aat tcg aat gca acg ctt aaa gaa ttt tta caa acc att aaa 147
 Ala Ile Asn Ser Asn Ala Thr Leu Lys Glu Phe Leu Gln Thr Ile Lys
 30 35 40

aac cat tgc cct aac atc aaa gag tgc atg gtg tta tcc aca tgc aat 195
 Asn His Cys Pro Asn Ile Lys Glu Cys Met Val Leu Ser Thr Cys Asn
 45 50 55 60

cgc ttt gaa atc tat gcg agc cta aaa cac gcc gct aat act aat gaa 243
 Arg Phe Glu Ile Tyr Ala Ser Leu Lys His Gly Ala Asn Thr Asn Glu
 65 70 75

caa aaa aac gca cta tta aag att ttg gct caa aat aaa aaa atg agc 291
 Gln Lys Asn Ala Leu Leu Lys Ile Leu Ala Gln Asn Lys Lys Met Ser
 80 85 90

gtg tct gat tta gaa aaa tgc gtt tta atg aac act gat gaa agc gca 339
 Val Ser Asp Leu Glu Lys Cys Val Leu Met Asn Thr Asp Glu Ser Ala
 95 100 105

gtc cat cat gtc ttt agc gtg tgc agc agt ttg gat agc ttg gtg gtt 387
 Val His His Val Phe Ser Val Cys Ser Ser Leu Asp Ser Leu Val Val
 110 115 120

ggg gaa act caa atc aca ggg cag atg aaa aac gct tat aaa ttc gct 435
 Gly Glu Thr Gln Ile Thr Gly Gln Met Lys Asn Ala Tyr Lys Phe Ala
 125 130 135 140

ttt gaa gag aaa ttt tgc tct aaa gat tta acc cga ttg ctc cat ttt 483
 Phe Glu Glu Lys Phe Cys Ser Lys Asp Leu Thr Arg Leu Leu His Phe
 145 150 155

gct ttc aaa tgc gcc gct aaa gtg cgc aat tta acc ggc att tcc aag	531
Ala Phe Lys Cys Ala Ala Lys Val Arg Asn Leu Thr Gly Ile Ser Lys	
160 165 170	
caa ggg gtt tcc atc tct tca gtg gcg gtc aaa gaa gcg ctt aat att	579
Gln Gly Val Ser Ile Ser Ser Val Ala Val Lys Glu Ala Leu Asn Ile	
175 180 185	
ttt gaa aaa gaa agg att aag gat aaa aaa gcc ctt gtg ata ggg ctt	627
Phe Glu Lys Glu Arg Ile Lys Asp Lys Lys Ala Leu Val Ile Gly Leu	
190 195 200	
ggc gag atg gct caa tta gtc atc aag cac ctt tta aac aag caa ttt	675
Gly Glu Met Ala Gln Leu Val Ile Lys His Leu Leu Asn Lys Gln Phe	
205 210 215 220	
gaa gcg ctt atc tta ggg cgt aat gcg gct aaa ttt gaa gat ttc atc	723
Glu Ala Leu Ile Leu Gly Arg Asn Ala Ala Lys Phe Glu Asp Phe Ile	
225 230 235	
aaa gaa tta gaa gaa cct aaa aaa gta agc ttt caa aat ata gaa aat	771
Lys Glu Leu Glu Glu Pro Lys Lys Val Ser Phe Gln Asn Ile Glu Asn	
240 245 250	
tta aac gct tat atc aat gaa tac gaa ctg ctt ttt tgc gcc act tct	819
Leu Asn Ala Tyr Ile Asn Glu Tyr Glu Leu Leu Phe Cys Ala Thr Ser	
255 260 265	
tcg ccg cat ttt atc gtg caa aat cgc atg tta aaa gaa acg att ttc	867
Ser Pro His Phe Ile Val Gln Asn Arg Met Leu Lys Glu Thr Ile Phe	
270 275 280	
agg cgt ttt tgg ttt gat tta gcc gtg cca cgg aat att gaa aag ccg	915
Arg Arg Phe Trp Phe Asp Leu Ala Val Pro Arg Asn Ile Glu Lys Pro	
285 290 295 300	
gta ttg gat aat att ttc tta tac agc gtt gat gat tta gag cct atg	963
Val Leu Asp Asn Ile Phe Leu Tyr Ser Val Asp Asp Leu Glu Pro Met	
305 310 315	
gtg aga gaa aat gtg gaa aac agg caa gag agc aga atg aga gct tat	1011
Val Arg Glu Asn Val Glu Asn Arg Gln Glu Ser Arg Met Arg Ala Tyr	
320 325 330	
gag att gta ggg ctt gcc aca atg gag ttt tac caa tgg att caa agt	1059
Glu Ile Val Gly Leu Ala Thr Met Glu Phe Tyr Gln Trp Ile Gln Ser	
335 340 345	
tta gaa gta gag cct gtg att aag gat tta agg gaa ttg gct agg att	1107
Leu Glu Val Glu Pro Val Ile Lys Asp Leu Arg Glu Leu Ala Arg Ile	
350 355 360	
tca gcc caa aaa gaa ttg caa aaa gcg ctt aaa aaa cgc tat gtg cct	1155
Ser Ala Gln Lys Glu Leu Gln Lys Ala Leu Lys Lys Arg Tyr Val Pro	
365 370 375 380	
aaa gaa tac gaa aac aac att gaa aag atc ttg cac aac gct ttc aac	1203
Lys Glu Tyr Glu Asn Asn Ile Glu Lys Ile Leu His Asn Ala Phe Asn	
385 390 395	

act ttt ttg cat aac cct acc atc gcc tta aaa aag aac gct caa aaa 1251
 Thr Phe Leu His Asn Pro Thr Ile Ala Leu Lys Lys Asn Ala Gln Lys
 400 405 410

gaa gaa tcc gat gtg ctt gtg ggt gcg att aaa aac ttg ttt aat tta 1299
 Glu Glu Ser Asp Val Leu Val Gly Ala Ile Lys Asn Leu Phe Asn Leu
 415 420 425

gac aaa tct aac gct aac cat gcc cag aat ttg aat ctc tat aaa tgc 1347
 Asp Lys Ser Asn Ala Asn His Ala Gln Asn Leu Asn Leu Tyr Lys Cys
 430 435 440

gaa tat tac gag gaa taatgcatgc tattttcaaa actctttgcc cccactctca 1402
 Glu Tyr Tyr Glu Glu
 445

aagaa 1407

<210> 508

<211> 449

<212> PRT

<213> Helicobacter pylori

<400> 508

Met Glu Leu Glu Thr His Leu Ser Lys Tyr Phe Thr Leu Ala Phe Thr
 1 5 10 15
 His Lys Ser Met Ser Leu Glu Met Arg Glu Lys Leu Ala Ile Asn Ser
 20 25 30
 Asn Ala Thr Leu Lys Glu Phe Leu Gln Thr Ile Lys Asn His Cys Pro
 35 40 45
 Asn Ile Lys Glu Cys Met Val Leu Ser Thr Cys Asn Arg Phe Glu Ile
 50 55 60
 Tyr Ala Ser Leu Lys His Gly Ala Asn Thr Asn Glu Gln Lys Asn Ala
 65 70 75 80
 Leu Leu Lys Ile Leu Ala Gln Asn Lys Lys Met Ser Val Ser Asp Leu
 85 90 95
 Glu Lys Cys Val Leu Met Asn Thr Asp Glu Ser Ala Val His His Val
 100 105 110
 Phe Ser Val Cys Ser Ser Leu Asp Ser Leu Val Val Gly Glu Thr Gln
 115 120 125
 Ile Thr Gly Gln Met Lys Asn Ala Tyr Lys Phe Ala Phe Glu Glu Lys
 130 135 140
 Phe Cys Ser Lys Asp Leu Thr Arg Leu Leu His Phe Ala Phe Lys Cys
 145 150 155 160
 Ala Ala Lys Val Arg Asn Leu Thr Gly Ile Ser Lys Gln Gly Val Ser
 165 170 175
 Ile Ser Ser Val Ala Val Lys Glu Ala Leu Asn Ile Phe Glu Lys Glu
 180 185 190
 Arg Ile Lys Asp Lys Lys Ala Leu Val Ile Gly Leu Gly Glu Met Ala
 195 200 205
 Gln Leu Val Ile Lys His Leu Leu Asn Lys Gln Phe Glu Ala Leu Ile
 210 215 220
 Leu Gly Arg Asn Ala Ala Lys Phe Glu Asp Phe Ile Lys Glu Leu Glu
 225 230 235 240
 Glu Pro Lys Lys Val Ser Phe Gln Asn Ile Glu Asn Leu Asn Ala Tyr
 245 250 255
 Ile Asn Glu Tyr Glu Leu Leu Phe Cys Ala Thr Ser Ser Pro His Phe
 260 265 270

Ile	Val	Gln	Asn	Arg	Met	Leu	Lys	Glu	Thr	Ile	Phe	Arg	Arg	Phe	Trp	
		275					280					285				
Phe	Asp	Leu	Ala	Val	Pro	Arg	Asn	Ile	Glu	Lys	Pro	Val	Leu	Asp	Asn	
		290				295					300					
Ile	Phe	Leu	Tyr	Ser	Val	Asp	Asp	Leu	Glu	Pro	Met	Val	Arg	Glu	Asn	
305				310					315					320		
Val	Glu	Asn	Arg	Gln	Glu	Ser	Arg	Met	Arg	Ala	Tyr	Glu	Ile	Val	Gly	
			325						330					335		
Leu	Ala	Thr	Met	Glu	Phe	Tyr	Gln	Trp	Ile	Gln	Ser	Leu	Glu	Val	Glu	
		340						345					350			
Pro	Val	Ile	Lys	Asp	Leu	Arg	Glu	Leu	Ala	Arg	Ile	Ser	Ala	Gln	Lys	
		355					360					365				
Glu	Leu	Gln	Lys	Ala	Leu	Lys	Lys	Arg	Tyr	Val	Pro	Lys	Glu	Tyr	Glu	
		370				375					380					
Asn	Asn	Ile	Glu	Lys	Ile	Leu	His	Asn	Ala	Phe	Asn	Thr	Phe	Leu	His	
385					390					395					400	
Asn	Pro	Thr	Ile	Ala	Leu	Lys	Lys	Asn	Ala	Gln	Lys	Glu	Glu	Ser	Asp	
			405						410					415		
Val	Leu	Val	Gly	Ala	Ile	Lys	Asn	Leu	Phe	Asn	Leu	Asp	Lys	Ser	Asn	
			420					425					430			
Ala	Asn	His	Ala	Gln	Asn	Leu	Asn	Leu	Tyr	Lys	Cys	Glu	Tyr	Tyr	Glu	
		435					440					445				
Glu																

<210> 509
 <211> 1202
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (40)...(1125)

<400> 509	
aaaacccaaa cgccgttaaa atatttaaaa aggaaattc atg ccc att gat ttg	54
Met Pro Ile Asp Leu	
1 5	
aac gaa cat tta aaa aag aaa aat tct caa aga gaa acc ccc acg cct	102
Asn Glu His Leu Lys Lys Lys Asn Ser Gln Arg Glu Thr Pro Thr Pro	
10 15 20	
aat acg cct aat aat ggg ggg cgt ttc atc ccg ccg tct aat tct ttt	150
Asn Thr Pro Asn Asn Gly Gly Arg Phe Ile Pro Pro Ser Asn Ser Phe	
25 30 35	
aat tct aaa aaa cta tcg gtt tta att gtc att gtc ctt tta ggc gtt	198
Asn Ser Lys Lys Leu Ser Val Leu Ile Val Ile Val Leu Leu Gly Val	
40 45 50	
atc gct ttt ttg gcc aag cct ttt gaa gtg att agc tca gga gaa att	246
Ile Ala Phe Leu Ala Lys Pro Phe Glu Val Ile Ser Ser Gly Glu Ile	
55 60 65	
ggc att aaa atc acc gcc ggg aaa tac gaa ccc acc ccc tta cag cca	294
Gly Ile Lys Ile Thr Ala Gly Lys Tyr Glu Pro Thr Pro Leu Gln Pro	
70 75 80 85	

ggg atc cac ttc ttt gtg cct atc att caa gac att ctc att gtg gat	342
Gly Ile His Phe Phe Val Pro Ile Ile Gln Asp Ile Leu Ile Val Asp	
90 95 100	
aca agg att agg aat atc aat ttt tca cgc acc gaa gac atg ggc gtg	390
Thr Arg Ile Arg Asn Ile Asn Phe Ser Arg Thr Glu Asp Met Gly Val	
105 110 115	
gcg ggt aaa aac caa ggg att ttt aga aac gac gct att aat gtg atg	438
Ala Gly Lys Asn Gln Gly Ile Phe Arg Asn Asp Ala Ile Asn Val Met	
120 125 130	
gat agt agg ggt ttg acc gtt tct att gaa ctc acc gtg caa tac cgc	486
Asp Ser Arg Gly Leu Thr Val Ser Ile Glu Leu Thr Val Gln Tyr Arg	
135 140 145	
tta aac ccc caa acc acc ccc caa acg atc gct act tat ggc ttg tct	534
Leu Asn Pro Gln Thr Thr Pro Gln Thr Ile Ala Thr Tyr Gly Leu Ser	
150 155 160 165	
tgg gag caa aaa atc atc aac cct gtg gtg cgc gat gtg gtg cgc tct	582
Trp Glu Gln Lys Ile Ile Asn Pro Val Val Arg Asp Val Val Arg Ser	
170 175 180	
gtc gtg ggg cgc tat ccg gct gaa gat tta ccc att aag cgc aat gaa	630
Val Val Gly Arg Tyr Pro Ala Glu Asp Leu Pro Ile Lys Arg Asn Glu	
185 190 195	
atc gcc gct ctt att aat agc ggt atc aat aaa gaa gtt tct aag ctc	678
Ile Ala Ala Leu Ile Asn Ser Gly Ile Asn Lys Glu Val Ser Lys Leu	
200 205 210	
cct aac acc cct gtg gaa tta agc tct atc caa ttg aga gaa atc gtc	726
Pro Asn Thr Pro Val Glu Leu Ser Ser Ile Gln Leu Arg Glu Ile Val	
215 220 225	
ttg ccc gct aag att aaa gag caa ata gaa aaa gtc caa atc gcg cgc	774
Leu Pro Ala Lys Ile Lys Glu Gln Ile Glu Lys Val Gln Ile Ala Arg	
230 235 240 245	
caa gaa tca gaa agg gtg aaa tac gag gtg gag cgc tcc aag caa gaa	822
Gln Glu Ser Glu Arg Val Lys Tyr Glu Val Glu Arg Ser Lys Gln Glu	
250 255 260	
gct caa aaa caa gcc gct ctg gct aaa ggg gaa gcg gac gct aac agg	870
Ala Gln Lys Gln Ala Ala Leu Ala Lys Gly Glu Ala Asp Ala Asn Arg	
265 270 275	
att aag gct cag ggc gtg gct gat gcg att gtg att gag gct aag gca	918
Ile Lys Ala Gln Gly Val Ala Asp Ala Ile Val Ile Glu Ala Lys Ala	
280 285 290	
aaa tct caa gct aat tta agc att tcg caa agc ttg agc gac aag ctt	966
Lys Ser Gln Ala Asn Leu Ser Ile Ser Gln Ser Leu Ser Asp Lys Leu	
295 300 305	
tta aga ctg cgc caa att gaa gtt caa ggc cag ttt aat gaa gcg tta	1014
Leu Arg Leu Arg Gln Ile Glu Val Gln Gly Gln Phe Asn Glu Ala Leu	

310	315	320	325	
aaa acg aac aat aac gct caa atc atg ctc act cca ggt ggg gct gtg				1062
Lys Thr Asn Asn Asn Ala Gln Ile Met Leu Thr Pro Gly Gly Ala Val				
	330	335	340	
cct aat att tgg att gac act aaa agc aag gtt aaa tct agt att gcc				1110
Pro Asn Ile Trp Ile Asp Thr Lys Ser Lys Val Lys Ser Ser Ile Ala				
	345	350	355	
gag act aaa gag cct taaaaacgca tggcatctct tgcctttatc caagcttttt				1165
Glu Thr Lys Glu Pro				
	360			

tggagtcttt taagggattt ttaagtcaag cgactct	1202
--	------

<210> 510

<211> 362

<212> PRT

<213> *Helicobacter pylori*

<400> 510

Met Pro Ile Asp Leu Asn Glu His Leu Lys Lys Lys Asn Ser Gln Arg	
1 5 10 15	
Glu Thr Pro Thr Pro Asn Thr Pro Asn Gly Gly Arg Phe Ile Pro	
20 25 30	
Pro Ser Asn Ser Phe Asn Ser Lys Lys Leu Ser Val Leu Ile Val Ile	
35 40 45	
Val Leu Leu Gly Val Ile Ala Phe Leu Ala Lys Pro Phe Glu Val Ile	
50 55 60	
Ser Ser Gly Glu Ile Gly Ile Lys Ile Thr Ala Gly Lys Tyr Glu Pro	
65 70 75 80	
Thr Pro Leu Gln Pro Gly Ile His Phe Phe Val Pro Ile Ile Gln Asp	
85 90 95	
Ile Leu Ile Val Asp Thr Arg Ile Arg Asn Ile Asn Phe Ser Arg Thr	
100 105 110	
Glu Asp Met Gly Val Ala Gly Lys Asn Gln Gly Ile Phe Arg Asn Asp	
115 120 125	
Ala Ile Asn Val Met Asp Ser Arg Gly Leu Thr Val Ser Ile Glu Leu	
130 135 140	
Thr Val Gln Tyr Arg Leu Asn Pro Gln Thr Thr Pro Gln Thr Ile Ala	
145 150 155 160	
Thr Tyr Gly Leu Ser Trp Glu Gln Lys Ile Ile Asn Pro Val Val Arg	
165 170 175	
Asp Val Val Arg Ser Val Val Gly Arg Tyr Pro Ala Glu Asp Leu Pro	
180 185 190	
Ile Lys Arg Asn Glu Ile Ala Ala Leu Ile Asn Ser Gly Ile Asn Lys	
195 200 205	
Glu Val Ser Lys Leu Pro Asn Thr Pro Val Glu Leu Ser Ser Ile Gln	
210 215 220	
Leu Arg Glu Ile Val Leu Pro Ala Lys Ile Lys Glu Gln Ile Glu Lys	
225 230 235 240	
Val Gln Ile Ala Arg Gln Glu Ser Glu Arg Val Lys Tyr Glu Val Glu	
245 250 255	
Arg Ser Lys Gln Glu Ala Gln Lys Gln Ala Ala Leu Ala Lys Gly Glu	
260 265 270	
Ala Asp Ala Asn Arg Ile Lys Ala Gln Gly Val Ala Asp Ala Ile Val	
275 280 285	
Ile Glu Ala Lys Ala Lys Ser Gln Ala Asn Leu Ser Ile Ser Gln Ser	

<400> 511																	
gactaaagag			ccttaaaaaac			gc	atg	gca	tct	ctt	gcc	ttt	atc	caa	gct	ttt	52
							Met	Ala	Ser	Leu	Ala	Phe	Ile	Gln	Ala	Phe	.
							1						5				10
ttg	gag	tct	ttt	aag	gga	ttt	tta	agt	caa	gcg	act	cta	atc	agc	gtt		100
Leu	Glu	Ser	Phe	Lys	Gly	Phe	Leu	Ser	Gln	Ala	Thr	Leu	Ile	Ser	Val		
				15					20					25			
tta	ata	gcg	agc	gtt	tta	atc	ctt	ttt	tgc	gcg	att	ttg	ctc	ctt	ttg		148
Leu	Ile	Ala	Ser	Val	Leu	Ile	Leu	Phe	Cys	Ala	Ile	Leu	Leu	Leu	Leu		
				30					35					40			
gct	ctg	ctt	ttg	aga	aac	cgc	tta	gct	agc	tat	ata	gca	aca	gca	gct		196
Ala	Leu	Leu	Leu	Arg	Asn	Arg	Leu	Ala	Ser	Tyr	Ile	Ala	Thr	Ala	Ala		
				45					50					55			
ttt	ttg	ggg	gcg	ttt	tta	agc	atg	cct	ttt	gtt	ttg	aac	att	tta	ctc		244
Phe	Leu	Gly	Ala	Phe	Leu	Ser	Met	Pro	Phe	Val	Leu	Asn	Ile	Leu	Leu		
				60					65					70			
act	caa	gcg	att	tac	ccc	ata	gaa	aca	cgc	atc	tta	cac	gct	aac	cct		292
Thr	Gln	Ala	Ile	Tyr	Pro	Ile	Glu	Thr	Arg	Ile	Leu	His	Ala	Asn	Pro		
75					80					85					90		
tta	agt	tac	agc	aac	gcc	ttt	tct	ttg	caa	gtg	gga	gtc	aaa	aac	cat		340
Leu	Ser	Tyr	Ser	Asn	Ala	Phe	Ser	Leu	Gln	Val	Gly	Val	Lys	Asn	His		
				95					100					105			
tcc	aaa	ttt	act	cta	aac	aaa	tgc	gtt	tta	cgc	cta	gaa	gtg	ctt	aaa		388
Ser	Lys	Phe	Thr	Leu	Asn	Lys	Cys	Val	Leu	Arg	Leu	Glu	Val	Leu	Lys		
				110					115					120			
aac	cct	cac	aat	ttt	gta	gaa	gag	cat	gct	ttt	aaa	tgg	ttt	gtc	aaa		436
Asn	Pro	His	Asn	Phe	Val	Glu	Glu	His	Ala	Phe	Lys	Trp	Phe	Val	Lys		
				125					130					135			
aaa	agc	tat	gaa	aaa	att	ttt	aaa	gaa	aag	att	ttg	ccc	aaa	gaa	tct		484
Lys	Ser	Tyr	Glu	Lys	Ile	Phe	Lys	Glu	Lys	Ile	Leu	Pro	Lys	Glu	Ser		

140	145	150	
aag gtc ttt tca ttc ttt att gac aac tac cct tat tca aaa acg gcc	532		
Lys Val Phe Ser Phe Phe Ile Asp Asn Tyr Pro Tyr Ser Lys Thr Ala			
155	160	165	170

cct tat caa gtt tct ttg ttt tgt tta taaaaaacta aaagataacg	579
Pro Tyr Gln Val Ser Leu Phe Cys Leu	
175	

cccaagataa cattcattaa aaagcgatta aaaacgctta aaggcataga t	630
--	-----

<210> 512
 <211> 179
 <212> PRT
 <213> Helicobacter pylori

<400> 512

Met	Ala	Ser	Leu	Ala	Phe	Ile	Gln	Ala	Phe	Leu	Glu	Ser	Phe	Lys	Gly
1				5					10					15	
Phe	Leu	Ser	Gln	Ala	Thr	Leu	Ile	Ser	Val	Leu	Ile	Ala	Ser	Val	Leu
			20					25					30		
Ile	Leu	Phe	Cys	Ala	Ile	Leu	Leu	Leu	Ala	Leu	Leu	Leu	Arg	Asn	
		35				40					45				
Arg	Leu	Ala	Ser	Tyr	Ile	Ala	Thr	Ala	Ala	Phe	Leu	Gly	Ala	Phe	Leu
	50				55						60				
Ser	Met	Pro	Phe	Val	Leu	Asn	Ile	Leu	Leu	Thr	Gln	Ala	Ile	Tyr	Pro
65					70					75					80
Ile	Glu	Thr	Arg	Ile	Leu	His	Ala	Asn	Pro	Leu	Ser	Tyr	Ser	Asn	Ala
			85					90						95	
Phe	Ser	Leu	Gln	Val	Gly	Val	Lys	Asn	His	Ser	Lys	Phe	Thr	Leu	Asn
			100					105					110		
Lys	Cys	Val	Leu	Arg	Leu	Glu	Val	Leu	Lys	Asn	Pro	His	Asn	Phe	Val
		115					120					125			
Glu	Glu	His	Ala	Phe	Lys	Trp	Phe	Val	Lys	Lys	Ser	Tyr	Glu	Lys	Ile
	130					135					140				
Phe	Lys	Glu	Lys	Ile	Leu	Pro	Lys	Glu	Ser	Lys	Val	Phe	Ser	Phe	Phe
145					150					155					160
Ile	Asp	Asn	Tyr	Pro	Tyr	Ser	Lys	Thr	Ala	Pro	Tyr	Gln	Val	Ser	Leu
				165					170					175	
Phe	Cys	Leu													

<210> 513
 <211> 1350
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (47)...(1273)

<400> 513

aaagaatgat cttaaaaggg caaaccacat ttattaagga gaatgc atg caa gaa	55
	Met Gln Glu
	1

atc ata gga gcg tct tta gtt ttt ttg tgc aat gaa aag tgc gaa gtg	103
---	-----

Ile	Ile	Gly	Ala	Ser	Leu	Val	Phe	Leu	Cys	Asn	Glu	Lys	Cys	Glu	Val		
5						10					15						
tta	gaa	gat	tat	ggc	gta	gtc	ttt	gat	gaa	aag	att	gtt	gaa	ata	ggc	151	
Leu	Glu	Asp	Tyr	Gly	Val	Val	Phe	Asp	Glu	Lys	Ile	Val	Glu	Ile	Gly		
20				25					30						35		
gat	tat	caa	agt	tta	acg	ctt	aaa	tac	cct	cac	tta	aag	gcg	cag	ttt	199	
Asp	Tyr	Gln	Ser	Leu	Thr	Leu	Lys	Tyr	Pro	His	Leu	Lys	Ala	Gln	Phe		
				40					45					50			
ttt	gaa	aat	tcc	gtt	ctg	ttg	ccc	gct	ttt	atc	aac	gcg	cac	acc	cat	247	
Phe	Glu	Asn	Ser	Val	Leu	Leu	Pro	Ala	Phe	Ile	Asn	Ala	His	Thr	His		
			55				60						65				
ttt	gaa	ttt	tcc	aac	aac	aag	gcg	agt	ttt	gat	tac	ggg	agt	ttt	tct	295	
Phe	Glu	Phe	Ser	Asn	Asn	Lys	Ala	Ser	Phe	Asp	Tyr	Gly	Ser	Phe	Ser		
		70					75					80					
ggc	tgg	tta	ggg	agc	gtg	tta	aac	aat	ggg	ggg	gcg	att	tta	gaa	aat	343	
Gly	Trp	Leu	Gly	Ser	Val	Leu	Asn	Asn	Gly	Gly	Ala	Ile	Leu	Glu	Asn		
	85					90					95						
tgc	caa	ggg	gct	att	caa	aac	gct	atc	agc	acg	caa	tta	aaa	agc	ggg	391	
Cys	Gln	Gly	Ala	Ile	Gln	Asn	Ala	Ile	Ser	Thr	Gln	Leu	Lys	Ser	Gly		
100					105					110					115		
gtg	ggg	agc	gtg	gga	gcg	att	tct	aac	cac	ctg	ata	gaa	gtt	aat	ttg	439	
Val	Gly	Ser	Val	Gly	Ala	Ile	Ser	Asn	His	Leu	Ile	Glu	Val	Asn	Leu		
				120					125					130			
tta	aaa	gaa	agc	cct	ttg	aat	gct	gtc	gtg	ttt	tta	gag	ttt	tta	ggg	487	
Leu	Lys	Glu	Ser	Pro	Leu	Asn	Ala	Val	Val	Phe	Leu	Glu	Phe	Leu	Gly		
				135				140					145				
agc	agt	tat	tct	tta	gaa	aaa	tta	aaa	gcg	ttt	gag	gcc	aaa	ttt	aag	535	
Ser	Ser	Tyr	Ser	Leu	Glu	Lys	Leu	Lys	Ala	Phe	Glu	Ala	Lys	Phe	Lys		
		150					155					160					
gaa	tta	aaa	gat	tta	gaa	gat	aaa	aaa	ctt	aaa	gcg	gct	ctc	gct	gtg	583	
Glu	Leu	Lys	Asp	Leu	Glu	Asp	Lys	Lys	Leu	Lys	Ala	Ala	Leu	Ala	Val		
	165					170					175						
cat	gcc	cct	tat	tcg	gtc	caa	aaa	gac	atg	gct	ttg	agc	gtc	atc	caa	631	
His	Ala	Pro	Tyr	Ser	Val	Gln	Lys	Asp	Met	Ala	Leu	Ser	Val	Ile	Gln		
180					185					190					195		
tta	gcc	aaa	gat	tca	caa	agc	ctg	ctt	tct	acg	cat	ttt	tta	gaa	tcg	679	
Leu	Ala	Lys	Asp	Ser	Gln	Ser	Leu	Leu	Ser	Thr	His	Phe	Leu	Glu	Ser		
				200					205					210			
ctt	gaa	gaa	tta	gaa	tgg	gta	gaa	aac	tct	aaa	ggg	tgg	ttt	gaa	aat	727	
Leu	Glu	Glu	Leu	Glu	Trp	Val	Glu	Asn	Ser	Lys	Gly	Trp	Phe	Glu	Asn		
			215					220					225				
ttt	tac	cag	cat	ttt	tta	aag	gag	tct	cat	ttc	aaa	tcg	ctc	tat	aag	775	
Phe	Tyr	Gln	His	Phe	Leu	Lys	Glu	Ser	His	Phe	Lys	Ser	Leu	Tyr	Lys		
		230					235					240					

ggc gcg aac gat tac att gac atg ttt aaa gac acg cac act tta ttc 823
 Gly Ala Asn Asp Tyr Ile Asp Met Phe Lys Asp Thr His Thr Leu Phe
 245 250 255
 gtg cat aac cag ttc gct tct tta gaa gcg tta aaa agg att aaa tct 871
 Val His Asn Gln Phe Ala Ser Leu Glu Ala Leu Lys Arg Ile Lys Ser
 260 265 270 275
 caa gtc aaa aac gct ttt tta atc aca tgc ccc ttt tct aac cgc cta 919
 Gln Val Lys Asn Ala Phe Leu Ile Thr Cys Pro Phe Ser Asn Arg Leu
 280 285 290
 ttg agc ggg caa gcg ttg gat tta gaa aga act aaa gaa gcc ggt ttg 967
 Leu Ser Gly Gln Ala Leu Asp Leu Glu Arg Thr Lys Glu Ala Gly Leu
 295 300 305
 agc gtg agc gtg gcc act gat ggc ttg agt tct aac att tcg ctg agc 1015
 Ser Val Ser Val Ala Thr Asp Gly Leu Ser Ser Asn Ile Ser Leu Ser
 310 315 320
 ctt tta gac gaa tta aga gcg ttt ttg ctc acc cat aac atg ccg tta 1063
 Leu Leu Asp Glu Leu Arg Ala Phe Leu Leu Thr His Asn Met Pro Leu
 325 330 335
 tta gaa tta gct aaa ata gcc ctt tta ggg gcg act agg cat ggg gct 1111
 Leu Glu Leu Ala Lys Ile Ala Leu Leu Gly Ala Thr Arg His Gly Ala
 340 345 350 355
 aaa gct tta gct ttg aat aat ggc gag ata gaa gcc aac aaa agg gcg 1159
 Lys Ala Leu Ala Leu Asn Asn Gly Glu Ile Glu Ala Asn Lys Arg Ala
 360 365 370
 gat ttg agc gtg ttt ggt ttt aat gaa aaa ttc act aaa gag caa gcg 1207
 Asp Leu Ser Val Phe Gly Phe Asn Glu Lys Phe Thr Lys Glu Gln Ala
 375 380 385
 att ttg caa ttt tta ttg cat gct aaa gaa gtg gag tgc ttg ttt tta 1255
 Ile Leu Gln Phe Leu Leu His Ala Lys Glu Val Glu Cys Leu Phe Leu
 390 395 400
 ggg ggg aaa agg gtg atc taatttgttt taaagacaga atgcgttaaa 1303
 Gly Gly Lys Arg Val Ile
 405

atgagaaatc taaatcaatt aaggaaagag tcaatgaaac tagtttt 1350

<210> 514

<211> 409

<212> PRT

<213> *Helicobacter pylori*

<400> 514

Met Gln Glu Ile Ile Gly Ala Ser Leu Val Phe Leu Cys Asn Glu Lys
 1 5 10 15
 Cys Glu Val Leu Glu Asp Tyr Gly Val Val Phe Asp Glu Lys Ile Val
 20 25 30
 Glu Ile Gly Asp Tyr Gln Ser Leu Thr Leu Lys Tyr Pro His Leu Lys
 35 40 45
 Ala Gln Phe Phe Glu Asn Ser Val Leu Leu Pro Ala Phe Ile Asn Ala

50		55		60													
His	Thr	His	Phe	Glu	Phe	Ser	Asn	Asn	Lys	Ala	Ser	Phe	Asp	Tyr	Gly		
65					70					75					80		
Ser	Phe	Ser	Gly	Trp	Leu	Gly	Ser	Val	Leu	Asn	Asn	Gly	Gly	Ala	Ile		
				85					90					95			
Leu	Glu	Asn	Cys	Gln	Gly	Ala	Ile	Gln	Asn	Ala	Ile	Ser	Thr	Gln	Leu		
			100					105					110				
Lys	Ser	Gly	Val	Gly	Ser	Val	Gly	Ala	Ile	Ser	Asn	His	Leu	Ile	Glu		
		115					120					125					
Val	Asn	Leu	Leu	Lys	Glu	Ser	Pro	Leu	Asn	Ala	Val	Val	Phe	Leu	Glu		
	130					135					140						
Phe	Leu	Gly	Ser	Ser	Tyr	Ser	Leu	Glu	Lys	Leu	Lys	Ala	Phe	Glu	Ala		
145					150					155					160		
Lys	Phe	Lys	Glu	Leu	Lys	Asp	Leu	Glu	Asp	Lys	Lys	Leu	Lys	Ala	Ala		
			165					170						175			
Leu	Ala	Val	His	Ala	Pro	Tyr	Ser	Val	Gln	Lys	Asp	Met	Ala	Leu	Ser		
		180						185				190					
Val	Ile	Gln	Leu	Ala	Lys	Asp	Ser	Gln	Ser	Leu	Leu	Ser	Thr	His	Phe		
	195						200					205					
Leu	Glu	Ser	Leu	Glu	Glu	Leu	Glu	Trp	Val	Glu	Asn	Ser	Lys	Gly	Trp		
	210				215						220						
Phe	Glu	Asn	Phe	Tyr	Gln	His	Phe	Leu	Lys	Glu	Ser	His	Phe	Lys	Ser		
225					230					235					240		
Leu	Tyr	Lys	Gly	Ala	Asn	Asp	Tyr	Ile	Asp	Met	Phe	Lys	Asp	Thr	His		
			245						250					255			
Thr	Leu	Phe	Val	His	Asn	Gln	Phe	Ala	Ser	Leu	Glu	Ala	Leu	Lys	Arg		
		260					265						270				
Ile	Lys	Ser	Gln	Val	Lys	Asn	Ala	Phe	Leu	Ile	Thr	Cys	Pro	Phe	Ser		
	275					280						285					
Asn	Arg	Leu	Leu	Ser	Gly	Gln	Ala	Leu	Asp	Leu	Glu	Arg	Thr	Lys	Glu		
	290				295						300						
Ala	Gly	Leu	Ser	Val	Ser	Val	Ala	Thr	Asp	Gly	Leu	Ser	Ser	Asn	Ile		
305					310					315					320		
Ser	Leu	Ser	Leu	Leu	Asp	Glu	Leu	Arg	Ala	Phe	Leu	Leu	Thr	His	Asn		
			325						330					335			
Met	Pro	Leu	Leu	Glu	Leu	Ala	Lys	Ile	Ala	Leu	Leu	Gly	Ala	Thr	Arg		
		340					345						350				
His	Gly	Ala	Lys	Ala	Leu	Ala	Leu	Asn	Asn	Gly	Glu	Ile	Glu	Ala	Asn		
	355					360						365					
Lys	Arg	Ala	Asp	Leu	Ser	Val	Phe	Gly	Phe	Asn	Glu	Lys	Phe	Thr	Lys		
	370				375						380						
Glu	Gln	Ala	Ile	Leu	Gln	Phe	Leu	Leu	His	Ala	Lys	Glu	Val	Glu	Cys		
385				390					395						400		
Leu	Phe	Leu	Gly	Gly	Lys	Arg	Val	Ile									
			405														

<210> 515
 <211> 1356
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (31)...(1320)

<400> 515
 aggccttgat tgaaagttta tattgaaacc atg ggt tgt gcc atg aat tct agg 54
 Met Gly Cys Ala Met Asn Ser Arg

1										5						
gat	agt	gag	cat	tta	ttg	agc	gag	ctg	tcc	aaa	cta	gac	tat	aaa	gag	102
Asp	Ser	Glu	His	Leu	Leu	Ser	Glu	Leu	Ser	Lys	Leu	Asp	Tyr	Lys	Glu	
10						15			20							
acc	aat	gac	cct	aaa	aca	gcg	gat	ttg	att	tta	atc	aac	act	tgc	agc	150
Thr	Asn	Asp	Pro	Lys	Thr	Ala	Asp	Leu	Ile	Leu	Ile	Asn	Thr	Cys	Ser	
25					30					35		40				
gtg	cgc	gaa	aag	cct	gaa	cga	aaa	ttg	ttt	tca	gaa	atc	ggg	caa	ttc	198
Val	Arg	Glu	Lys	Pro	Glu	Arg	Lys	Leu	Phe	Ser	Glu	Ile	Gly	Gln	Phe	
				45					50		55					
gct	aaa	atc	aaa	aaa	ccc	aac	gcc	aaa	atc	ggg	gtt	tgc	ggg	tgc	act	246
Ala	Lys	Ile	Lys	Lys	Pro	Asn	Ala	Lys	Ile	Gly	Val	Cys	Gly	Cys	Thr	
				60		65			70							
gca	agc	cac	atg	gga	gcg	gat	att	ttg	aaa	aaa	gcc	cca	agc	gtg	agc	294
Ala	Ser	His	Met	Gly	Ala	Asp	Ile	Leu	Lys	Lys	Ala	Pro	Ser	Val	Ser	
75						80			85							
ttt	gtg	tta	ggg	gct	agg	aat	gtg	tct	aaa	atc	tct	caa	gtg	atc	cat	342
Phe	Val	Leu	Gly	Ala	Arg	Asn	Val	Ser	Lys	Ile	Ser	Gln	Val	Ile	His	
90					95		100									
aaa	gaa	aaa	gcg	gtt	gaa	gtg	gcg	att	gat	tat	gat	gaa	agc	gcg	tat	390
Lys	Glu	Lys	Ala	Val	Glu	Val	Ala	Ile	Asp	Tyr	Asp	Glu	Ser	Ala	Tyr	
105					110		115			120						
gcg	ttt	gaa	ttt	ttt	gaa	aaa	aag	gct	caa	atc	cga	tcg	ttg	cta	aat	438
Ala	Phe	Glu	Phe	Phe	Glu	Lys	Lys	Ala	Gln	Ile	Arg	Ser	Leu	Leu	Asn	
				125		130			135							
atc	tct	ata	ggg	tgc	gat	aag	aaa	tgc	gct	tat	tgc	atc	gtc	ccg	cac	486
Ile	Ser	Ile	Gly	Cys	Asp	Lys	Lys	Cys	Ala	Tyr	Cys	Ile	Val	Pro	His	
140						145			150							
act	agg	ggg	aaa	gaa	att	tct	atc	cct	atg	gat	ttg	att	tta	aaa	gaa	534
Thr	Arg	Gly	Lys	Glu	Ile	Ser	Ile	Pro	Met	Asp	Leu	Ile	Leu	Lys	Glu	
155						160			165							
gct	gag	aaa	tta	gcg	aat	aac	ggc	acc	aaa	gag	ctt	atg	ctt	tta	ggg	582
Ala	Glu	Lys	Leu	Ala	Asn	Asn	Gly	Thr	Lys	Glu	Leu	Met	Leu	Leu	Gly	
170					175			180								
cag	aat	gtg	aat	aat	tac	ggc	gcg	cgt	ttc	agc	agc	gag	cat	gcg	aaa	630
Gln	Asn	Val	Asn	Asn	Tyr	Gly	Ala	Arg	Phe	Ser	Ser	Glu	His	Ala	Lys	
185					190		195			200						
gtg	gat	ttt	agc	gat	ttg	ttg	gat	aaa	ttg	agc	gaa	atc	cag	ggg	att	678
Val	Asp	Phe	Ser	Asp	Leu	Leu	Asp	Lys	Leu	Ser	Glu	Ile	Gln	Gly	Ile	
				205		210			215							
gaa	agg	ata	cga	ttc	act	tcg	cct	cac	ccc	ttg	cac	atg	aat	gat	gga	726
Glu	Arg	Ile	Arg	Phe	Thr	Ser	Pro	His	Pro	Leu	His	Met	Asn	Asp	Gly	
220						225			230							
ttt	tta	gag	cgt	ttt	gcc	aaa	aac	cct	aaa	gtg	tgc	aag	agt	atc	cac	774

Phe	Leu	Glu	Arg	Phe	Ala	Lys	Asn	Pro	Lys	Val	Cys	Lys	Ser	Ile	His											
	235						240					245														
atg	cct	tta	cag	agc	gga	tct	agc	gcg	gtg	tta	aag	atg	atg	cga	agg	822										
Met	Pro	Leu	Gln	Ser	Gly	Ser	Ser	Ala	Val	Leu	Lys	Met	Met	Arg	Arg											
	250					255					260															
ggt	tat	agt	aag	gag	tgg	ttt	tta	aat	agg	gtg	gag	agg	tta	aaa	gct	870										
Gly	Tyr	Ser	Lys	Glu	Trp	Phe	Leu	Asn	Arg	Val	Glu	Arg	Leu	Lys	Ala											
265					270					275					280											
tta	gtg	cct	gaa	gtg	ggc	att	agc	acg	gat	att	atc	gta	ggc	ttc	cct	918										
Leu	Val	Pro	Glu	Val	Gly	Ile	Ser	Thr	Asp	Ile	Ile	Val	Gly	Phe	Pro											
				285					290					295												
aat	gag	agc	gat	aag	gat	ttt	gaa	gac	aca	atg	gag	gtg	cta	gaa	aaa	966										
Asn	Glu	Ser	Asp	Lys	Asp	Phe	Glu	Asp	Thr	Met	Glu	Val	Leu	Glu	Lys											
			300					305					310													
gtg	cgc	ttt	gac	acg	ctc	tat	agt	ttc	att	tat	tcc	cca	cgc	cct	ttc	1014										
Val	Arg	Phe	Asp	Thr	Leu	Tyr	Ser	Phe	Ile	Tyr	Ser	Pro	Arg	Pro	Phe											
	315						320					325														
act	gaa	gcg	gga	gct	tgg	aag	gaa	aga	gtg	ccg	tta	gaa	gtt	tca	tct	1062										
Thr	Glu	Ala	Gly	Ala	Trp	Lys	Glu	Arg	Val	Pro	Leu	Glu	Val	Ser	Ser											
	330					335					340															
tca	agg	ttg	gag	agg	ttg	caa	aac	agg	cac	aaa	gaa	att	tta	gaa	gaa	1110										
Ser	Arg	Leu	Glu	Arg	Leu	Gln	Asn	Arg	His	Lys	Glu	Ile	Leu	Glu	Glu											
345					350					355					360											
aaa	gcc	aag	cta	gaa	gtg	ggc	aaa	acg	cat	gtg	gtg	ttg	gtg	gaa	aac	1158										
Lys	Ala	Lys	Leu	Glu	Val	Gly	Lys	Thr	His	Val	Val	Leu	Val	Glu	Asn											
				365					370					375												
agg	cgt	gaa	atg	gat	aat	caa	atc	gtg	ggt	ttt	gaa	ggg	cgt	agc	gat	1206										
Arg	Arg	Glu	Met	Asp	Asn	Gln	Ile	Val	Gly	Phe	Glu	Gly	Arg	Ser	Asp											
			380					385					390													
acg	ggg	aaa	ttc	att	gaa	gta	act	tgt	aag	gaa	aaa	aga	aac	ccg	ggc	1254										
Thr	Gly	Lys	Phe	Ile	Glu	Val	Thr	Cys	Lys	Glu	Lys	Arg	Asn	Pro	Gly											
	395						400					405														
gag	ctt	gta	aaa	gtg	gag	att	att	tct	cat	tcc	aaa	ggg	cgc	ttg	atg	1302										
Glu	Leu	Val	Lys	Val	Glu	Ile	Ile	Ser	His	Ser	Lys	Gly	Arg	Leu	Met											
	410					415					420															
gcg	gcc	act	aaa	ggc	aac	taataaaaaat aaccaatgaa aaagcgggtt										1350										
Ala	Ala	Thr	Lys	Gly	Asn																					
425					430																					
taaagg																1356										
<210> 516																										
<211> 430																										
<212> PRT																										
<213> Helicobacter pylori																										
<400> 516																										

Met	Gly	Cys	Ala	Met	Asn	Ser	Arg	Asp	Ser	Glu	His	Leu	Leu	Ser	Glu
1				5					10					15	
Leu	Ser	Lys	Leu	Asp	Tyr	Lys	Glu	Thr	Asn	Asp	Pro	Lys	Thr	Ala	Asp
			20					25					30		
Leu	Ile	Leu	Ile	Asn	Thr	Cys	Ser	Val	Arg	Glu	Lys	Pro	Glu	Arg	Lys
		35					40					45			
Leu	Phe	Ser	Glu	Ile	Gly	Gln	Phe	Ala	Lys	Ile	Lys	Lys	Pro	Asn	Ala
	50					55					60				
Lys	Ile	Gly	Val	Cys	Gly	Cys	Thr	Ala	Ser	His	Met	Gly	Ala	Asp	Ile
65					70					75					80
Leu	Lys	Lys	Ala	Pro	Ser	Val	Ser	Phe	Val	Leu	Gly	Ala	Arg	Asn	Val
				85					90					95	
Ser	Lys	Ile	Ser	Gln	Val	Ile	His	Lys	Glu	Lys	Ala	Val	Glu	Val	Ala
			100					105					110		
Ile	Asp	Tyr	Asp	Glu	Ser	Ala	Tyr	Ala	Phe	Glu	Phe	Phe	Glu	Lys	Lys
		115					120					125			
Ala	Gln	Ile	Arg	Ser	Leu	Leu	Asn	Ile	Ser	Ile	Gly	Cys	Asp	Lys	Lys
	130					135					140				
Cys	Ala	Tyr	Cys	Ile	Val	Pro	His	Thr	Arg	Gly	Lys	Glu	Ile	Ser	Ile
145					150					155					160
Pro	Met	Asp	Leu	Ile	Leu	Lys	Glu	Ala	Glu	Lys	Leu	Ala	Asn	Asn	Gly
				165					170					175	
Thr	Lys	Glu	Leu	Met	Leu	Leu	Gly	Gln	Asn	Val	Asn	Asn	Tyr	Gly	Ala
			180					185					190		
Arg	Phe	Ser	Ser	Glu	His	Ala	Lys	Val	Asp	Phe	Ser	Asp	Leu	Leu	Asp
		195					200					205			
Lys	Leu	Ser	Glu	Ile	Gln	Gly	Ile	Glu	Arg	Ile	Arg	Phe	Thr	Ser	Pro
	210					215					220				
His	Pro	Leu	His	Met	Asn	Asp	Gly	Phe	Leu	Glu	Arg	Phe	Ala	Lys	Asn
225					230					235					240
Pro	Lys	Val	Cys	Lys	Ser	Ile	His	Met	Pro	Leu	Gln	Ser	Gly	Ser	Ser
				245					250					255	
Ala	Val	Leu	Lys	Met	Met	Arg	Arg	Gly	Tyr	Ser	Lys	Glu	Trp	Phe	Leu
			260					265					270		
Asn	Arg	Val	Glu	Arg	Leu	Lys	Ala	Leu	Val	Pro	Glu	Val	Gly	Ile	Ser
		275					280					285			
Thr	Asp	Ile	Ile	Val	Gly	Phe	Pro	Asn	Glu	Ser	Asp	Lys	Asp	Phe	Glu
	290					295					300				
Asp	Thr	Met	Glu	Val	Leu	Glu	Lys	Val	Arg	Phe	Asp	Thr	Leu	Tyr	Ser
305					310					315					320
Phe	Ile	Tyr	Ser	Pro	Arg	Pro	Phe	Thr	Glu	Ala	Gly	Ala	Trp	Lys	Glu
				325					330					335	
Arg	Val	Pro	Leu	Glu	Val	Ser	Ser	Ser	Arg	Leu	Glu	Arg	Leu	Gln	Asn
			340					345					350		
Arg	His	Lys	Glu	Ile	Leu	Glu	Glu	Lys	Ala	Lys	Leu	Glu	Val	Gly	Lys
		355					360					365			
Thr	His	Val	Val	Leu	Val	Glu	Asn	Arg	Arg	Glu	Met	Asp	Asn	Gln	Ile
	370					375					380				
Val	Gly	Phe	Glu	Gly	Arg	Ser	Asp	Thr	Gly	Lys	Phe	Ile	Glu	Val	Thr
385					390					395					400
Cys	Lys	Glu	Lys	Arg	Asn	Pro	Gly	Glu	Leu	Val	Lys	Val	Glu	Ile	Ile
				405					410					415	
Ser	His	Ser	Lys	Gly	Arg	Leu	Met	Ala	Ala	Thr	Lys	Gly	Asn		
			420					425					430		

<210> 517
 <211> 1530
 <212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (50)...(1501)

<400> 517

attgaaatac aaatacgaaa gcttaaaaaga gcaagattaa aggctagca atg gct aaa 58
Met Ala Lys
1

atc aca acc gtg att gat ata ggc tct aat tca gtg cgt ttg gct gtc 106
Ile Thr Thr Val Ile Asp Ile Gly Ser Asn Ser Val Arg Leu Ala Val
5 10 15

ttt aaa aag acg agc cag ttt ggg ttt tac ttg ctt ttt gag act aag 154
Phe Lys Lys Thr Ser Gln Phe Gly Phe Tyr Leu Leu Phe Glu Thr Lys
20 25 30 35

tct aag gtt agg att tca gag ggc tgt tat gcg ttt aat gga atc ttg 202
Ser Lys Val Arg Ile Ser Glu Gly Cys Tyr Ala Phe Asn Gly Ile Leu
40 45 50

caa gaa atc ccc atg caa cga gcc gtt aaa gcc ttg agc gaa ttt aaa 250
Gln Glu Ile Pro Met Gln Arg Ala Val Lys Ala Leu Ser Glu Phe Lys
55 60 65

gaa atc gct ctc aaa tac aaa agc aaa aaa atc ctg tgc gtg gcg acc 296
Glu Ile Ala Leu Lys Tyr Lys Ser Lys Lys Ile Leu Cys Val Ala Thr
70 75 80

tca gcg gtg cgc gat gcc cct aat cgg ctg gag ttt gta gcg agg gtg 346
Ser Ala Val Arg Asp Ala Pro Asn Arg Leu Glu Phe Val Ala Arg Val
85 90 95

aaa aag gct tgc ggt ttg caa atc aaa atc att gat ggg caa aaa gaa 394
Lys Lys Ala Cys Gly Leu Gln Ile Lys Ile Ile Asp Gly Gln Lys Glu
100 105 110 115

gcg ctc tat ggc ggg att gcg tgc gcg aat ttg ttg cat aaa aat tca 442
Ala Leu Tyr Gly Gly Ile Ala Cys Ala Asn Leu Leu His Lys Asn Ser
120 125 130

ggg atc acg ata gat att gga ggg ggt agc acc gag tgc gcg ttg att 490
Gly Ile Thr Ile Asp Ile Gly Gly Gly Ser Thr Glu Cys Ala Leu Ile
135 140 145

gaa aaa ggc aag att aag gac tta atc tcg ctt gat gtt ggg acg att 538
Glu Lys Gly Lys Ile Lys Asp Leu Ile Ser Leu Asp Val Gly Thr Ile
150 155 160

cgc att aaa gaa atg ttt tta gac aaa gac tta gag gtc aaa ttg gct 586
Arg Ile Lys Glu Met Phe Leu Asp Lys Asp Leu Glu Val Lys Leu Ala
165 170 175

aaa gcc ttt atc caa aaa gaa gtc tct aaa ctg ccc ttt aaa cac aaa 634
Lys Ala Phe Ile Gln Lys Glu Val Ser Lys Leu Pro Phe Lys His Lys
180 185 190 195

aac gcc ttt ggg gtg ggg ggg acg atc aga gcg ttg agt aag gta ttg	682
Asn Ala Phe Gly Val Gly Gly Thr Ile Arg Ala Leu Ser Lys Val Leu	
200 205 210	
atg aaa cgc ttt tgt tac cct att gat tct ttg cat ggc tat gaa ata	730
Met Lys Arg Phe Cys Tyr Pro Ile Asp Ser Leu His Gly Tyr Glu Ile	
215 220 225	
gat gca cat aaa aat tta gcg ttc att gaa aaa atc gtc atg ctc aaa	778
Asp Ala His Lys Asn Leu Ala Phe Ile Glu Lys Ile Val Met Leu Lys	
230 235 240	
gaa gat caa tta cgg ctt tta ggg gtg aat gaa gag cgt ttg gat agc	826
Glu Asp Gln Leu Arg Leu Leu Gly Val Asn Glu Glu Arg Leu Asp Ser	
245 250 255	
atc agg agc ggg gcg ttg att tta tca gtc gtt ttg gag cat tta aaa	874
Ile Arg Ser Gly Ala Leu Ile Leu Ser Val Val Leu Glu His Leu Lys	
260 265 270 275	
act tct tta atg atc act agt ggg gtg ggg gtg aga gaa ggc gtg ttt	922
Thr Ser Leu Met Ile Thr Ser Gly Val Gly Val Arg Glu Gly Val Phe	
280 285 290	
ttg agc gat tta ttg cgc cat cat tac cat aaa ttc ccc ccc aat atc	970
Leu Ser Asp Leu Leu Arg His His Tyr His Lys Phe Pro Pro Asn Ile	
295 300 305	
aac ccc tct ctc atc tct tta aaa gat gcg ttt ttg ccc cat gaa aag	1018
Asn Pro Ser Leu Ile Ser Leu Lys Asp Arg Phe Leu Pro His Glu Lys	
310 315 320	
cac agc caa aag gtc aaa aaa gaa tgc gtg aaa ttg ttt gaa gcc tta	1066
His Ser Gln Lys Val Lys Lys Glu Cys Val Lys Leu Phe Glu Ala Leu	
325 330 335	
tcg cct ttg cat aaa ata gat gaa aaa tac ctt ttc cat tta aag att	1114
Ser Pro Leu His Lys Ile Asp Glu Lys Tyr Leu Phe His Leu Lys Ile	
340 345 350 355	
gcg ggg gaa tta gcg agc atg ggt aag att tta agc gtc tat tta gcc	1162
Ala Gly Glu Leu Ala Ser Met Gly Lys Ile Leu Ser Val Tyr Leu Ala	
360 365 370	
cac aag cac agc gcg tat ttt att tta aac gct ttg agt tat ggc ttt	1210
His Lys His Ser Ala Tyr Phe Ile Leu Asn Ala Leu Ser Tyr Gly Phe	
375 380 385	
agc cac cag gat aga gcg atc att tgc tta tta gcc caa ttc agc cat	1258
Ser His Gln Asp Arg Ala Ile Ile Cys Leu Leu Ala Gln Phe Ser His	
390 395 400	
aaa aaa atc cct aaa gac aac gct atc gcc cac atg agc gcg atg atg	1306
Lys Lys Ile Pro Lys Asp Asn Ala Ile Ala His Met Ser Ala Met Met	
405 410 415	
cca agc ctt tta acc tta caa tgg ctg agt ttt atc ctt tct tta gcc	1354
Pro Ser Leu Leu Thr Leu Gln Trp Leu Ser Phe Ile Leu Ser Leu Ala	
420 425 430 435	

gaa aat ttg tgc cta aca gac agc cat cat tta aaa tac acg cta gaa	1402
Glu Asn Leu Cys Leu Thr Asp Ser His His Leu Lys Tyr Thr Leu Glu	
440 445 450	
aaa aac aag ctt gtg atc cat tct aat gac acg ctt tac ttg gct aaa	1450
Lys Asn Lys Leu Val Ile His Ser Asn Asp Thr Leu Tyr Leu Ala Lys	
455 460 465	
gaa atg ctc ccc aaa ctc gtt aag ccc att cct ttg acg ata gag ttt	1498
Glu Met Leu Pro Lys Leu Val Lys Pro Ile Pro Leu Thr Ile Glu Phe	
470 475 480	
gct tgaaaatagc gattgtcagg ctttcagcg	1530
Ala	

<210> 518
 <211> 484
 <212> PRT
 <213> Helicobacter pylori

<400> 518

Met Ala Lys Ile Thr Thr Val Ile Asp Ile Gly Ser Asn Ser Val Arg	
1 5 10 15	
Leu Ala Val Phe Lys Lys Thr Ser Gln Phe Gly Phe Tyr Leu Leu Phe	
20 25 30	
Glu Thr Lys Ser Lys Val Arg Ile Ser Glu Gly Cys Tyr Ala Phe Asn	
35 40 45	
Gly Ile Leu Gln Glu Ile Pro Met Gln Arg Ala Val Lys Ala Leu Ser	
50 55 60	
Glu Phe Lys Glu Ile Ala Leu Lys Tyr Lys Ser Lys Lys Ile Leu Cys	
65 70 75 80	
Val Ala Thr Ser Ala Val Arg Asp Ala Pro Asn Arg Leu Glu Phe Val	
85 90 95	
Ala Arg Val Lys Lys Ala Cys Gly Leu Gln Ile Lys Ile Ile Asp Gly	
100 105 110	
Gln Lys Glu Ala Leu Tyr Gly Gly Ile Ala Cys Ala Asn Leu Leu His	
115 120 125	
Lys Asn Ser Gly Ile Thr Ile Asp Ile Gly Gly Gly Ser Thr Glu Cys	
130 135 140	
Ala Leu Ile Glu Lys Gly Lys Ile Lys Asp Leu Ile Ser Leu Asp Val	
145 150 155 160	
Gly Thr Ile Arg Ile Lys Glu Met Phe Leu Asp Lys Asp Leu Glu Val	
165 170 175	
Lys Leu Ala Lys Ala Phe Ile Gln Lys Glu Val Ser Lys Leu Pro Phe	
180 185 190	
Lys His Lys Asn Ala Phe Gly Val Gly Gly Thr Ile Arg Ala Leu Ser	
195 200 205	
Lys Val Leu Met Lys Arg Phe Cys Tyr Pro Ile Asp Ser Leu His Gly	
210 215 220	
Tyr Glu Ile Asp Ala His Lys Asn Leu Ala Phe Ile Glu Lys Ile Val	
225 230 235 240	
Met Leu Lys Glu Asp Gln Leu Arg Leu Leu Gly Val Asn Glu Glu Arg	
245 250 255	
Leu Asp Ser Ile Arg Ser Gly Ala Leu Ile Leu Ser Val Val Leu Glu	
260 265 270	
His Leu Lys Thr Ser Leu Met Ile Thr Ser Gly Val Gly Val Arg Glu	

ttt gac gct aag gcc aat ttg gat ttt gtg ttt ggg gat tct aaa agc	347
Phe Asp Ala Lys Ala Asn Leu Asp Phe Val Phe Gly Asp Ser Lys Ser	
85 90 95	
gaa gaa gag aaa aaa agg atc att aaa aag ggt tat gaa aat ttt gct	395
Glu Glu Glu Lys Lys Arg Ile Ile Lys Lys Gly Tyr Glu Asn Phe Ala	
100 105 110	
ttc att att tta gaa act att aga gtg atc ttt atc cct aaa gat gaa	443
Phe Ile Ile Leu Glu Thr Ile Arg Val Ile Phe Ile Pro Lys Asp Glu	
115 120 125	
tac gac gct cgt ttc acg ctc atc aat gaa gaa aat gtg tgg aaa tct	491
Tyr Asp Ala Arg Phe Thr Leu Ile Asn Glu Glu Asn Val Trp Lys Ser	
130 135 140	
tta aac aag gaa ggc caa gcg atc act tta tgc atg cat ttt ggc tat	539
Leu Asn Lys Glu Gly Gln Ala Ile Thr Leu Cys Met His Phe Gly Tyr	
145 150 155 160	
tgg gaa gcg gta ggc acg act tta gcg caa tat tat gaa aat tat ggt	587
Trp Glu Ala Val Gly Thr Thr Leu Ala Gln Tyr Tyr Glu Asn Tyr Gly	
165 170 175	
agg ggg tgt ttg ggg cgt ttg act aaa ttt gcc cct atc aat cac atg	635
Arg Gly Cys Leu Gly Arg Leu Thr Lys Phe Ala Pro Ile Asn His Met	
180 185 190	
att atg agt agg cga gag gcg ttt ggg gtg cgt ttt gtc aat aaa ata	683
Ile Met Ser Arg Arg Glu Ala Phe Gly Val Arg Phe Val Asn Lys Ile	
195 200 205	
ggg gcg atg aaa gaa ctc att aaa atg tat aat caa ggc aat ggt ctg	731
Gly Ala Met Lys Glu Leu Ile Lys Met Tyr Asn Gln Gly Asn Gly Leu	
210 215 220	
gtg ggg att tta gtg gat caa aat gtc gtg cct aaa gat ggg gtg gtg	779
Val Gly Ile Leu Val Asp Gln Asn Val Val Pro Lys Asp Gly Val Val	
225 230 235 240	
gtg aaa ttc ttt gat aga gac gct acg cac acc acg atc gct tct att	827
Val Lys Phe Phe Asp Arg Asp Ala Thr His Thr Thr Ile Ala Ser Ile	
245 250 255	
ttg tcg cgc cgt tat aat ata gat att cag ccg gta ttc att gat ttt	875
Leu Ser Arg Arg Tyr Asn Ile Asp Ile Gln Pro Val Phe Ile Asp Phe	
260 265 270	
aat gac gat tat tcg cat tat aca gcg acc tat tat ccg agt atc cgc	923
Asn Asp Asp Tyr Ser His Tyr Thr Ala Thr Tyr Tyr Pro Ser Ile Arg	
275 280 285	
tct caa atc acc gat aac gcg caa aac gat att tta gaa tgc acg caa	971
Ser Gln Ile Thr Asp Asn Ala Gln Asn Asp Ile Leu Glu Cys Thr Gln	
290 295 300	
gcc caa gcg agt ttg tgc gaa gag gtg att aga aac cac ccg gaa agt	1019
Ala Gln Ala Ser Leu Cys Glu Glu Val Ile Arg Asn His Pro Glu Ser	

305	310	315	320	
tat ttt tgg ttc cat agg cgt ttt aaa agc acc cac cct gag att tat				1067
Tyr Phe Trp Phe His Arg Arg Phe Lys Ser Thr His Pro Glu Ile Tyr				
	325	330	335	
caa aga taggggttttg ttttaatacaa aaattaaaaa ctaaagcctt attttttaaga				1123
Gln Arg				
aaacttt				1130
<210> 520				
<211> 338				
<212> PRT				
<213> Helicobacter pylori				
<400> 520				
Met Arg Phe Lys His Leu Lys Gly Lys Arg Met Thr Tyr Lys Glu Arg				
1 5 10 15				
Leu Ile His Glu Lys Ile Leu Lys Gln Asp Asp Lys Gly Phe Lys Thr				
20 25 30				
Glu Leu Arg Ile Leu Ser Ile Phe Ile Val Glu Ser Leu Val Asn Ile				
35 40 45				
Leu Gly Phe Ile Leu Ala Lys Met Pro His Ser Trp Phe Leu Arg Cys				
50 55 60				
Ile Lys Ala Val Ala Trp Leu Met Lys Thr Phe Asp Lys Cys Arg Tyr				
65 70 75 80				
Phe Asp Ala Lys Ala Asn Leu Asp Phe Val Phe Gly Asp Ser Lys Ser				
85 90 95				
Glu Glu Glu Lys Lys Arg Ile Ile Lys Lys Gly Tyr Glu Asn Phe Ala				
100 105 110				
Phe Ile Ile Leu Glu Thr Ile Arg Val Ile Phe Ile Pro Lys Asp Glu				
115 120 125				
Tyr Asp Ala Arg Phe Thr Leu Ile Asn Glu Glu Asn Val Trp Lys Ser				
130 135 140				
Leu Asn Lys Glu Gly Gln Ala Ile Thr Leu Cys Met His Phe Gly Tyr				
145 150 155 160				
Trp Glu Ala Val Gly Thr Thr Leu Ala Gln Tyr Tyr Glu Asn Tyr Gly				
165 170 175				
Arg Gly Cys Leu Gly Arg Leu Thr Lys Phe Ala Pro Ile Asn His Met				
180 185 190				
Ile Met Ser Arg Arg Glu Ala Phe Gly Val Arg Phe Val Asn Lys Ile				
195 200 205				
Gly Ala Met Lys Glu Leu Ile Lys Met Tyr Asn Gln Gly Asn Gly Leu				
210 215 220				
Val Gly Ile Leu Val Asp Gln Asn Val Val Pro Lys Asp Gly Val Val				
225 230 235 240				
Val Lys Phe Phe Asp Arg Asp Ala Thr His Thr Thr Ile Ala Ser Ile				
245 250 255				
Leu Ser Arg Arg Tyr Asn Ile Asp Ile Gln Pro Val Phe Ile Asp Phe				
260 265 270				
Asn Asp Asp Tyr Ser His Tyr Thr Ala Thr Tyr Tyr Pro Ser Ile Arg				
275 280 285				
Ser Gln Ile Thr Asp Asn Ala Gln Asn Asp Ile Leu Glu Cys Thr Gln				
290 295 300				
Ala Gln Ala Ser Leu Cys Glu Glu Val Ile Arg Asn His Pro Glu Ser				
305 310 315 320				
Tyr Phe Trp Phe His Arg Arg Phe Lys Ser Thr His Pro Glu Ile Tyr				

Gln Arg 325 330 335

<210> 521
 <211> 8748
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (16)...(8694)

<400> 521
 agagggtagc attta atg aaa aag ttt aaa aag aaa cca aaa agt atc aaa 51
 Met Lys Lys Phe Lys Lys Lys Pro Lys Ser Ile Lys
 1 5 10

cga tcg cat caa aat caa aaa aca atc tta aag cgt cct tta tgg ctt 99
 Arg Ser His Gln Asn Gln Lys Thr Ile Leu Lys Arg Pro Leu Trp Leu
 15 20 25

atg cct tta ctc atc agc ggg ttt gct agt ggg gtg tat gcg aat aat 147
 Met Pro Leu Leu Ile Ser Gly Phe Ala Ser Gly Val Tyr Ala Asn Asn
 30 35 40

ctg tgg gat ttg tta aac cca aaa gtg ggg ggt gag tat gtg cat tgg 195
 Leu Trp Asp Leu Leu Asn Pro Lys Val Gly Gly Glu Tyr Val His Trp
 45 50 55 60

gtt aag ggc agt cag tat tgt gca tgg tgg gaa ttt gct ggg tgt tta 243
 Val Lys Gly Ser Gln Tyr Cys Ala Trp Trp Glu Phe Ala Gly Cys Leu
 65 70 75

aag aat gta tgg ggg gca aat cat aaa ggc tat gat gct gga aac gcc 291
 Lys Asn Val Trp Gly Ala Asn His Lys Gly Tyr Asp Ala Gly Asn Ala
 80 85 90

gct aac tat ttg tct tct caa aac tat caa gct att tcg gtg ggt agt 339
 Ala Asn Tyr Leu Ser Ser Gln Asn Tyr Gln Ala Ile Ser Val Gly Ser
 95 100 105

ggg aat gaa acg ggg act tat agt tta agc ggt ttt acc aat tat gtt 387
 Gly Asn Glu Thr Gly Thr Tyr Ser Leu Ser Gly Phe Thr Asn Tyr Val
 110 115 120

ggg ggc aat ctc acg atc aat cta ggc aat agc gtt gtt tta gat tta 435
 Gly Gly Asn Leu Thr Ile Asn Leu Gly Asn Ser Val Val Leu Asp Leu
 125 130 135 140

agc ggt tct aat agt ttc act tcg tat caa ggt tat aat caa ggc aaa 483
 Ser Gly Ser Asn Ser Phe Thr Ser Tyr Gln Gly Tyr Asn Gln Gly Lys
 145 150 155

gat gat gta aca ttt acg gtt ggc gca atc aat tta aac ggc act tta 531
 Asp Asp Val Thr Phe Thr Val Gly Ala Ile Asn Leu Asn Gly Thr Leu
 160 165 170

gaa gtg ggt aat cgt gtg gga tcg gga gct ggc acg cac acc ggc aca	579
Glu Val Gly Asn Arg Val Gly Ser Gly Ala Gly Thr His Thr Gly Thr	
175 180 185	
gcc act tta aac ttg aac gct aat aag gtc aat atc aat tcc aat atc	627
Ala Thr Leu Asn Leu Asn Ala Asn Lys Val Asn Ile Asn Ser Asn Ile	
190 195 200	
aac gcg tat aaa act tcg caa gtg aat ata ggc aac gct aac agc gtt	675
Asn Ala Tyr Lys Thr Ser Gln Val Asn Ile Gly Asn Ala Asn Ser Val	
205 210 215 220	
att acc att ggt tcg gtt tct ttg agt ggg gat gtt tgc agt tct tta	723
Ile Thr Ile Gly Ser Val Ser Leu Ser Gly Asp Val Cys Ser Ser Leu	
225 230 235	
gct agc gtt ggg ata ggg gct aat tgc tcc act tct ggg cct agc tat	771
Ala Ser Val Gly Ile Gly Ala Asn Cys Ser Thr Ser Gly Pro Ser Tyr	
240 245 250	
tct ttt aaa ggg acg act aac gct act aac acg gcg ttt agt aat gca	819
Ser Phe Lys Gly Thr Thr Asn Ala Thr Asn Thr Ala Phe Ser Asn Ala	
255 260 265	
agc ggc agt ttc act ttt gaa gag aac gcc act ttt agc ggg gcg aaa	867
Ser Gly Ser Phe Thr Phe Glu Glu Asn Ala Thr Phe Ser Gly Ala Lys	
270 275 280	
tgg aat ggg ggg act tat acc ttt aat aaa gag ttt agc gct acc aat	915
Trp Asn Gly Gly Thr Tyr Thr Phe Asn Lys Glu Phe Ser Ala Thr Asn	
285 290 295 300	
aac acc gcc ttt agt agc ggt agt ttt aat ttt aaa ggt gta agc tct	963
Asn Thr Ala Phe Ser Ser Gly Ser Phe Asn Phe Lys Gly Val Ser Ser	
305 310 315	
ttt aat ggt act tcg ttt agt aac gct tct tat act ttt gac aat caa	1011
Phe Asn Gly Thr Ser Phe Ser Asn Ala Ser Tyr Thr Phe Asp Asn Gln	
320 325 330	
gcc act ttc caa aac agc tcc ttt aat ggg ggg act ttt act ttt aat	1059
Ala Thr Phe Gln Asn Ser Ser Phe Asn Gly Gly Thr Phe Thr Phe Asn	
335 340 345	
aac caa act aat cca act aac aac gct cag cac ccc caa att caa aac	1107
Asn Gln Thr Asn Pro Thr Asn Asn Ala Gln His Pro Gln Ile Gln Asn	
350 355 360	
agc tct ttt agt ggt aac gct acc act ctt aag ggc ttt gtg aat ttc	1155
Ser Ser Phe Ser Gly Asn Ala Thr Thr Leu Lys Gly Phe Val Asn Phe	
365 370 375 380	
cag caa gcc ttt aac aat tca aac cac caa cta acg atc caa aac gct	1203
Gln Gln Ala Phe Asn Asn Ser Asn His Gln Leu Thr Ile Gln Asn Ala	
385 390 395	
tcc ttt aat aac gcc act ttt aac aat acc ggt aaa atc act ata gaa	1251
Ser Phe Asn Asn Ala Thr Phe Asn Asn Thr Gly Lys Ile Thr Ile Glu	
400 405 410	

aaa gat gcg agt ttt aat aac acg aca ttc aac act tct gtt gat aca	1299
Lys Asp Ala Ser Phe Asn Asn Thr Thr Phe Asn Thr Ser Val Asp Thr	
415 420 425	
aac aac atg agt gtt acc ggt ggc gtt act tta agc ggt aaa aat gac	1347
Asn Asn Met Ser Val Thr Gly Gly Val Thr Leu Ser Gly Lys Asn Asp	
430 435 440	
ttg aaa aat ggc tca acc ctt gat ttt ggg agt tct aaa atc act ctc	1395
Leu Lys Asn Gly Ser Thr Leu Asp Phe Gly Ser Ser Lys Ile Thr Leu	
445 450 455 460	
gct caa ggg acg act ttc aac ctc aca agt tta ggc agt gag aag agc	1443
Ala Gln Gly Thr Thr Phe Asn Leu Thr Ser Leu Gly Ser Glu Lys Ser	
465 470 475	
gta acg att tta aat tct agc ggt ggg atc act tat agt aac ctt tta	1491
Val Thr Ile Leu Asn Ser Ser Gly Gly Ile Thr Tyr Ser Asn Leu Leu	
480 485 490	
aac cat gca atc aac ggc ttg aca agt gcc tta aaa acg aac gaa agc	1539
Asn His Ala Ile Asn Gly Leu Thr Ser Ala Leu Lys Thr Asn Glu Ser	
495 500 505	
ctt tca aat ccg caa agt ttc gct caa ggt ttg tgg gat ata atc act	1587
Leu Ser Asn Pro Gln Ser Phe Ala Gln Gly Leu Trp Asp Ile Ile Thr	
510 515 520	
tac aat ggg gtt acc ggg cag ctt ttg aat gaa aac gct gca aca tct	1635
Tyr Asn Gly Val Thr Gly Gln Leu Leu Asn Glu Asn Ala Ala Thr Ser	
525 530 535 540	
aaa ccc act gac tct tcg ccc tct aaa tcc tct aca aac tct acg caa	1683
Lys Pro Thr Asp Ser Ser Pro Ser Lys Ser Ser Thr Asn Ser Thr Gln	
545 550 555	
gtc tat caa gtg ggt tac aaa ata ggg gat act atc tac aaa ctg caa	1731
Val Tyr Gln Val Gly Tyr Lys Ile Gly Asp Thr Ile Tyr Lys Leu Gln	
560 565 570	
gaa act ttc agc cac aat tcc att att att cag gct tta gag agc ggg	1779
Glu Thr Phe Ser His Asn Ser Ile Ile Ile Gln Ala Leu Glu Ser Gly	
575 580 585	
act tac acg cca ccc cct gtc att aac ggc tcc aaa ttt gac tta tcc	1827
Thr Tyr Thr Pro Pro Pro Val Ile Asn Gly Ser Lys Phe Asp Leu Ser	
590 595 600	
gct tca aat tat atc aat gct gac atg cct tgg tat gac cat aaa tat	1875
Ala Ser Asn Tyr Ile Asn Ala Asp Met Pro Trp Tyr Asp His Lys Tyr	
605 610 615 620	
tac atc cct aaa tcc caa aat ttt aca gag agc ggg act tat tac ttg	1923
Tyr Ile Pro Lys Ser Gln Asn Phe Thr Glu Ser Gly Thr Tyr Tyr Leu	
625 630 635	
ccg agc gtc caa ata tgg ggg agc tac act aac tcg ttt aaa caa act	1971
Pro Ser Val Gln Ile Trp Gly Ser Tyr Thr Asn Ser Phe Lys Gln Thr	

640					645					650						
ttt	agc	gca	aat	ggc	agt	aat	ctg	gtg	att	ggg	tat	aac	tca	aca	tgg	2019
Phe	Ser	Ala	Asn	Gly	Ser	Asn	Leu	Val	Ile	Gly	Tyr	Asn	Ser	Thr	Trp	
		655					660					665				
act	gat	cat	aat	gtc	tct	tct	agc	ggc	acg	gtg	tct	ttt	ggg	gac	act	2067
Thr	Asp	His	Asn	Val	Ser	Ser	Ser	Gly	Thr	Val	Ser	Phe	Gly	Asp	Thr	
	670					675					680					
tca	ggg	agc	gct	ctt	aat	ggg	cat	tgc	gga	cct	tgg	ccg	tat	tac	caa	2115
Ser	Gly	Ser	Ala	Leu	Asn	Gly	His	Cys	Gly	Pro	Trp	Pro	Tyr	Tyr	Gln	
	685				690					695					700	
tgc	aca	ggc	acg	act	aac	ggc	act	tat	agc	gcc	tat	cat	gtg	tat	atc	2163
Cys	Thr	Gly	Thr	Thr	Asn	Gly	Thr	Tyr	Ser	Ala	Tyr	His	Val	Tyr	Ile	
				705					710					715		
aca	gcg	aat	ctg	cgt	tct	ggc	aat	cgt	ata	ggc	acc	ggc	ggg	gca	gct	2211
Thr	Ala	Asn	Leu	Arg	Ser	Gly	Asn	Arg	Ile	Gly	Thr	Gly	Gly	Ala	Ala	
			720					725					730			
aat	cta	atc	ttt	aat	ggg	gta	gat	agt	atc	aat	atc	gct	aac	gct	acc	2259
Asn	Leu	Ile	Phe	Asn	Gly	Val	Asp	Ser	Ile	Asn	Ile	Ala	Asn	Ala	Thr	
		735					740					745				
atc	acg	caa	cat	aac	gcc	gga	atc	tat	tca	agc	tct	atg	act	ttt	tcc	2307
Ile	Thr	Gln	His	Asn	Ala	Gly	Ile	Tyr	Ser	Ser	Ser	Met	Thr	Phe	Ser	
	750					755					760					
acg	caa	agc	atg	gat	aat	tcg	cag	aat	ttg	aat	ggc	cta	aat	tct	aac	2355
Thr	Gln	Ser	Met	Asp	Asn	Ser	Gln	Asn	Leu	Asn	Gly	Leu	Asn	Ser	Asn	
	765				770					775					780	
ggc	aaa	ctt	tcg	gtg	tat	ggc	acc	act	ttc	act	aac	gaa	gct	aaa	gat	2403
Gly	Lys	Leu	Ser	Val	Tyr	Gly	Thr	Thr	Phe	Thr	Asn	Glu	Ala	Lys	Asp	
				785					790					795		
ggg	aaa	ttc	att	ttc	aat	gca	ggg	caa	gcg	ggt	ttt	gaa	aac	acc	aac	2451
Gly	Lys	Phe	Ile	Phe	Asn	Ala	Gly	Gln	Ala	Val	Phe	Glu	Asn	Thr	Asn	
			800					805					810			
ttt	aat	gga	ggg	agt	tac	caa	ttc	agc	ggc	gat	agc	ttg	aat	ttt	tca	2499
Phe	Asn	Gly	Gly	Ser	Tyr	Gln	Phe	Ser	Gly	Asp	Ser	Leu	Asn	Phe	Ser	
		815					820					825				
aac	aac	aac	cag	ttc	aat	agc	ggc	tcg	ttt	gaa	att	agc	gca	aaa	aac	2547
Asn	Asn	Asn	Gln	Phe	Asn	Ser	Gly	Ser	Phe	Glu	Ile	Ser	Ala	Lys	Asn	
		830				835					840					
gct	tcg	ttc	aat	aac	gct	aac	ttt	aac	aac	agc	gct	tct	ttt	aat	ttc	2595
Ala	Ser	Phe	Asn	Asn	Ala	Asn	Phe	Asn	Asn	Ser	Ala	Ser	Phe	Asn	Phe	
	845				850					855					860	
aat	aat	tct	aac	gcg	acc	act	tcg	ttt	gtg	ggg	gat	ttc	act	aac	gct	2643
Asn	Asn	Ser	Asn	Ala	Thr	Thr	Ser	Phe	Val	Gly	Asp	Phe	Thr	Asn	Ala	
				865					870					875		
aat	tca	aat	ttg	caa	atc	gcc	ggg	aac	gct	ggt	ttt	ggg	aac	tct	act	2691

Asn Ser Asn Leu Gln Ile Ala Gly Asn Ala Val Phe Gly Asn Ser Thr	
880 885 890	
aat ggc tct caa aat acc gct aat ttt aat aat acc ggc tct gtt aat	2739
Asn Gly Ser Gln Asn Thr Ala Asn Phe Asn Asn Thr Gly Ser Val Asn	
895 900 905	
att tca ggg aat gca acc ttt gat aat gtg gtg ttt aat ggc cct acg	2787
Ile Ser Gly Asn Ala Thr Phe Asp Asn Val Val Phe Asn Gly Pro Thr	
910 915 920	
aac acg agc gtg aaa ggg cag gtt act tta aat aac atc act tta aaa	2835
Asn Thr Ser Val Lys Gly Gln Val Thr Leu Asn Asn Ile Thr Leu Lys	
925 930 935 940	
aac ctg aac gcc cct ttg tct ttt ggc gat ggg acg att act ttt aac	2883
Asn Leu Asn Ala Pro Leu Ser Phe Gly Asp Gly Thr Ile Thr Phe Asn	
945 950 955	
gct cat tcg gtg att aat att gct gaa tct atc act aat ggc aac cct	2931
Ala His Ser Val Ile Asn Ile Ala Glu Ser Ile Thr Asn Gly Asn Pro	
960 965 970	
atc act ctt gta agc tct tct aaa gaa att gaa tac aac aac gct ttc	2979
Ile Thr Leu Val Ser Ser Ser Lys Glu Ile Glu Tyr Asn Asn Ala Phe	
975 980 985	
agt aaa aat cta tgg cag ctc atc aac tac caa ggg cat ggg gca agc	3027
Ser Lys Asn Leu Trp Gln Leu Ile Asn Tyr Gln Gly His Gly Ala Ser	
990 995 1000	
agt gaa aag ctc gtc tct agc gcg ggt aat ggc gtt tat gat gtg gtg	3075
Ser Glu Lys Leu Val Ser Ser Ala Gly Asn Gly Val Tyr Asp Val Val	
1005 1010 1015 1020	
tat tct ttc aat aac caa acc tac aat ttc caa gag gtt ttt tca caa	3123
Tyr Ser Phe Asn Asn Gln Thr Tyr Asn Phe Gln Glu Val Phe Ser Gln	
1025 1030 1035	
aac agc att tct atc cgg cgt ttg ggc gtt aac atg gtg ttt gat tat	3171
Asn Ser Ile Ser Ile Arg Arg Leu Gly Val Asn Met Val Phe Asp Tyr	
1040 1045 1050	
gtg gat atg gaa aaa tcg gat cat tta tat tat caa aac gct ctc ggt	3219
Val Asp Met Glu Lys Ser Asp His Leu Tyr Tyr Gln Asn Ala Leu Gly	
1055 1060 1065	
ttt atg acc tac atg cct aat agc tat aac aat aat tta ggg aat gca	3267
Phe Met Thr Tyr Met Pro Asn Ser Tyr Asn Asn Asn Leu Gly Asn Ala	
1070 1075 1080	
aac aac acc att tac tat tac gac aag agc att gat ttt tat gcg agc	3315
Asn Asn Thr Ile Tyr Tyr Tyr Asp Lys Ser Ile Asp Phe Tyr Ala Ser	
1085 1090 1095 1100	
ggg aaa act cta ttc act aaa gcg gaa ttt tct caa aca ttc acc ggg	3363
Gly Lys Thr Leu Phe Thr Lys Ala Glu Phe Ser Gln Thr Phe Thr Gly	
1105 1110 1115	

caa aac agc gcg atc gtt ttt ggg gct aaa agc ata tgg acg agc tta	3411
Gln Asn Ser Ala Ile Val Phe Gly Ala Lys Ser Ile Trp Thr Ser Leu	
1120 1125 1130	
agc gat gca ccg cag tct aac acc atc att cgc ttt ggg gac aat aag	3459
Ser Asp Ala Pro Gln Ser Asn Thr Ile Ile Arg Phe Gly Asp Asn Lys	
1135 1140 1145	
gga gca ggg agt aat gat gcg agc ggg cat tgc tgg aat ttg caa tgc	3507
Gly Ala Gly Ser Asn Asp Ala Ser Gly His Cys Trp Asn Leu Gln Cys	
1150 1155 1160	
ata ggc ttt att aca ggg cat tat gaa gcg caa aag att tac atc acc	3555
Ile Gly Phe Ile Thr Gly His Tyr Glu Ala Gln Lys Ile Tyr Ile Thr	
1165 1170 1175 1180	
ggt agc att gaa agc ggg aat cgc att tct agc ggt ggg ggc gcg agc	3603
Gly Ser Ile Glu Ser Gly Asn Arg Ile Ser Ser Gly Gly Ala Ser	
1185 1190 1195	
ctt aat ttt aac ggg ctt caa ggc att ctt tta acg aac gcg act ttg	3651
Leu Asn Phe Asn Gly Leu Gln Gly Ile Leu Leu Thr Asn Ala Thr Leu	
1200 1205 1210	
tat aac cgc gcc gct ggc acg caa agc tcg tct atg aat ttt atc tct	3699
Tyr Asn Arg Ala Ala Gly Thr Gln Ser Ser Ser Met Asn Phe Ile Ser	
1215 1220 1225	
aac agc gcg aac att cag gct caa aac tcc tat ttt ata gac gat acc	3747
Asn Ser Ala Asn Ile Gln Ala Gln Asn Ser Tyr Phe Ile Asp Asp Thr	
1230 1235 1240	
gca caa aat ggc ggt aac cct aat ttc agt ttc aac gct ttg aat ctg	3795
Ala Gln Asn Gly Gly Asn Pro Asn Phe Ser Phe Asn Ala Leu Asn Leu	
1245 1250 1255 1260	
gat ttt tct aac agc tct ttt aga ggc tat gtg ggg aaa acg caa tct	3843
Asp Phe Ser Asn Ser Ser Phe Arg Gly Tyr Val Gly Lys Thr Gln Ser	
1265 1270 1275	
gtt ttt aaa ttc aat gcc aag aat gcg atc agt ttc acc aac agc acg	3891
Val Phe Lys Phe Asn Ala Lys Asn Ala Ile Ser Phe Thr Asn Ser Thr	
1280 1285 1290	
aat tta agc tct ggt ttg tat caa atg caa gct aaa agc gtg ttg ttt	3939
Asn Leu Ser Ser Gly Leu Tyr Gln Met Gln Ala Lys Ser Val Leu Phe	
1295 1300 1305	
gac aat tcc aat tta agc gtt tca gtg ggg aca agc agt att aaa gcc	3987
Asp Asn Ser Asn Leu Ser Val Ser Val Gly Thr Ser Ser Ile Lys Ala	
1310 1315 1320	
aat gcg atc aat ctt tct caa aat gcc tct att aat gcg agc aac cat	4035
Asn Ala Ile Asn Leu Ser Gln Asn Ala Ser Ile Asn Ala Ser Asn His	
1325 1330 1335 1340	
tca acc tta gaa ctt caa ggc gat ttg aat gtg aac gac acc agc tcg	4083
Ser Thr Leu Glu Leu Gln Gly Asp Leu Asn Val Asn Asp Thr Ser Ser	
1345 1350 1355	

ctc aac ctc aac caa agc acg att aat gtt tcc aat aac gcc acg atc	4131
Leu Asn Leu Asn Gln Ser Thr Ile Asn Val Ser Asn Asn Ala Thr Ile	
1360 1365 1370	
aac gat tat gcg agc ttg att gcg agt aat ggc tct cac ctt aat ttt	4179
Asn Asp Tyr Ala Ser Leu Ile Ala Ser Asn Gly Ser His Leu Asn Phe	
1375 1380 1385	
aac ggg gcg gtt aat ttc aat tca gcg aat att act acg agt ttg aat	4227
Asn Gly Ala Val Asn Phe Asn Ser Ala Asn Ile Thr Thr Ser Leu Asn	
1390 1395 1400	
aat tcc tct atc gtg ttt aag ggg gcg gtc tct tta gga ggg cag ttt	4275
Asn Ser Ser Ile Val Phe Lys Gly Ala Val Ser Leu Gly Gly Gln Phe	
1405 1410 1415 1420	
aat tta agc aat aac tct tct tta gat ttc caa ggc tct agc gct atc	4323
Asn Leu Ser Asn Asn Ser Ser Leu Asp Phe Gln Gly Ser Ser Ala Ile	
1425 1430 1435	
acc tct aac acg gcg ttt aat ttc tat gat aac gct ttt tct caa agc	4371
Thr Ser Asn Thr Ala Phe Asn Phe Tyr Asp Asn Ala Phe Ser Gln Ser	
1440 1445 1450	
ccc atc act ttc cat caa gcc ctt gac att aaa gcg ccc tta agt ttg	4419
Pro Ile Thr Phe His Gln Ala Leu Asp Ile Lys Ala Pro Leu Ser Leu	
1455 1460 1465	
gga ggc aac ctt tta aac cct aac aac agc agc gtg ctg gat tta aaa	4467
Gly Gly Asn Leu Leu Asn Pro Asn Asn Ser Ser Val Leu Asp Leu Lys	
1470 1475 1480	
aac agc cag ctt gtt ttt ggc gat caa ggg agt ttg aat atc gct aac	4515
Asn Ser Gln Leu Val Phe Gly Asp Gln Gly Ser Leu Asn Ile Ala Asn	
1485 1490 1495 1500	
att gat tta cta agc gat cta aat gat aat aaa aat cgt gtg tat aac	4563
Ile Asp Leu Leu Ser Asp Leu Asn Asp Asn Lys Asn Arg Val Tyr Asn	
1505 1510 1515	
atc att caa gcg gac atg aat agt aat tgg tat gag cgt atc agc ttc	4611
Ile Ile Gln Ala Asp Met Asn Ser Asn Trp Tyr Glu Arg Ile Ser Phe	
1520 1525 1530	
ttt ggc atg cac atc aat gac ggg att tat gat gct aaa aac caa act	4659
Phe Gly Met His Ile Asn Asp Gly Ile Tyr Asp Ala Lys Asn Gln Thr	
1535 1540 1545	
tat agt ttc act aac ccc ctt aat aac gcc cta aaa atc acc gag agc	4707
Tyr Ser Phe Thr Asn Pro Leu Asn Asn Ala Leu Lys Ile Thr Glu Ser	
1550 1555 1560	
ttt aaa gac aac caa cta agc gtt acg ctc tct caa atc ccg ggt att	4755
Phe Lys Asp Asn Gln Leu Ser Val Thr Leu Ser Gln Ile Pro Gly Ile	
1565 1570 1575 1580	
aaa aac acg ctc tat aac att ggc tct gaa att ttt aac tac caa aaa	4803
Lys Asn Thr Leu Tyr Asn Ile Gly Ser Glu Ile Phe Asn Tyr Gln Lys	

1585	1590	1595	
gtt tat aac aac gct aat ggc gtg tat tct tat agc gat gat gca caa Val Tyr Asn Asn Ala Asn Gly Val Tyr Ser Tyr Ser Asp Asp Ala Gln 1600 1605 1610			4851
ggc gtg ttt tat ctc aca agc aac gtg aaa ggc tat tac aac cct aac Gly Val Phe Tyr Leu Thr Ser Asn Val Lys Gly Tyr Tyr Asn Pro Asn 1615 1620 1625			4899
caa tcc tat caa gcc agc ggc agt aac aac acc acg aaa aat aat aat Gln Ser Tyr Gln Ala Ser Gly Ser Asn Asn Thr Thr Lys Asn Asn Asn 1630 1635 1640			4947
cta acc tct gaa tct tct atc atc tcg caa acc tat aac gcg caa ggc Leu Thr Ser Glu Ser Ile Ile Ser Gln Thr Tyr Asn Ala Gln Gly 1645 1650 1655 1660			4995
aac cct att agc gcg ttg cac atc tat aac aag ggc tat aat ttc aac Asn Pro Ile Ser Ala Leu His Ile Tyr Asn Lys Gly Tyr Asn Phe Asn 1665 1670 1675			5043
aat atc aaa gcg tta ggg caa atg gct ctc aaa ctc tac cct gaa atc Asn Ile Lys Ala Leu Gly Gln Met Ala Leu Lys Leu Tyr Pro Glu Ile 1680 1685 1690			5091
aaa aag gta tta ggg aat gat ttt tcg ccc tca agt ttg aac gct tta Lys Lys Val Leu Gly Asn Asp Phe Ser Pro Ser Ser Leu Asn Ala Leu 1695 1700 1705			5139
aac tct aat gcg cta aac caa ctt acc aaa ctc atc acg cct aac gac Asn Ser Asn Ala Leu Asn Gln Leu Thr Lys Leu Ile Thr Pro Asn Asp 1710 1715 1720			5187
tgg aaa aac att aac gag ttg att gat aac gca aac aat tcg gtg gtg Trp Lys Asn Ile Asn Glu Leu Ile Asp Asn Ala Asn Asn Ser Val Val 1725 1730 1735 1740			5235
caa aat ttc aat aac ggc act ttg att gtg gga gcg act caa ata ggc Gln Asn Phe Asn Asn Gly Thr Leu Ile Val Gly Ala Thr Gln Ile Gly 1745 1750 1755			5283
caa aca gac acc aat agc gcg gtt gtt ttt ggg ggc ttg ggc tat caa Gln Thr Asp Thr Asn Ser Ala Val Val Phe Gly Gly Leu Gly Tyr Gln 1760 1765 1770			5331
aca cct tgt gat tat act gat att gtg tgc caa aaa ttt aga ggc act Thr Pro Cys Asp Tyr Thr Asp Ile Val Cys Gln Lys Phe Arg Gly Thr 1775 1780 1785			5379
tat tta gga cag ctt tta gag tcc agc tcg gct gat ttg ggc tat att Tyr Leu Gly Gln Leu Leu Glu Ser Ser Ser Ala Asp Leu Gly Tyr Ile 1790 1795 1800			5427
gac acg act ttt aac gct aaa gaa att tat ctt acc ggc act tta ggc Asp Thr Thr Phe Asn Ala Lys Glu Ile Tyr Leu Thr Gly Thr Leu Gly 1805 1810 1815 1820			5475
agc ggg aac gca tgg ggg act ggg ggg agc gcg agc gta act ttt aac			5523

Ser Gly Asn Ala Trp Gly Thr Gly Gly Ser Ala Ser Val Thr Phe Asn	
1825 1830 1835	
agc caa act tcg ctc att ctc aat cag gct aat atc gta agc tcg caa	5571
Ser Gln Thr Ser Leu Ile Leu Asn Gln Ala Asn Ile Val Ser Ser Gln	
1840 1845 1850	
acc gat ggg atc ttt agc atg ctg ggt caa gag ggt att aat aag gtt	5619
Thr Asp Gly Ile Phe Ser Met Leu Gly Gln Glu Gly Ile Asn Lys Val	
1855 1860 1865	
ttc aat caa gcc ggg ctc gct aat att ttg ggc gaa gtg gcg gtg caa	5667
Phe Asn Gln Ala Gly Leu Ala Asn Ile Leu Gly Glu Val Ala Val Gln	
1870 1875 1880	
tcc atc aac aaa gcc ggg gga tta ggg aat ttg ata gta aat acg cta	5715
Ser Ile Asn Lys Ala Gly Gly Leu Gly Asn Leu Ile Val Asn Thr Leu	
1885 1890 1895 1900	
ggg agt aat agc gtg att ggg ggg tat tta acg cct gaa caa aaa aat	5763
Gly Ser Asn Ser Val Ile Gly Gly Tyr Leu Thr Pro Glu Gln Lys Asn	
1905 1910 1915	
caa acc cta agc cag ctt tta ggg cag aat aac ttt gat aat ctc atg	5811
Gln Thr Leu Ser Gln Leu Leu Gly Gln Asn Asn Phe Asp Asn Leu Met	
1920 1925 1930	
aac gat agc ggt ttg aat acg gcg att aag gat ttg atc aga caa aaa	5859
Asn Asp Ser Gly Leu Asn Thr Ala Ile Lys Asp Leu Ile Arg Gln Lys	
1935 1940 1945	
tta ggc ttt tgg acc ggg cta gtg ggg gga tta gcc gga cta ggg ggc	5907
Leu Gly Phe Trp Thr Gly Leu Val Gly Gly Leu Ala Gly Leu Gly Gly	
1950 1955 1960	
att gat ttg caa aac cct gaa aag ctt ata ggc agc atg tca atc aat	5955
Ile Asp Leu Gln Asn Pro Glu Lys Leu Ile Gly Ser Met Ser Ile Asn	
1965 1970 1975 1980	
gat tta ttg agt aaa aaa ggg ttg ttc aat cag atc acc ggc ttt att	6003
Asp Leu Leu Ser Lys Lys Gly Leu Phe Asn Gln Ile Thr Gly Phe Ile	
1985 1990 1995	
tcc gct aac gat ata ggg caa gtc ata agc gta atg ttg caa gat att	6051
Ser Ala Asn Asp Ile Gly Gln Val Ile Ser Val Met Leu Gln Asp Ile	
2000 2005 2010	
gtc aaa ccg agc aac gct tta aaa aac gat gta gcg gct tta ggc aag	6099
Val Lys Pro Ser Asn Ala Leu Lys Asn Asp Val Ala Ala Leu Gly Lys	
2015 2020 2025	
caa atg att ggc gaa ttt tta ggc caa gac acg ctc aat tct tta gaa	6147
Gln Met Ile Gly Glu Phe Leu Gly Gln Asp Thr Leu Asn Ser Leu Glu	
2030 2035 2040	
agc ttg ttg caa aac cag cag att aaa agc gtt tta gac aaa gtc cta	6195
Ser Leu Leu Gln Asn Gln Gln Ile Lys Ser Val Leu Asp Lys Val Leu	
2045 2050 2055 2060	

gcg gct aaa ggt tta ggg cct att tat gaa caa ggc ttg ggg gat ttg	6243
Ala Ala Lys Gly Leu Gly Pro Ile Tyr Glu Gln Gly Leu Gly Asp Leu	
2065 2070 2075	
ata cct aat ctt ggt aaa aaa ggg ctt ttc gct cct tat ggc ttg agt	6291
Ile Pro Asn Leu Gly Lys Lys Gly Leu Phe Ala Pro Tyr Gly Leu Ser	
2080 2085 2090	
caa gtg tgg caa aaa ggg gat ttt agt ttc aac gca caa ggc aat gtt	6339
Gln Val Trp Gln Lys Gly Asp Phe Ser Phe Asn Ala Gln Gly Asn Val	
2095 2100 2105	
ttt gtg caa aat tcc act ttc tct aac gcc aat gga ggc acg ctc tct	6387
Phe Val Gln Asn Ser Thr Phe Ser Asn Ala Asn Gly Gly Thr Leu Ser	
2110 2115 2120	
ttt aac gca gga aat tcg ctc att ttt gcc gga aac aat cat att gca	6435
Phe Asn Ala Gly Asn Ser Leu Ile Phe Ala Gly Asn Asn His Ile Ala	
2125 2130 2135 2140	
ttc act aac cac gct gga act ctt caa tta ttg tcc gat caa gtt tct	6483
Phe Thr Asn His Ala Gly Thr Leu Gln Leu Leu Ser Asp Gln Val Ser	
2145 2150 2155	
aac att aac atc acc acg ctt aac gct agc aac ggc ctt aag att aac	6531
Asn Ile Asn Ile Thr Thr Leu Asn Ala Ser Asn Gly Leu Lys Ile Asn	
2160 2165 2170	
gcc gct aat aac aat gtt tct gtg tct caa ggc aat ctg ttt gtc agc	6579
Ala Ala Asn Asn Asn Val Ser Val Ser Gln Gly Asn Leu Phe Val Ser	
2175 2180 2185	
gct agc tgc gcg caa caa agc gat cca act aca gct aat att gca aac	6627
Ala Ser Cys Ala Gln Gln Ser Asp Pro Thr Thr Ala Asn Ile Ala Asn	
2190 2195 2200	
cct tgc gcg ctt agc gcc caa agc acg aat ggc gct tct tct aat aat	6675
Pro Cys Ala Leu Ser Ala Gln Ser Thr Asn Gly Ala Ser Ser Asn Asn	
2205 2210 2215 2220	
gcg tca aat aac gcg cca atc gcc ttg agt aat aac gat gaa agc ttg	6723
Ala Ser Asn Asn Ala Pro Ile Ala Leu Ser Asn Asn Asp Glu Ser Leu	
2225 2230 2235	
atg gtt gcg gcg aat gat ttc aat ttt tca ggc aat att tac gct aat	6771
Met Val Ala Ala Asn Asp Phe Asn Phe Ser Gly Asn Ile Tyr Ala Asn	
2240 2245 2250	
ggg gtg gtt gat ttt tca aag att aaa ggc tct gca aac att aaa aac	6819
Gly Val Val Asp Phe Ser Lys Ile Lys Gly Ser Ala Asn Ile Lys Asn	
2255 2260 2265	
ctg tat ctt tac aat aac gct caa ttc caa gcc aac aat ctc act att	6867
Leu Tyr Leu Tyr Asn Asn Ala Gln Phe Gln Ala Asn Asn Leu Thr Ile	
2270 2275 2280	
tcc aat caa gcg gtg tta gaa aaa aac gcc agc ttt gta acg aat aat	6915
Ser Asn Gln Ala Val Leu Glu Lys Asn Ala Ser Phe Val Thr Asn Asn	
2285 2290 2295 2300	

tta aac att caa gga gcg ttt aac aac aac gcc acg caa aaa ata gag	6963
Leu Asn Ile Gln Gly Ala Phe Asn Asn Asn Ala Thr Gln Lys Ile Glu	
2305 2310 2315	
gtg ctt caa aat tta gtg atc gct tca aac gct tct tta agc acc ggc	7011
Val Leu Gln Asn Leu Val Ile Ala Ser Asn Ala Ser Leu Ser Thr Gly	
2320 2325 2330	
att tat ggg tta gaa gta ggg ggg gct ttg aat aat tct gga gcg atc	7059
Ile Tyr Gly Leu Glu Val Gly Gly Ala Leu Asn Asn Ser Gly Ala Ile	
2335 2340 2345	
cat ttt aat tta gaa aat acc caa acg cca acg ccg ctc att caa gca	7107
His Phe Asn Leu Glu Asn Thr Gln Thr Pro Thr Pro Leu Ile Gln Ala	
2350 2355 2360	
gag ggg atc att aac ctc aac acc acc caa acg cct ttt atg aat gtc	7155
Glu Gly Ile Ile Asn Leu Asn Thr Thr Gln Thr Pro Phe Met Asn Val	
2365 2370 2375 2380	
aat aac agc atg gcc aat aat acg act tac act tta tta aaa agc agc	7203
Asn Asn Ser Met Ala Asn Asn Thr Thr Tyr Thr Leu Leu Lys Ser Ser	
2385 2390 2395	
cgt tac att gat tac aat atc aac ccc aac agc ttg caa tcg tat ttg	7251
Arg Tyr Ile Asp Tyr Asn Ile Asn Pro Asn Ser Leu Gln Ser Tyr Leu	
2400 2405 2410	
aat ctc tac act tta atc aat atc aac ggg aac cac ata gag gaa aaa	7299
Asn Leu Tyr Thr Leu Ile Asn Ile Asn Gly Asn His Ile Glu Glu Lys	
2415 2420 2425	
aac ggc gca ttg act tat ttg ggc caa cgg gtt ttg ttg caa gat aac	7347
Asn Gly Ala Leu Thr Tyr Leu Gly Gln Arg Val Leu Leu Gln Asp Lys	
2430 2435 2440	
ggg tta ttg tta agc gta gcg ctg ccc aac tca aac aac gct tct caa	7395
Gly Leu Leu Leu Ser Val Ala Leu Pro Asn Ser Asn Asn Ala Ser Gln	
2445 2450 2455 2460	
aac aac att tta agc ctt tct gtc ctt tat aac caa gtt aaa atg tct	7443
Asn Asn Ile Leu Ser Leu Ser Val Leu Tyr Asn Gln Val Lys Met Ser	
2465 2470 2475	
tgc ggc gat aaa gcg atg gat ttt acc ccc cct acc tta caa gat tac	7491
Cys Gly Asp Lys Ala Met Asp Phe Thr Pro Pro Thr Leu Gln Asp Tyr	
2480 2485 2490	
att gtg ggc att caa ggg caa agc gcg ctc aat caa att gaa gct gtt	7539
Ile Val Gly Ile Gln Gly Gln Ser Ala Leu Asn Gln Ile Glu Ala Val	
2495 2500 2505	
ggg ggg aac gct atc aag tgg ctt tca aca ttg atg atg gag act aaa	7587
Gly Gly Asn Ala Ile Lys Trp Leu Ser Thr Leu Met Met Glu Thr Lys	
2510 2515 2520	
gaa aac ccg ttt ttt gcg ccg att tat tta aaa aac cac tct ttg aat	7635
Glu Asn Pro Phe Phe Ala Pro Ile Tyr Leu Lys Asn His Ser Leu Asn	

2525	2530	2535	2540	
gaa atc tta ggc gta aca aaa gat ctt caa aac acc gca agc ttg att				7683
Glu Ile Leu Gly Val Thr Lys Asp Leu Gln Asn Thr Ala Ser Leu Ile	2545	2550	2555	
tct aac cct aat ttt aga gat aac gct acc aat ctt tta gaa ttg gcg				7731
Ser Asn Pro Asn Phe Arg Asp Asn Ala Thr Asn Leu Leu Glu Leu Ala	2560	2565	2570	
agt tac acc caa caa acc agc cgt tta aca aaa ctc tct gat ttt aga				7779
Ser Tyr Thr Gln Gln Thr Ser Arg Leu Thr Lys Leu Ser Asp Phe Arg	2575	2580	2585	
tct aga gag gga gag tct gat ttt tct ttg tta gag ctt aaa aac aag				7827
Ser Arg Glu Gly Glu Ser Asp Phe Ser Leu Leu Glu Leu Lys Asn Lys	2590	2595	2600	
cgt ttt agc gat cct aat cca gag gtt ttt gtc aaa tac tct caa ctt				7875
Arg Phe Ser Asp Pro Asn Pro Glu Val Phe Val Lys Tyr Ser Gln Leu	2605	2610	2615	2620
agc aaa cac cca aat aac ctt tgg gtt caa ggg gtg gga gga gcg agc				7923
Ser Lys His Pro Asn Asn Leu Trp Val Gln Gly Val Gly Gly Ala Ser	2625	2630	2635	
ttt att tct ggg ggc aat ggc acg ctt tat ggc ttg aat gcg ggc tat				7971
Phe Ile Ser Gly Gly Asn Gly Thr Leu Tyr Gly Leu Asn Ala Gly Tyr	2640	2645	2650	
gac agg ttg gtt aaa aat gtg atc ctt ggg ggt tat gtg gct tat ggc				8019
Asp Arg Leu Val Lys Asn Val Ile Leu Gly Gly Tyr Val Ala Tyr Gly	2655	2660	2665	
tat agc gac ttt aat ggg aac atc atg cat tct ttg ggt aat aat gtg				8067
Tyr Ser Asp Phe Asn Gly Asn Ile Met His Ser Leu Gly Asn Asn Val	2670	2675	2680	
gat gtg ggg atg tat gcg agg gct ttt tta aaa agg aac gaa ttc act				8115
Asp Val Gly Met Tyr Ala Arg Ala Phe Leu Lys Arg Asn Glu Phe Thr	2685	2690	2695	2700
ttg agc gcg aat gaa act tat gga ggc aat gca act agt atc aat tct				8163
Leu Ser Ala Asn Glu Thr Tyr Gly Gly Asn Ala Thr Ser Ile Asn Ser	2705	2710	2715	
tct aat tct ttg ctc tct gtg ttg aac caa cgc tac aac tac aac acc				8211
Ser Asn Ser Leu Leu Ser Val Leu Asn Gln Arg Tyr Asn Tyr Asn Thr	2720	2725	2730	
tgg aca acg agc gtg aac ggg aat tac ggc tat gat ttc atg ttc aaa				8259
Trp Thr Thr Ser Val Asn Gly Asn Tyr Gly Tyr Asp Phe Met Phe Lys	2735	2740	2745	
caa aaa agc gtg gtg cta aaa cct caa gtg ggt ttg agc tat cat ttc				8307
Gln Lys Ser Val Val Leu Lys Pro Gln Val Gly Leu Ser Tyr His Phe	2750	2755	2760	
ata ggt cta agt ggg atg aaa ggc aat gat gcc gct tac aaa caa ttc				8355

Ile Gly Leu Ser Gly Met Lys Gly Asn Asp Ala Ala Tyr Lys Gln Phe
 2765 2770 2775 2780

ctc atg cat tca aac ccc tct aac gaa tcg gtt tta acg ctc aac atg 8403
 Leu Met His Ser Asn Pro Ser Asn Glu Ser Val Leu Thr Leu Asn Met
 2785 2790 2795

ggg ttg gag agc cgt aaa tat ttt ggt aaa aat tcc tat tat ttt gta 8451
 Gly Leu Glu Ser Arg Lys Tyr Phe Gly Lys Asn Ser Tyr Tyr Phe Val
 2800 2805 2810

acg gcg aga cta ggt agg gat ctt ttg atc aaa tct aaa ggc agc aat 8499
 Thr Ala Arg Leu Gly Arg Asp Leu Leu Ile Lys Ser Lys Gly Ser Asn
 2815 2820 2825

acg gtg cgt ttt gtg ggc gaa aac act tta ttg tat cgc aag ggg gaa 8547
 Thr Val Arg Phe Val Gly Glu Asn Thr Leu Leu Tyr Arg Lys Gly Glu
 2830 2835 2840

gtt ttt aac act ttt gcg agc gtg att aca ggg ggc gaa atg cat ttg 8595
 Val Phe Asn Thr Phe Ala Ser Val Ile Thr Gly Gly Glu Met His Leu
 2845 2850 2855 2860

tgg cgt ttg gtg tat gtg aat gcg ggg gtg ggg ctt aag atg ggc ttg 8643
 Trp Arg Leu Val Tyr Val Asn Ala Gly Val Gly Leu Lys Met Gly Leu
 2865 2870 2875

caa tac caa gat att aat ata acc ggg aat gtg ggc atg cga gtg gcg 8691
 Gln Tyr Gln Asp Ile Asn Ile Thr Gly Asn Val Gly Met Arg Val Ala
 2880 2885 2890

ttt tagctttttt gctataatgc ttcgttcaaa ttttatgggt aggtttttct 8744
 Phe

atgt 8748

<210> 522

<211> 2893

<212> PRT

<213> Helicobacter pylori

<400> 522

Met Lys Lys Phe Lys Lys Lys Pro Lys Ser Ile Lys Arg Ser His Gln
 1 5 10 15
 Asn Gln Lys Thr Ile Leu Lys Arg Pro Leu Trp Leu Met Pro Leu Leu
 20 25 30
 Ile Ser Gly Phe Ala Ser Gly Val Tyr Ala Asn Asn Leu Trp Asp Leu
 35 40 45
 Leu Asn Pro Lys Val Gly Gly Glu Tyr Val His Trp Val Lys Gly Ser
 50 55 60
 Gln Tyr Cys Ala Trp Trp Glu Phe Ala Gly Cys Leu Lys Asn Val Trp
 65 70 75 80
 Gly Ala Asn His Lys Gly Tyr Asp Ala Gly Asn Ala Ala Asn Tyr Leu
 85 90 95
 Ser Ser Gln Asn Tyr Gln Ala Ile Ser Val Gly Ser Gly Asn Glu Thr
 100 105 110
 Gly Thr Tyr Ser Leu Ser Gly Phe Thr Asn Tyr Val Gly Gly Asn Leu
 115 120 125

Thr	Ile	Asn	Leu	Gly	Asn	Ser	Val	Val	Leu	Asp	Leu	Ser	Gly	Ser	Asn
130						135					140				
Ser	Phe	Thr	Ser	Tyr	Gln	Gly	Tyr	Asn	Gln	Gly	Lys	Asp	Asp	Val	Thr
145					150					155					160
Phe	Thr	Val	Gly	Ala	Ile	Asn	Leu	Asn	Gly	Thr	Leu	Glu	Val	Gly	Asn
				165					170					175	
Arg	Val	Gly	Ser	Gly	Ala	Gly	Thr	His	Thr	Gly	Thr	Ala	Thr	Leu	Asn
			180					185					190		
Leu	Asn	Ala	Asn	Lys	Val	Asn	Ile	Asn	Ser	Asn	Ile	Asn	Ala	Tyr	Lys
		195					200					205			
Thr	Ser	Gln	Val	Asn	Ile	Gly	Asn	Ala	Asn	Ser	Val	Ile	Thr	Ile	Gly
	210					215					220				
Ser	Val	Ser	Leu	Ser	Gly	Asp	Val	Cys	Ser	Ser	Leu	Ala	Ser	Val	Gly
225					230					235					240
Ile	Gly	Ala	Asn	Cys	Ser	Thr	Ser	Gly	Pro	Ser	Tyr	Ser	Phe	Lys	Gly
				245					250					255	
Thr	Thr	Asn	Ala	Thr	Asn	Thr	Ala	Phe	Ser	Asn	Ala	Ser	Gly	Ser	Phe
			260					265					270		
Thr	Phe	Glu	Glu	Asn	Ala	Thr	Phe	Ser	Gly	Ala	Lys	Trp	Asn	Gly	Gly
		275					280					285			
Thr	Tyr	Thr	Phe	Asn	Lys	Glu	Phe	Ser	Ala	Thr	Asn	Asn	Thr	Ala	Phe
	290					295					300				
Ser	Ser	Gly	Ser	Phe	Asn	Phe	Lys	Gly	Val	Ser	Ser	Phe	Asn	Gly	Thr
305					310					315					320
Ser	Phe	Ser	Asn	Ala	Ser	Tyr	Thr	Phe	Asp	Asn	Gln	Ala	Thr	Phe	Gln
				325					330					335	
Asn	Ser	Ser	Phe	Asn	Gly	Gly	Thr	Phe	Thr	Phe	Asn	Asn	Gln	Thr	Asn
			340					345					350		
Pro	Thr	Asn	Asn	Ala	Gln	His	Pro	Gln	Ile	Gln	Asn	Ser	Ser	Phe	Ser
		355					360					365			
Gly	Asn	Ala	Thr	Thr	Leu	Lys	Gly	Phe	Val	Asn	Phe	Gln	Gln	Ala	Phe
	370					375					380				
Asn	Asn	Ser	Asn	His	Gln	Leu	Thr	Ile	Gln	Asn	Ala	Ser	Phe	Asn	Asn
385					390					395					400
Ala	Thr	Phe	Asn	Asn	Thr	Gly	Lys	Ile	Thr	Ile	Glu	Lys	Asp	Ala	Ser
				405					410					415	
Phe	Asn	Asn	Thr	Thr	Phe	Asn	Thr	Ser	Val	Asp	Thr	Asn	Asn	Met	Ser
			420					425					430		
Val	Thr	Gly	Gly	Val	Thr	Leu	Ser	Gly	Lys	Asn	Asp	Leu	Lys	Asn	Gly
		435					440					445			
Ser	Thr	Leu	Asp	Phe	Gly	Ser	Ser	Lys	Ile	Thr	Leu	Ala	Gln	Gly	Thr
	450					455					460				
Thr	Phe	Asn	Leu	Thr	Ser	Leu	Gly	Ser	Glu	Lys	Ser	Val	Thr	Ile	Leu
465					470					475					480
Asn	Ser	Ser	Gly	Gly	Ile	Thr	Tyr	Ser	Asn	Leu	Leu	Asn	His	Ala	Ile
				485					490					495	
Asn	Gly	Leu	Thr	Ser	Ala	Leu	Lys	Thr	Asn	Glu	Ser	Leu	Ser	Asn	Pro
			500					505					510		
Gln	Ser	Phe	Ala	Gln	Gly	Leu	Trp	Asp	Ile	Ile	Thr	Tyr	Asn	Gly	Val
		515					520					525			
Thr	Gly	Gln	Leu	Leu	Asn	Glu	Asn	Ala	Ala	Thr	Ser	Lys	Pro	Thr	Asp
	530					535					540				
Ser	Ser	Pro	Ser	Lys	Ser	Ser	Thr	Asn	Ser	Thr	Gln	Val	Tyr	Gln	Val
545					550					555					560
Gly	Tyr	Lys	Ile	Gly	Asp	Thr	Ile	Tyr	Lys	Leu	Gln	Glu	Thr	Phe	Ser
				565					570					575	
His	Asn	Ser	Ile	Ile	Ile	Gln	Ala	Leu	Glu	Ser	Gly	Thr	Tyr	Thr	Pro
			580					585					590		
Pro	Pro	Val	Ile	Asn	Gly	Ser	Lys	Phe	Asp	Leu	Ser	Ala	Ser	Asn	Tyr

		595					600					605					
Ile	Asn	Ala	Asp	Met	Pro	Trp	Tyr	Asp	His	Lys	Tyr	Tyr	Ile	Pro	Lys		
	610						615					620					
Ser	Gln	Asn	Phe	Thr	Glu	Ser	Gly	Thr	Tyr	Tyr	Leu	Pro	Ser	Val	Gln		
625					630					635					640		
Ile	Trp	Gly	Ser	Tyr	Thr	Asn	Ser	Phe	Lys	Gln	Thr	Phe	Ser	Ala	Asn		
				645					650						655		
Gly	Ser	Asn	Leu	Val	Ile	Gly	Tyr	Asn	Ser	Thr	Trp	Thr	Asp	His	Asn		
			660					665					670				
Val	Ser	Ser	Ser	Gly	Thr	Val	Ser	Phe	Gly	Asp	Thr	Ser	Gly	Ser	Ala		
		675					680					685					
Leu	Asn	Gly	His	Cys	Gly	Pro	Trp	Pro	Tyr	Tyr	Gln	Cys	Thr	Gly	Thr		
	690					695					700						
Thr	Asn	Gly	Thr	Tyr	Ser	Ala	Tyr	His	Val	Tyr	Ile	Thr	Ala	Asn	Leu		
705					710					715					720		
Arg	Ser	Gly	Asn	Arg	Ile	Gly	Thr	Gly	Gly	Ala	Ala	Asn	Leu	Ile	Phe		
				725					730					735			
Asn	Gly	Val	Asp	Ser	Ile	Asn	Ile	Ala	Asn	Ala	Thr	Ile	Thr	Gln	His		
			740					745					750				
Asn	Ala	Gly	Ile	Tyr	Ser	Ser	Ser	Met	Thr	Phe	Ser	Thr	Gln	Ser	Met		
		755					760					765					
Asp	Asn	Ser	Gln	Asn	Leu	Asn	Gly	Leu	Asn	Ser	Asn	Gly	Lys	Leu	Ser		
	770					775					780						
Val	Tyr	Gly	Thr	Thr	Phe	Thr	Asn	Glu	Ala	Lys	Asp	Gly	Lys	Phe	Ile		
785					790					795					800		
Phe	Asn	Ala	Gly	Gln	Ala	Val	Phe	Glu	Asn	Thr	Asn	Phe	Asn	Gly	Gly		
				805					810					815			
Ser	Tyr	Gln	Phe	Ser	Gly	Asp	Ser	Leu	Asn	Phe	Ser	Asn	Asn	Asn	Gln		
			820					825					830				
Phe	Asn	Ser	Gly	Ser	Phe	Glu	Ile	Ser	Ala	Lys	Asn	Ala	Ser	Phe	Asn		
		835					840					845					
Asn	Ala	Asn	Phe	Asn	Asn	Ser	Ala	Ser	Phe	Asn	Phe	Asn	Asn	Ser	Asn		
	850					855					860						
Ala	Thr	Thr	Ser	Phe	Val	Gly	Asp	Phe	Thr	Asn	Ala	Asn	Ser	Asn	Leu		
865					870					875					880		
Gln	Ile	Ala	Gly	Asn	Ala	Val	Phe	Gly	Asn	Ser	Thr	Asn	Gly	Ser	Gln		
				885					890					895			
Asn	Thr	Ala	Asn	Phe	Asn	Asn	Thr	Gly	Ser	Val	Asn	Ile	Ser	Gly	Asn		
			900					905					910				
Ala	Thr	Phe	Asp	Asn	Val	Val	Phe	Asn	Gly	Pro	Thr	Asn	Thr	Ser	Val		
		915						920					925				
Lys	Gly	Gln	Val	Thr	Leu	Asn	Asn	Ile	Thr	Leu	Lys	Asn	Leu	Asn	Ala		
	930					935					940						
Pro	Leu	Ser	Phe	Gly	Asp	Gly	Thr	Ile	Thr	Phe	Asn	Ala	His	Ser	Val		
945					950					955					960		
Ile	Asn	Ile	Ala	Glu	Ser	Ile	Thr	Asn	Gly	Asn	Pro	Ile	Thr	Leu	Val		
				965					970					975			
Ser	Ser	Ser	Lys	Glu	Ile	Glu	Tyr	Asn	Asn	Ala	Phe	Ser	Lys	Asn	Leu		
			980					985					990				
Trp	Gln	Leu	Ile	Asn	Tyr	Gln	Gly	His	Gly	Ala	Ser	Ser	Glu	Lys	Leu		
			995				1000						1005				
Val	Ser	Ser	Ala	Gly	Asn	Gly	Val	Tyr	Asp	Val	Val	Tyr	Ser	Phe	Asn		
	1010					1015					1020						
Asn	Gln	Thr	Tyr	Asn	Phe	Gln	Glu	Val	Phe	Ser	Gln	Asn	Ser	Ile	Ser		
1025					1030					1035					1040		
Ile	Arg	Arg	Leu	Gly	Val	Asn	Met	Val	Phe	Asp	Tyr	Val	Asp	Met	Glu		
				1045					1050					1055			
Lys	Ser	Asp	His	Leu	Tyr	Tyr	Gln	Asn	Ala	Leu	Gly	Phe	Met	Thr	Tyr		
			1060					1065					1070				

Met	Pro	Asn	Ser	Tyr	Asn	Asn	Asn	Leu	Gly	Asn	Ala	Asn	Asn	Thr	Ile		
		1075					1080					1085					
Tyr	Tyr	Tyr	Asp	Lys	Ser	Ile	Asp	Phe	Tyr	Ala	Ser	Gly	Lys	Thr	Leu		
		1090					1095				1100						
Phe	Thr	Lys	Ala	Glu	Phe	Ser	Gln	Thr	Phe	Thr	Gly	Gln	Asn	Ser	Ala		
1105						1110				1115					1120		
Ile	Val	Phe	Gly	Ala	Lys	Ser	Ile	Trp	Thr	Ser	Leu	Ser	Asp	Ala	Pro		
			1125						1130						1135		
Gln	Ser	Asn	Thr	Ile	Ile	Arg	Phe	Gly	Asp	Asn	Lys	Gly	Ala	Gly	Ser		
			1140					1145						1150			
Asn	Asp	Ala	Ser	Gly	His	Cys	Trp	Asn	Leu	Gln	Cys	Ile	Gly	Phe	Ile		
		1155					1160					1165					
Thr	Gly	His	Tyr	Glu	Ala	Gln	Lys	Ile	Tyr	Ile	Thr	Gly	Ser	Ile	Glu		
	1170					1175				1180							
Ser	Gly	Asn	Arg	Ile	Ser	Ser	Gly	Gly	Gly	Ala	Ser	Leu	Asn	Phe	Asn		
1185					1190					1195					1200		
Gly	Leu	Gln	Gly	Ile	Leu	Leu	Thr	Asn	Ala	Thr	Leu	Tyr	Asn	Arg	Ala		
			1205					1210						1215			
Ala	Gly	Thr	Gln	Ser	Ser	Ser	Met	Asn	Phe	Ile	Ser	Asn	Ser	Ala	Asn		
			1220					1225						1230			
Ile	Gln	Ala	Gln	Asn	Ser	Tyr	Phe	Ile	Asp	Asp	Thr	Ala	Gln	Asn	Gly		
		1235					1240						1245				
Gly	Asn	Pro	Asn	Phe	Ser	Phe	Asn	Ala	Leu	Asn	Leu	Asp	Phe	Ser	Asn		
	1250					1255					1260						
Ser	Ser	Phe	Arg	Gly	Tyr	Val	Gly	Lys	Thr	Gln	Ser	Val	Phe	Lys	Phe		
1265					1270					1275					1280		
Asn	Ala	Lys	Asn	Ala	Ile	Ser	Phe	Thr	Asn	Ser	Thr	Asn	Leu	Ser	Ser		
			1285					1290						1295			
Gly	Leu	Tyr	Gln	Met	Gln	Ala	Lys	Ser	Val	Leu	Phe	Asp	Asn	Ser	Asn		
		1300						1305					1310				
Leu	Ser	Val	Ser	Val	Gly	Thr	Ser	Ser	Ile	Lys	Ala	Asn	Ala	Ile	Asn		
	1315					1320						1325					
Leu	Ser	Gln	Asn	Ala	Ser	Ile	Asn	Ala	Ser	Asn	His	Ser	Thr	Leu	Glu		
	1330					1335					1340						
Leu	Gln	Gly	Asp	Leu	Asn	Val	Asn	Asp	Thr	Ser	Ser	Leu	Asn	Leu	Asn		
1345					1350				1355					1360			
Gln	Ser	Thr	Ile	Asn	Val	Ser	Asn	Asn	Ala	Thr	Ile	Asn	Asp	Tyr	Ala		
			1365					1370						1375			
Ser	Leu	Ile	Ala	Ser	Asn	Gly	Ser	His	Leu	Asn	Phe	Asn	Gly	Ala	Val		
		1380				1385							1390				
Asn	Phe	Asn	Ser	Ala	Asn	Ile	Thr	Thr	Ser	Leu	Asn	Asn	Ser	Ser	Ile		
	1395					1400						1405					
Val	Phe	Lys	Gly	Ala	Val	Ser	Leu	Gly	Gly	Gln	Phe	Asn	Leu	Ser	Asn		
	1410					1415				1420							
Asn	Ser	Ser	Leu	Asp	Phe	Gln	Gly	Ser	Ser	Ala	Ile	Thr	Ser	Asn	Thr		
1425					1430					1435					1440		
Ala	Phe	Asn	Phe	Tyr	Asp	Asn	Ala	Phe	Ser	Gln	Ser	Pro	Ile	Thr	Phe		
			1445					1450						1455			
His	Gln	Ala	Leu	Asp	Ile	Lys	Ala	Pro	Leu	Ser	Leu	Gly	Gly	Asn	Leu		
		1460						1465					1470				
Leu	Asn	Pro	Asn	Asn	Ser	Ser	Val	Leu	Asp	Leu	Lys	Asn	Ser	Gln	Leu		
	1475					1480					1485						
Val	Phe	Gly	Asp	Gln	Gly	Ser	Leu	Asn	Ile	Ala	Asn	Ile	Asp	Leu	Leu		
	1490					1495					1500						
Ser	Asp	Leu	Asn	Asp	Asn	Lys	Asn	Arg	Val	Tyr	Asn	Ile	Ile	Gln	Ala		
1505					1510				1515					1520			
Asp	Met	Asn	Ser	Asn	Trp	Tyr	Glu	Arg	Ile	Ser	Phe	Phe	Gly	Met	His		
			1525					1530						1535			
Ile	Asn	Asp	Gly	Ile	Tyr	Asp	Ala	Lys	Asn	Gln	Thr	Tyr	Ser	Phe	Thr		

Asn	Ala	Leu	Lys	Asn	Asp	Val	Ala	Ala	Leu	Gly	Lys	Gln	Met	Ile	Gly
			2020					2025					2030		
Glu	Phe	Leu	Gly	Gln	Asp	Thr	Leu	Asn	Ser	Leu	Glu	Ser	Leu	Leu	Gln
		2035					2040					2045			
Asn	Gln	Gln	Ile	Lys	Ser	Val	Leu	Asp	Lys	Val	Leu	Ala	Ala	Lys	Gly
	2050				2055					2060					
Leu	Gly	Pro	Ile	Tyr	Glu	Gln	Gly	Leu	Gly	Asp	Leu	Ile	Pro	Asn	Leu
2065				2070					2075					2080	
Gly	Lys	Lys	Gly	Leu	Phe	Ala	Pro	Tyr	Gly	Leu	Ser	Gln	Val	Trp	Gln
			2085					2090					2095		
Lys	Gly	Asp	Phe	Ser	Phe	Asn	Ala	Gln	Gly	Asn	Val	Phe	Val	Gln	Asn
		2100					2105					2110			
Ser	Thr	Phe	Ser	Asn	Ala	Asn	Gly	Gly	Thr	Leu	Ser	Phe	Asn	Ala	Gly
	2115						2120					2125			
Asn	Ser	Leu	Ile	Phe	Ala	Gly	Asn	Asn	His	Ile	Ala	Phe	Thr	Asn	His
	2130					2135					2140				
Ala	Gly	Thr	Leu	Gln	Leu	Leu	Ser	Asp	Gln	Val	Ser	Asn	Ile	Asn	Ile
2145				2150					2155					2160	
Thr	Thr	Leu	Asn	Ala	Ser	Asn	Gly	Leu	Lys	Ile	Asn	Ala	Ala	Asn	Asn
			2165					2170						2175	
Asn	Val	Ser	Val	Ser	Gln	Gly	Asn	Leu	Phe	Val	Ser	Ala	Ser	Cys	Ala
		2180					2185						2190		
Gln	Gln	Ser	Asp	Pro	Thr	Thr	Ala	Asn	Ile	Ala	Asn	Pro	Cys	Ala	Leu
	2195						2200					2205			
Ser	Ala	Gln	Ser	Thr	Asn	Gly	Ala	Ser	Ser	Asn	Asn	Ala	Ser	Asn	Asn
	2210					2215				2220					
Ala	Pro	Ile	Ala	Leu	Ser	Asn	Asn	Asp	Glu	Ser	Leu	Met	Val	Ala	Ala
2225				2230					2235					2240	
Asn	Asp	Phe	Asn	Phe	Ser	Gly	Asn	Ile	Tyr	Ala	Asn	Gly	Val	Val	Asp
			2245					2250						2255	
Phe	Ser	Lys	Ile	Lys	Gly	Ser	Ala	Asn	Ile	Lys	Asn	Leu	Tyr	Leu	Tyr
	2260						2265						2270		
Asn	Asn	Ala	Gln	Phe	Gln	Ala	Asn	Asn	Leu	Thr	Ile	Ser	Asn	Gln	Ala
	2275						2280					2285			
Val	Leu	Glu	Lys	Asn	Ala	Ser	Phe	Val	Thr	Asn	Asn	Leu	Asn	Ile	Gln
	2290					2295					2300				
Gly	Ala	Phe	Asn	Asn	Asn	Ala	Thr	Gln	Lys	Ile	Glu	Val	Leu	Gln	Asn
2305				2310					2315					2320	
Leu	Val	Ile	Ala	Ser	Asn	Ala	Ser	Leu	Ser	Thr	Gly	Ile	Tyr	Gly	Leu
			2325					2330						2335	
Glu	Val	Gly	Gly	Ala	Leu	Asn	Asn	Ser	Gly	Ala	Ile	His	Phe	Asn	Leu
	2340						2345					2350			
Glu	Asn	Thr	Gln	Thr	Pro	Thr	Pro	Leu	Ile	Gln	Ala	Glu	Gly	Ile	Ile
	2355						2360					2365			
Asn	Leu	Asn	Thr	Thr	Gln	Thr	Pro	Phe	Met	Asn	Val	Asn	Asn	Ser	Met
	2370					2375					2380				
Ala	Asn	Asn	Thr	Thr	Tyr	Thr	Leu	Leu	Lys	Ser	Ser	Arg	Tyr	Ile	Asp
2385				2390					2395					2400	
Tyr	Asn	Ile	Asn	Pro	Asn	Ser	Leu	Gln	Ser	Tyr	Leu	Asn	Leu	Tyr	Thr
			2405					2410						2415	
Leu	Ile	Asn	Ile	Asn	Gly	Asn	His	Ile	Glu	Glu	Lys	Asn	Gly	Ala	Leu
	2420						2425						2430		
Thr	Tyr	Leu	Gly	Gln	Arg	Val	Leu	Leu	Gln	Asp	Lys	Gly	Leu	Leu	Leu
	2435						2440					2445			
Ser	Val	Ala	Leu	Pro	Asn	Ser	Asn	Asn	Ala	Ser	Gln	Asn	Asn	Ile	Leu
	2450					2455					2460				
Ser	Leu	Ser	Val	Leu	Tyr	Asn	Gln	Val	Lys	Met	Ser	Cys	Gly	Asp	Lys
2465				2470					2475					2480	
Ala	Met	Asp	Phe	Thr	Pro	Pro	Thr	Leu	Gln	Asp	Tyr	Ile	Val	Gly	Ile

<221> CDS

<222> (32)...(1048)

<400> 523

```
ggaactctca tcaaaaaaca aggaacataa t atg aga cat gga gat att agt 52
                               Met Arg His Gly Asp Ile Ser
                               1                               5

agc agc cca gat act gtg ggt gta gcg gta gtt aat tat aag atg cct 100
Ser Ser Pro Asp Thr Val Gly Val Ala Val Val Asn Tyr Lys Met Pro
          10                      15                      20

aga ctc cac act aag aat gag gtg ttg gaa aat tgt cgc aat atc gct 148
Arg Leu His Thr Lys Asn Glu Val Leu Glu Asn Cys Arg Asn Ile Ala
          25                      30                      35

aag gtg att ggt ggg gtc aaa cag ggt ttg cct ggg ttg gat ctg att 196
Lys Val Ile Gly Gly Val Lys Gln Gly Leu Pro Gly Leu Asp Leu Ile
          40                      45                      50                      55

att ttc cct gaa tac agc acg cat ggg att atg tat gac aga caa gaa 244
Ile Phe Pro Glu Tyr Ser Thr His Gly Ile Met Tyr Asp Arg Gln Glu
                      60                      65                      70

atg ttt gat aca gcc gca agc gtt cct gga gaa gaa acc gcg atc ttt 292
Met Phe Asp Thr Ala Ala Ser Val Pro Gly Glu Glu Thr Ala Ile Phe
          75                      80                      85

gct gaa gct tgt aag aaa aac aag gtt tgg gga gtg ttc tct ttg aca 340
Ala Glu Ala Cys Lys Lys Asn Lys Val Trp Gly Val Phe Ser Leu Thr
          90                      95                      100

ggg gaa aaa cac gag caa gcc aaa aag aat ccc tat aac act ttg att 388
Gly Glu Lys His Glu Gln Ala Lys Lys Asn Pro Tyr Asn Thr Leu Ile
          105                      110                      115

ctt gtc aat gat aag ggt gag atc gtg caa aaa tac cgc aaa atc ttg 436
Leu Val Asn Asp Lys Gly Glu Ile Val Gln Lys Tyr Arg Lys Ile Leu
          120                      125                      130                      135

cct tgg tgc cct att gaa tgt tgg tat cct ggg gat aaa act tat gtg 484
Pro Trp Cys Pro Ile Glu Cys Trp Tyr Pro Gly Asp Lys Thr Tyr Val
          140                      145                      150

gtt gat ggg cct aag ggc ttg aaa gtt tct ttg att att tgc gat gat 532
Val Asp Gly Pro Lys Gly Leu Lys Val Ser Leu Ile Ile Cys Asp Asp
          155                      160                      165

gga aac tac cct gaa att tgg cgc gat tgc gcg atg cgt ggg gca gaa 580
Gly Asn Tyr Pro Glu Ile Trp Arg Asp Cys Ala Met Arg Gly Ala Glu
          170                      175                      180

ctc att gtg cgc tgt caa ggt tac atg tat ccg gct aag gag caa caa 628
Leu Ile Val Arg Cys Gln Gly Tyr Met Tyr Pro Ala Lys Glu Gln Gln
          185                      190                      195

att gca ata gta aaa gct atg gcg tgg gcc aat caa tgt tat gta gcg 676
Ile Ala Ile Val Lys Ala Met Ala Trp Ala Asn Gln Cys Tyr Val Ala
          200                      205                      210                      215
```

gta gcg aat gcg acc ggt ttt gat ggg gtg tat tcc tat ttt ggg cat 724
 Val Ala Asn Ala Thr Gly Phe Asp Gly Val Tyr Ser Tyr Phe Gly His
 220 225 230
 tct agc att att ggt ttt gac ggg cat act ttg ggc gaa tgc ggg gaa 772
 Ser Ser Ile Ile Gly Phe Asp Gly His Thr Leu Gly Glu Cys Gly Glu
 235 240 245
 gaa gaa aat ggt ctt caa tac gct caa ctt tct gtg caa caa atc cgt 820
 Glu Glu Asn Gly Leu Gln Tyr Ala Gln Leu Ser Val Gln Gln Ile Arg
 250 255 260
 gat gcg aga aaa tac gac caa agc caa aac caa ctc ttc aaa ctc ttg 868
 Asp Ala Arg Lys Tyr Asp Gln Ser Gln Asn Gln Leu Phe Lys Leu Leu
 265 270 275
 cac aga ggt tat agt ggg gtt ttt gct agt ggc gat ggg gat aag ggt 916
 His Arg Gly Tyr Ser Gly Val Phe Ala Ser Gly Asp Gly Asp Lys Gly
 280 285 290 295
 gtg gcg gaa tgc cct ttt gag ttc tat aaa act tgg gtg aat gac ccc 964
 Val Ala Glu Cys Pro Phe Glu Phe Tyr Lys Thr Trp Val Asn Asp Pro
 300 305 310
 aaa aaa gct caa gaa aat gta gaa aaa atc acc cgc cca agc gtg ggt 1012
 Lys Lys Ala Gln Glu Asn Val Glu Lys Ile Thr Arg Pro Ser Val Gly
 315 320 325
 gtg gcc gct tgt cct gtg ggc gat ttg ccc acg aaa taaagggcaa 1058
 Val Ala Ala Cys Pro Val Gly Asp Leu Pro Thr Lys
 330 335
 aaggaggagg gggggggc 1075
 <210> 524
 <211> 339
 <212> PRT
 <213> Helicobacter pylori

<400> 524
 Met Arg His Gly Asp Ile Ser Ser Ser Pro Asp Thr Val Gly Val Ala
 1 5 10 15
 Val Val Asn Tyr Lys Met Pro Arg Leu His Thr Lys Asn Glu Val Leu
 20 25 30
 Glu Asn Cys Arg Asn Ile Ala Lys Val Ile Gly Gly Val Lys Gln Gly
 35 40 45
 Leu Pro Gly Leu Asp Leu Ile Ile Phe Pro Glu Tyr Ser Thr His Gly
 50 55 60
 Ile Met Tyr Asp Arg Gln Glu Met Phe Asp Thr Ala Ala Ser Val Pro
 65 70 75 80
 Gly Glu Glu Thr Ala Ile Phe Ala Glu Ala Cys Lys Lys Asn Lys Val
 85 90 95
 Trp Gly Val Phe Ser Leu Thr Gly Glu Lys His Glu Gln Ala Lys Lys
 100 105 110
 Asn Pro Tyr Asn Thr Leu Ile Leu Val Asn Asp Lys Gly Glu Ile Val
 115 120 125
 Gln Lys Tyr Arg Lys Ile Leu Pro Trp Cys Pro Ile Glu Cys Trp Tyr
 130 135 140

Pro	Gly	Asp	Lys	Thr	Tyr	Val	Val	Asp	Gly	Pro	Lys	Gly	Leu	Lys	Val
145					150					155					160
Ser	Leu	Ile	Ile	Cys	Asp	Asp	Gly	Asn	Tyr	Pro	Glu	Ile	Trp	Arg	Asp
				165					170						175
Cys	Ala	Met	Arg	Gly	Ala	Glu	Leu	Ile	Val	Arg	Cys	Gln	Gly	Tyr	Met
			180					185					190		
Tyr	Pro	Ala	Lys	Glu	Gln	Gln	Ile	Ala	Ile	Val	Lys	Ala	Met	Ala	Trp
		195					200					205			
Ala	Asn	Gln	Cys	Tyr	Val	Ala	Val	Ala	Asn	Ala	Thr	Gly	Phe	Asp	Gly
	210					215					220				
Val	Tyr	Ser	Tyr	Phe	Gly	His	Ser	Ser	Ile	Ile	Gly	Phe	Asp	Gly	His
225					230					235					240
Thr	Leu	Gly	Glu	Cys	Gly	Glu	Glu	Glu	Asn	Gly	Leu	Gln	Tyr	Ala	Gln
			245						250						255
Leu	Ser	Val	Gln	Gln	Ile	Arg	Asp	Ala	Arg	Lys	Tyr	Asp	Gln	Ser	Gln
			260					265					270		
Asn	Gln	Leu	Phe	Lys	Leu	Leu	His	Arg	Gly	Tyr	Ser	Gly	Val	Phe	Ala
	275						280					285			
Ser	Gly	Asp	Gly	Asp	Lys	Gly	Val	Ala	Glu	Cys	Pro	Phe	Glu	Phe	Tyr
	290					295					300				
Lys	Thr	Trp	Val	Asn	Asp	Pro	Lys	Lys	Ala	Gln	Glu	Asn	Val	Glu	Lys
305				310						315					320
Ile	Thr	Arg	Pro	Ser	Val	Gly	Val	Ala	Ala	Cys	Pro	Val	Gly	Asp	Leu
				325					330					335	
Pro	Thr	Lys													

<210> 525
 <211> 1722
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (40)...(1686)

<400> 525																
atctctatcc	tttatagaat	ttgttggtgga	gactggcctt	atg	aat	aat	ggt	ttt							54	
				Met	Asn	Asn	Val	Phe								
				1				5								
ggt	aag	ggt	ttg	ttt	ttt	ttt	ctt	tta	ttg	ttt	ggg	ttt	ttt	ttg	aaa	102
Val	Lys	Gly	Leu	Phe	Phe	Phe	Leu	Leu	Leu	Phe	Gly	Phe	Phe	Leu	Lys	
				10					15					20		
gct	tca	gaa	agc	cca	aac	gct	act	ctt	aat	cca	tct	aaa	gaa	aat	ggt	150
Ala	Ser	Glu	Ser	Pro	Asn	Ala	Thr	Leu	Asn	Pro	Ser	Lys	Glu	Asn	Val	
			25					30					35			
tct	ggt	gaa	gag	caa	aag	cgt	ttt	gga	ggc	ggt	tta	ggt	ttt	gca	aga	198
Ser	Val	Glu	Glu	Gln	Lys	Arg	Phe	Gly	Gly	Val	Leu	Val	Phe	Ala	Arg	
		40					45					50				
ggc	gct	gat	ggc	tcg	agc	atg	gat	cct	gct	tta	gtg	act	gat	ggc	gaa	246
Gly	Ala	Asp	Gly	Ser	Ser	Met	Asp	Pro	Ala	Leu	Val	Thr	Asp	Gly	Glu	
		55				60					65					
agc	tat	gta	gca	acg	ggc	aat	att	tat	gac	acg	ctc	gtg	caa	ttc	aga	294

Ser 70	Tyr	Val	Ala	Thr	Gly 75	Asn	Ile	Tyr	Asp	Thr 80	Leu	Val	Gln	Phe	Arg 85	
tac	ggc	acc	aca	gaa	gtt	gaa	ccc	gcc	tta	gcg	aca	agc	tgg	gac	ata	342
Tyr	Gly	Thr	Thr	Glu	Val	Glu	Pro	Ala	Leu	Ala	Thr	Ser	Trp	Asp	Ile	
				90					95					100		
tcc	cca	gat	ggg	ctt	gta	tat	acc	ttt	cat	tta	cgc	aaa	ggg	gtt	tat	390
Ser	Pro	Asp	Gly	Leu	Val	Tyr	Thr	Phe	His	Leu	Arg	Lys	Gly	Val	Tyr	
			105					110					115			
ttc	cac	caa	acg	aag	tat	tgg	aat	aaa	aaa	gta	gag	ttt	agc	gct	aaa	438
Phe	His	Gln	Thr	Lys	Tyr	Trp	Asn	Lys	Lys	Val	Glu	Phe	Ser	Ala	Lys	
		120					125					130				
gat	gtg	ctg	ttt	tgc	ttt	gaa	cgc	cag	atg	gat	aaa	gct	aaa	cga	tat	486
Asp	Val	Leu	Phe	Ser	Phe	Glu	Arg	Gln	Met	Asp	Lys	Ala	Lys	Arg	Tyr	
	135					140					145					
tat	agc	ccg	ggg	gct	aaa	agc	tat	aag	tat	tgg	gaa	ggc	atg	ggc	atg	534
Tyr	Ser	Pro	Gly	Ala	Lys	Ser	Tyr	Lys	Tyr	Trp	Glu	Gly	Met	Gly	Met	
150					155					160					165	
tct	cat	att	att	aag	agc	att	gaa	gct	tta	gat	gac	tat	acc	att	aga	582
Ser	His	Ile	Ile	Lys	Ser	Ile	Glu	Ala	Leu	Asp	Asp	Tyr	Thr	Ile	Arg	
				170					175					180		
ttc	aca	ctt	aat	ggg	cca	gaa	gcc	ccg	ttt	tta	gcg	aat	ttg	ggc	atg	630
Phe	Thr	Leu	Asn	Gly	Pro	Glu	Ala	Pro	Phe	Leu	Ala	Asn	Leu	Gly	Met	
			185					190					195			
gac	ttt	ttg	agc	att	ttg	agt	aag	gat	tac	gct	gat	tac	ctg	gct	caa	678
Asp	Phe	Leu	Ser	Ile	Leu	Ser	Lys	Asp	Tyr	Ala	Asp	Tyr	Leu	Ala	Gln	
		200					205					210				
aat	aat	aaa	aaa	gac	gag	ttg	gct	aaa	aaa	cct	att	ggg	aca	ggg	cct	726
Asn	Asn	Lys	Lys	Asp	Glu	Leu	Ala	Lys	Lys	Pro	Ile	Gly	Thr	Gly	Pro	
	215					220					225					
ttc	aaa	ttc	ttt	ttg	tgg	aat	aaa	gat	gaa	aaa	atc	att	ctt	tta	aaa	774
Phe	Lys	Phe	Phe	Leu	Trp	Asn	Lys	Asp	Glu	Lys	Ile	Ile	Leu	Leu	Lys	
230					235					240					245	
aat	caa	gat	tat	tgg	ggg	cct	aaa	gcg	tat	ttg	gat	aag	gtg	gtg	gtg	822
Asn	Gln	Asp	Tyr	Trp	Gly	Pro	Lys	Ala	Tyr	Leu	Asp	Lys	Val	Val	Val	
				250					255					260		
cgc	acc	att	cct	aat	tct	tcc	act	cgc	gct	tta	gcg	ttg	cgc	acc	ggc	870
Arg	Thr	Ile	Pro	Asn	Ser	Ser	Thr	Arg	Ala	Leu	Ala	Leu	Arg	Thr	Gly	
			265					270					275			
gaa	atc	atg	ctc	atg	act	ggg	cct	aat	ctc	aat	gaa	gtg	gag	caa	tta	918
Glu	Ile	Met	Leu	Met	Thr	Gly	Pro	Asn	Leu	Asn	Glu	Val	Glu	Gln	Leu	
		280					285					290				
gaa	aaa	gtc	cct	aat	atc	gtg	gtg	gac	aaa	agt	gct	ggg	ttg	ttg	gcg	966
Glu	Lys	Val	Pro	Asn	Ile	Val	Val	Asp	Lys	Ser	Ala	Gly	Leu	Leu	Ala	
	295					300					305					

agt tgg ctt tcg ttg aac acg caa aaa aag tat ttt gac aac cct ttg	1014
Ser Trp Leu Ser Leu Asn Thr Gln Lys Lys Tyr Phe Asp Asn Pro Leu	
310 315 320 325	
gtg cgt ttg gct atc aat cat gcg atc aat gca gat gat tac atc aaa	1062
Val Arg Leu Ala Ile Asn His Ala Ile Asn Ala Asp Asp Tyr Ile Lys	
330 335 340	
gtg ctt tat gaa ggc ttt gct caa aaa atg gtc aat cct ttc ccg ccc	1110
Val Leu Tyr Glu Gly Phe Ala Gln Lys Met Val Asn Pro Phe Pro Pro	
345 350 355	
acc ata tgg ggt tat aac tac aat atc aaa ccc tat gaa tac gat ttg	1158
Thr Ile Trp Gly Tyr Asn Tyr Asn Ile Lys Pro Tyr Glu Tyr Asp Leu	
360 365 370	
aaa aag gct aag gag ttg ttg aaa caa gcg ggc tat cct aac ggc ttt	1206
Lys Lys Ala Lys Glu Leu Leu Lys Gln Ala Gly Tyr Pro Asn Gly Phe	
375 380 385	
aaa acc act att ttt acc act gcc act cgt aac cca aaa gga gcg gtg	1254
Lys Thr Thr Ile Phe Thr Thr Ala Thr Arg Asn Pro Lys Gly Ala Val	
390 395 400 405	
ttc ata cag gcg agc ctg gct aaa att ggc att gat gtg aaa att gaa	1302
Phe Ile Gln Ala Ser Leu Ala Lys Ile Gly Ile Asp Val Lys Ile Glu	
410 415 420	
gtg tat gag tgg ggg gct tat ttg aaa aga acg ggt ctg ggc gaa cat	1350
Val Tyr Glu Trp Gly Ala Tyr Leu Lys Arg Thr Gly Leu Gly Glu His	
425 430 435	
gaa atg gcg ttt tca ggc tgg atg gca gac att gcg gat ccg gat aat	1398
Glu Met Ala Phe Ser Gly Trp Met Ala Asp Ile Ala Asp Pro Asp Asn	
440 445 450	
ttc tta tac acc tta tgg agc gag caa gcc gcc tca gct ata ccc act	1446
Phe Leu Tyr Thr Leu Trp Ser Glu Gln Ala Ala Ser Ala Ile Pro Thr	
455 460 465	
caa aac cat tcc ttt tat aaa aat aag gag ttt tcc aat ctg ctc ata	1494
Gln Asn His Ser Phe Tyr Lys Asn Lys Glu Phe Ser Asn Leu Leu Ile	
470 475 480 485	
aag gct aaa cgc gtt tcg gat caa aaa gag agg gaa gcc ctt tat tta	1542
Lys Ala Lys Arg Val Ser Asp Gln Lys Glu Arg Glu Ala Leu Tyr Leu	
490 495 500	
aag gca caa gaa att atc cat aaa gac gcg cct tat gtg cct tta gcc	1590
Lys Ala Gln Glu Ile Ile His Lys Asp Ala Pro Tyr Val Pro Leu Ala	
505 510 515	
tat cct tat tcg gtg gtg ccg cat ttg tct aaa gtt aag ggt tat aaa	1638
Tyr Pro Tyr Ser Val Val Pro His Leu Ser Lys Val Lys Gly Tyr Lys	
520 525 530	
acg acc gga gtg agc gtg aat cgc ttc ttt aag gtg tat tta gaa aaa	1686
Thr Thr Gly Val Ser Val Asn Arg Phe Phe Lys Val Tyr Leu Glu Lys	
535 540 545	

taaaaggggt tgcattgctga gttttatcat taagcg

1722

<210> 526

<211> 549

<212> PRT

<213> *Helicobacter pylori*

<400> 526

Met	Asn	Asn	Val	Phe	Val	Lys	Gly	Leu	Phe	Phe	Phe	Leu	Leu	Leu	Phe
1				5					10					15	
Gly	Phe	Phe	Leu	Lys	Ala	Ser	Glu	Ser	Pro	Asn	Ala	Thr	Leu	Asn	Pro
			20					25					30		
Ser	Lys	Glu	Asn	Val	Ser	Val	Glu	Gln	Lys	Arg	Phe	Gly	Gly	Val	
		35					40				45				
Leu	Val	Phe	Ala	Arg	Gly	Ala	Asp	Gly	Ser	Ser	Met	Asp	Pro	Ala	Leu
		50				55					60				
Val	Thr	Asp	Gly	Glu	Ser	Tyr	Val	Ala	Thr	Gly	Asn	Ile	Tyr	Asp	Thr
65					70					75					80
Leu	Val	Gln	Phe	Arg	Tyr	Gly	Thr	Thr	Glu	Val	Glu	Pro	Ala	Leu	Ala
				85					90					95	
Thr	Ser	Trp	Asp	Ile	Ser	Pro	Asp	Gly	Leu	Val	Tyr	Thr	Phe	His	Leu
			100					105					110		
Arg	Lys	Gly	Val	Tyr	Phe	His	Gln	Thr	Lys	Tyr	Trp	Asn	Lys	Lys	Val
		115					120					125			
Glu	Phe	Ser	Ala	Lys	Asp	Val	Leu	Phe	Ser	Phe	Glu	Arg	Gln	Met	Asp
		130				135					140				
Lys	Ala	Lys	Arg	Tyr	Tyr	Ser	Pro	Gly	Ala	Lys	Ser	Tyr	Lys	Tyr	Trp
145					150					155					160
Glu	Gly	Met	Gly	Met	Ser	His	Ile	Ile	Lys	Ser	Ile	Glu	Ala	Leu	Asp
			165						170					175	
Asp	Tyr	Thr	Ile	Arg	Phe	Thr	Leu	Asn	Gly	Pro	Glu	Ala	Pro	Phe	Leu
			180					185					190		
Ala	Asn	Leu	Gly	Met	Asp	Phe	Leu	Ser	Ile	Leu	Ser	Lys	Asp	Tyr	Ala
		195					200					205			
Asp	Tyr	Leu	Ala	Gln	Asn	Asn	Lys	Lys	Asp	Glu	Leu	Ala	Lys	Lys	Pro
		210				215					220				
Ile	Gly	Thr	Gly	Pro	Phe	Lys	Phe	Phe	Leu	Trp	Asn	Lys	Asp	Glu	Lys
225					230					235					240
Ile	Ile	Leu	Leu	Lys	Asn	Gln	Asp	Tyr	Trp	Gly	Pro	Lys	Ala	Tyr	Leu
			245						250					255	
Asp	Lys	Val	Val	Val	Arg	Thr	Ile	Pro	Asn	Ser	Ser	Thr	Arg	Ala	Leu
			260					265					270		
Ala	Leu	Arg	Thr	Gly	Glu	Ile	Met	Leu	Met	Thr	Gly	Pro	Asn	Leu	Asn
		275				280						285			
Glu	Val	Glu	Gln	Leu	Glu	Lys	Val	Pro	Asn	Ile	Val	Val	Asp	Lys	Ser
		290				295					300				
Ala	Gly	Leu	Leu	Ala	Ser	Trp	Leu	Ser	Leu	Asn	Thr	Gln	Lys	Lys	Tyr
305					310					315					320
Phe	Asp	Asn	Pro	Leu	Val	Arg	Leu	Ala	Ile	Asn	His	Ala	Ile	Asn	Ala
			325						330					335	
Asp	Asp	Tyr	Ile	Lys	Val	Leu	Tyr	Glu	Gly	Phe	Ala	Gln	Lys	Met	Val
			340					345					350		
Asn	Pro	Phe	Pro	Pro	Thr	Ile	Trp	Gly	Tyr	Asn	Tyr	Asn	Ile	Lys	Pro
		355					360					365			
Tyr	Glu	Tyr	Asp	Leu	Lys	Lys	Ala	Lys	Glu	Leu	Leu	Lys	Gln	Ala	Gly
	370					375					380				
Tyr	Pro	Asn	Gly	Phe	Lys	Thr	Thr	Ile	Phe	Thr	Thr	Ala	Thr	Arg	Asn
385					390					395					400

gaa tta gct ttg atc gct ctg ttt atg gct ctt gtt ttg ggt att agc	393
Glu Leu Ala Leu Ile Ala Leu Phe Met Ala Leu Val Leu Gly Ile Ser	
100 105 110 115	
ggt ggc gtg tta gct gcg atc aaa cgc tat agc gtg ttt gat tat tcc	441
Val Gly Val Leu Ala Ala Ile Lys Arg Tyr Ser Val Phe Asp Tyr Ser	
120 125 130	
agc atg act ttt gct tta gcc ggg att tct atg ccg gtg ttt tgg cta	489
Ser Met Thr Phe Ala Leu Ala Gly Ile Ser Met Pro Val Phe Trp Leu	
135 140 145	
ggg ctc atg ctg att tat atc ttt agc gtg caa ttg ggg tgg ttg cct	537
Gly Leu Met Leu Ile Tyr Ile Phe Ser Val Gln Leu Gly Trp Leu Pro	
150 155 160	
gtt ttt ggg cgt ttg agc gat gtg tat tat tta gat ggc ccc aca ggt	585
Val Phe Gly Arg Leu Ser Asp Val Tyr Tyr Leu Asp Gly Pro Thr Gly	
165 170 175	
ctt tat ttg ata gac agc ctg atc gca agg gat tat ggg gcg ttt atg	633
Leu Tyr Leu Ile Asp Ser Leu Ile Ala Arg Asp Tyr Gly Ala Phe Met	
180 185 190 195	
gat acg atc aag cac ttg att ttg cct agc att gtg tta gcc acg gtt	681
Asp Thr Ile Lys His Leu Ile Leu Pro Ser Ile Val Leu Ala Thr Val	
200 205 210	
tct acc gct gtt att gcc aqa atg act cgc gcg agc atg gca gaa gtc	729
Ser Thr Ala Val Ile Ala Arg Met Thr Arg Ala Ser Met Ala Glu Val	
215 220 225	
tct aaa gaa gat tat gtg cgt acc gct aaa gct aag ggg tgt agc tcc	777
Ser Lys Glu Asp Tyr Val Arg Thr Ala Lys Ala Lys Gly Cys Ser Ser	
230 235 240	
ttt agg gtg att ttt gtg cac act ttg cgt aat gct tta atc cct gta	825
Phe Arg Val Ile Phe Val His Thr Leu Arg Asn Ala Leu Ile Pro Val	
245 250 255	
acg act atc gca ggc ttg atg ttg gcc ggg ctt tta ggg ggg agc atg	873
Thr Thr Ile Ala Gly Leu Met Leu Ala Gly Leu Leu Gly Gly Ser Met	
260 265 270 275	
ata act gaa acg gtt ttc tca tgg cct ggg att ggt aag tgg att gtt	921
Ile Thr Glu Thr Val Phe Ser Trp Pro Gly Ile Gly Lys Trp Ile Val	
280 285 290	
aat gcg ctc aac cag cgc gat ttc ccg att atc cag tcc atg tct ttg	969
Asn Ala Leu Asn Gln Arg Asp Phe Pro Ile Ile Gln Ser Met Ser Leu	
295 300 305	
att att gcc atg atg tat att ggg gct aat ctc tta gtg gat att tta	1017
Ile Ile Ala Met Met Tyr Ile Gly Ala Asn Leu Leu Val Asp Ile Leu	
310 315 320	
tac gct ttt att gat cct aga ata agg ttg tca taatggagtc ttttagagag	1070
Tyr Ala Phe Ile Asp Pro Arg Ile Arg Leu Ser	

325

330

tttatccaac

1080

<210> 528

<211> 334

<212> PRT

<213> *Helicobacter pylori*

<400> 528

```

Met Leu Ser Phe Ile Ile Lys Arg Ile Leu Trp Ala Ile Pro Thr Leu
 1           5           10           15
Phe Gly Val Ser Ile Ile Val Phe Met Met Val His Leu Val Pro Gly
          20           25           30
Asp Pro Ala Leu Val Ile Leu Gly Glu Lys Ala Asn Gln Ala Ala Ile
          35           40           45
Asp Ala Leu Arg Glu Gln Phe Gly Leu Asn Lys Pro Leu Ile Glu Gln
          50           55           60
Tyr Phe Phe Phe Ile Asn Asn Val Leu His Gly Asn Phe Gly Thr Ser
65           70           75           80
Ile Met Thr Gly Glu Pro Val Met His Glu Phe Trp Gln Arg Phe Pro
          85           90           95
Ala Thr Val Glu Leu Ala Leu Ile Ala Leu Phe Met Ala Leu Val Leu
          100          105          110
Gly Ile Ser Val Gly Val Leu Ala Ala Ile Lys Arg Tyr Ser Val Phe
          115          120          125
Asp Tyr Ser Ser Met Thr Phe Ala Leu Ala Gly Ile Ser Met Pro Val
          130          135          140
Phe Trp Leu Gly Leu Met Leu Ile Tyr Ile Phe Ser Val Gln Leu Gly
          145          150          155          160
Trp Leu Pro Val Phe Gly Arg Leu Ser Asp Val Tyr Tyr Leu Asp Gly
          165          170          175
Pro Thr Gly Leu Tyr Leu Ile Asp Ser Leu Ile Ala Arg Asp Tyr Gly
          180          185          190
Ala Phe Met Asp Thr Ile Lys His Leu Ile Leu Pro Ser Ile Val Leu
          195          200          205
Ala Thr Val Ser Thr Ala Val Ile Ala Arg Met Thr Arg Ala Ser Met
          210          215          220
Ala Glu Val Ser Lys Glu Asp Tyr Val Arg Thr Ala Lys Ala Lys Gly
          225          230          235          240
Cys Ser Ser Phe Arg Val Ile Phe Val His Thr Leu Arg Asn Ala Leu
          245          250          255
Ile Pro Val Thr Thr Ile Ala Gly Leu Met Leu Ala Gly Leu Leu Gly
          260          265          270
Gly Ser Met Ile Thr Glu Thr Val Phe Ser Trp Pro Gly Ile Gly Lys
          275          280          285
Trp Ile Val Asn Ala Leu Asn Gln Arg Asp Phe Pro Ile Ile Gln Ser
          290          295          300
Met Ser Leu Ile Ile Ala Met Met Tyr Ile Gly Ala Asn Leu Leu Val
          305          310          315          320
Asp Ile Leu Tyr Ala Phe Ile Asp Pro Arg Ile Arg Leu Ser
          325          330

```

<210> 529

<211> 955

<212> DNA

<213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (32)...(892)

<400> 529

atcctaaacg cacctcttaa aaggagcttg c atg att tta gaa gtt aaa gat	52
Met Ile Leu Glu Val Lys Asp	
1 5	
tta aaa act tat ttt ttc acc gat aag ggc gtg aat aaa gca gtg gat	100
Leu Lys Thr Tyr Phe Phe Thr Asp Lys Gly Val Asn Lys Ala Val Asp	
10 15 20	
ggt gtg agt ttt ggt ttg aaa aag tct caa acg ctc tgc att gta ggg	148
Gly Val Ser Phe Gly Leu Lys Lys Ser Gln Thr Leu Cys Ile Val Gly	
25 30 35	
gag agc ggg agc ggg aaa agc atc act tcg ctc tct att tta ggg ttg	196
Glu Ser Gly Ser Gly Lys Ser Ile Thr Ser Leu Ser Ile Leu Gly Leu	
40 45 50 55	
att gaa aaa ccg ggt caa att gtg gga ggg agc att caa ttt tta ggg	244
Ile Glu Lys Pro Gly Gln Ile Val Gly Gly Ser Ile Gln Phe Leu Gly	
60 65 70	
cag gat ttg ttg caa ctc aaa gaa aag cag atg caa aaa gaa att agg	292
Gln Asp Leu Leu Gln Leu Lys Glu Lys Gln Met Gln Lys Glu Ile Arg	
75 80 85	
ggt aaa aaa att ggc atg atc ttt caa gag cct atg aca agc cta aac	340
Gly Lys Lys Ile Gly Met Ile Phe Gln Glu Pro Met Thr Ser Leu Asn	
90 95 100	
cct tcc tac acg gtg ggg ttt caa atc aat gaa gtg ttg aaa atc cac	388
Pro Ser Tyr Thr Val Gly Phe Gln Ile Asn Glu Val Leu Lys Ile His	
105 110 115	
cac cct aac ctc aat aaa aaa gaa cgc tta gaa agg gtg gtt tat gaa	436
His Pro Asn Leu Asn Lys Lys Glu Arg Leu Glu Arg Val Val Tyr Glu	
120 125 130 135	
tta gag cgt gtg ggc att ccc cat gca ggg gat aaa tac cac gaa tac	484
Leu Glu Arg Val Gly Ile Pro His Ala Gly Asp Lys Tyr His Glu Tyr	
140 145 150	
cct ttc aat ctc agc ggg ggg cag cgc caa agg gtg atg atc gct atg	532
Pro Phe Asn Leu Ser Gly Gly Gln Arg Gln Arg Val Met Ile Ala Met	
155 160 165	
gct atg gtg tgt gag cct gaa atc ttg atc gct gat gag cct acg aca	580
Ala Met Val Cys Glu Pro Glu Ile Leu Ile Ala Asp Glu Pro Thr Thr	
170 175 180	
gcc tta gat gta acc att caa gcg caa att tta gaa ttg atg aaa gaa	628
Ala Leu Asp Val Thr Ile Gln Ala Gln Ile Leu Glu Leu Met Lys Glu	
185 190 195	
ttg caa caa aaa aaa ggc act tct att ttg ttt atc acc cat gat tta	676
Leu Gln Gln Lys Lys Gly Thr Ser Ile Leu Phe Ile Thr His Asp Leu	

200	205	210	215	
ggc gtg gtg gcg caa atc gct gat gaa gtg gtg gtg atg tat aaa ggc				724
Gly Val Val Ala Gln Ile Ala Asp Glu Val Val Val Met Tyr Lys Gly				
	220	225	230	
cat gtg gtg gag caa gcg agt gcg aaa gag ctt ttt gct gat cca aga				772
His Val Val Glu Gln Ala Ser Ala Lys Glu Leu Phe Ala Asp Pro Arg				
	235	240	245	
cac cct tat acg aaa gct ctt tta agc gcg atc cct aaa ccg ggc aaa				820
His Pro Tyr Thr Lys Ala Leu Leu Ser Ala Ile Pro Lys Pro Gly Lys				
	250	255	260	
gaa tac cgc aaa aaa cgc tta gag acc gtg gat gaa aat gtg gat tat				868
Glu Tyr Arg Lys Lys Arg Leu Glu Thr Val Asp Glu Asn Val Asp Tyr				
	265	270	275	
ttg agt ttt caa aag gag ttg cga tgaagctctt agaaattaaa gaattgaaaa				922
Leu Ser Phe Gln Lys Glu Leu Arg				
	280	285		
aatcctatgc gatagacagg ggggtattca agc				955

<210> 530

<211> 287

<212> PRT

<213> *Helicobacter pylori*

<400> 530

Met Ile Leu Glu Val Lys Asp Leu Lys Thr Tyr Phe Phe Thr Asp Lys	
1 5 10 15	
Gly Val Asn Lys Ala Val Asp Gly Val Ser Phe Gly Leu Lys Lys Ser	
20 25 30	
Gln Thr Leu Cys Ile Val Gly Glu Ser Gly Ser Gly Lys Ser Ile Thr	
35 40 45	
Ser Leu Ser Ile Leu Gly Leu Ile Glu Lys Pro Gly Gln Ile Val Gly	
50 55 60	
Gly Ser Ile Gln Phe Leu Gly Gln Asp Leu Leu Gln Leu Lys Glu Lys	
65 70 75 80	
Gln Met Gln Lys Glu Ile Arg Gly Lys Lys Ile Gly Met Ile Phe Gln	
85 90 95	
Glu Pro Met Thr Ser Leu Asn Pro Ser Tyr Thr Val Gly Phe Gln Ile	
100 105 110	
Asn Glu Val Leu Lys Ile His His Pro Asn Leu Asn Lys Lys Glu Arg	
115 120 125	
Leu Glu Arg Val Val Tyr Glu Leu Glu Arg Val Gly Ile Pro His Ala	
130 135 140	
Gly Asp Lys Tyr His Glu Tyr Pro Phe Asn Leu Ser Gly Gly Gln Arg	
145 150 155 160	
Gln Arg Val Met Ile Ala Met Ala Met Val Cys Glu Pro Glu Ile Leu	
165 170 175	
Ile Ala Asp Glu Pro Thr Thr Ala Leu Asp Val Thr Ile Gln Ala Gln	
180 185 190	
Ile Leu Glu Leu Met Lys Glu Leu Gln Gln Lys Lys Gly Thr Ser Ile	
195 200 205	
Leu Phe Ile Thr His Asp Leu Gly Val Val Ala Gln Ile Ala Asp Glu	
210 215 220	
Val Val Val Met Tyr Lys Gly His Val Val Glu Gln Ala Ser Ala Lys	

225					230					235					240
Glu	Leu	Phe	Ala	Asp	Pro	Arg	His	Pro	Tyr	Thr	Lys	Ala	Leu	Leu	Ser
				245					250					255	
Ala	Ile	Pro	Lys	Pro	Gly	Lys	Glu	Tyr	Arg	Lys	Lys	Arg	Leu	Glu	Thr
			260					265					270		
Val	Asp	Glu	Asn	Val	Asp	Tyr	Leu	Ser	Phe	Gln	Lys	Glu	Leu	Arg	
		275					280					285			

<210> 531
 <211> 894
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (37)...(840)

<400> 531	
aaatgtggat tatttgagtt ttcaaaaagga gttgacg atg aag ctc tta gaa att	54
Met Lys Leu Leu Glu Ile	
1 5	
aaa gaa ttg aaa aaa tcc tat gcg ata gac agg ggg tta ttc aag cct	102
Lys Glu Leu Lys Lys Ser Tyr Ala Ile Asp Arg Gly Leu Phe Lys Pro	
10 15 20	
aaa aga gtg atc cat gcg ctc aat ggg atc agt ttt gaa gtg gaa caa	150
Lys Arg Val Ile His Ala Leu Asn Gly Ile Ser Phe Glu Val Glu Gln	
25 30 35	
aat gaa gtt ttg agc att gtg ggg gag agc ggt tgc ggg aaa agc acg	198
Asn Glu Val Leu Ser Ile Val Gly Glu Ser Gly Cys Gly Lys Ser Thr	
40 45 50	
aca gcc aaa att tta gcc ggg att gaa agg caa gat agc ggg gcg att	246
Thr Ala Lys Ile Leu Ala Gly Ile Glu Arg Gln Asp Ser Gly Ala Ile	
55 60 65 70	
tat ttc aat ggt aag cgc cat ttg cat ttt agc aaa cag gat tgg ttt	294
Tyr Phe Asn Gly Lys Arg His Leu His Phe Ser Lys Gln Asp Trp Phe	
75 80 85	
gat tac cgc aaa aag gtg caa atg att ttt caa gac cct tat tct agc	342
Asp Tyr Arg Lys Lys Val Gln Met Ile Phe Gln Asp Pro Tyr Ser Ser	
90 95 100	
cta aac cct cgg tgg aaa gtg ggc gag atc atc gct gaa ccc ttg ctt	390
Leu Asn Pro Arg Trp Lys Val Gly Glu Ile Ile Ala Glu Pro Leu Leu	
105 110 115	
tta aat tct cat ttt tca aaa aaa gaa atc aaa aca aaa gtg cta gag	438
Leu Asn Ser His Phe Ser Lys Lys Glu Ile Lys Thr Lys Val Leu Glu	
120 125 130	
atc atg caa aaa gtg ggc ttg aaa tta gaa tgg atc gat cgt tac ccc	486
Ile Met Gln Lys Val Gly Leu Lys Leu Glu Trp Ile Asp Arg Tyr Pro	
135 140 145 150	

cac	caa	ttt	tca	ggc	ggg	caa	agg	caa	cga	atc	ggc	att	gct	agg	gcg	534	
His	Gln	Phe	Ser	Gly	Gly	Gln	Arg	Gln	Arg	Ile	Gly	Ile	Ala	Arg	Ala		
				155					160					165			
ctc	att	ttg	cat	cct	agc	gtg	gtg	att	tgc	gat	gag	cct	gtg	tct	gcg	582	
Leu	Ile	Leu	His	Pro	Ser	Val	Val	Ile	Cys	Asp	Glu	Pro	Val	Ser	Ala		
			170					175					180				
cta	gac	gtg	tcc	att	caa	gcg	caa	gtg	ttg	aat	ttg	ctc	ttg	gat	ttg	630	
Leu	Asp	Val	Ser	Ile	Gln	Ala	Gln	Val	Leu	Asn	Leu	Leu	Leu	Asp	Leu		
		185					190					195					
caa	aaa	gaa	atg	ggg	ctg	act	tat	att	ttt	atc	agc	cat	gat	tta	ggg	678	
Gln	Lys	Glu	Met	Gly	Leu	Thr	Tyr	Ile	Phe	Ile	Ser	His	Asp	Leu	Gly		
	200					205					210						
gtg	gtg	gag	cat	ata	agc	gat	aaa	atc	atc	gta	atg	aat	cag	ggg	caa	726	
Val	Val	Glu	His	Ile	Ser	Asp	Lys	Ile	Ile	Val	Met	Asn	Gln	Gly	Gln		
215					220					225					230		
atc	gta	gaa	acg	ggg	gat	gtg	gat	agc	gtg	ata	agc	gct	cca	aag	cac	774	
Ile	Val	Glu	Thr	Gly	Asp	Val	Asp	Ser	Val	Ile	Ser	Ala	Pro	Lys	His		
				235					240					245			
cct	tat	acg	cag	aaa	tta	ctc	aat	gcg	gtg	ccg	cat	ttg	gaa	aaa	tcc	822	
Pro	Tyr	Thr	Gln	Lys	Leu	Leu	Asn	Ala	Val	Pro	His	Leu	Glu	Lys	Ser		
			250					255					260				
atg	caa	aga	ttt	gcc	aaa	taaaagaaaag	gatttttaag	ctgtgtttgt								870	
Met	Gln	Arg	Phe	Ala	Lys												
			265														
agatagcgtg gaaattatca tcgc															894		

<210> 532

<211> 268

<212> PRT

<213> *Helicobacter pylori*

<400> 532

Met	Lys	Leu	Leu	Glu	Ile	Lys	Glu	Leu	Lys	Lys	Ser	Tyr	Ala	Ile	Asp
1				5					10					15	
Arg	Gly	Leu	Phe	Lys	Pro	Lys	Arg	Val	Ile	His	Ala	Leu	Asn	Gly	Ile
			20					25					30		
Ser	Phe	Glu	Val	Glu	Gln	Asn	Glu	Val	Leu	Ser	Ile	Val	Gly	Glu	Ser
		35					40					45			
Gly	Cys	Gly	Lys	Ser	Thr	Thr	Ala	Lys	Ile	Leu	Ala	Gly	Ile	Glu	Arg
	50					55					60				
Gln	Asp	Ser	Gly	Ala	Ile	Tyr	Phe	Asn	Gly	Lys	Arg	His	Leu	His	Phe
65					70					75				80	
Ser	Lys	Gln	Asp	Trp	Phe	Asp	Tyr	Arg	Lys	Lys	Val	Gln	Met	Ile	Phe
			85						90				95		
Gln	Asp	Pro	Tyr	Ser	Ser	Leu	Asn	Pro	Arg	Trp	Lys	Val	Gly	Glu	Ile
		100						105					110		
Ile	Ala	Glu	Pro	Leu	Leu	Leu	Asn	Ser	His	Phe	Ser	Lys	Lys	Glu	Ile
		115					120					125			
Lys	Thr	Lys	Val	Leu	Glu	Ile	Met	Gln	Lys	Val	Gly	Leu	Lys	Leu	Glu
	130					135					140				
Trp	Ile	Asp	Arg	Tyr	Pro	His	Gln	Phe	Ser	Gly	Gly	Gln	Arg	Gln	Arg

145		150		155		160
Ile Gly Ile Ala Arg	Ala Leu Ile Leu His	Pro Ser Val Val	Ile Cys			
	165	170	175			
Asp Glu Pro Val Ser	Ala Leu Asp Val Ser	Ile Gln Ala Gln	Val Leu			
	180	185	190			
Asn Leu Leu Leu Asp	Leu Gln Lys Met Gly	Leu Thr Tyr Ile	Phe			
	195	200	205			
Ile Ser His Asp Leu	Gly Val Val Glu His	Ile Ser Asp Lys	Ile Ile			
	210	215	220			
Val Met Asn Gln Gly	Gln Ile Val Glu Thr	Gly Asp Val Asp	Ser Val			
225	230	235	240			
Ile Ser Ala Pro Lys	His Pro Tyr Thr	Gln Lys Leu Leu	Asn Ala Val			
	245	250	255			
Pro His Leu Glu Lys	Ser Met Gln Arg	Phe Ala Lys				
	260	265				

<210> 533
 <211> 1141
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (62)...(1087)

<400> 533
 ttaagctgtg ttgtagata gcgtggaaat tatcatcgct tcgggtaagg gggggcctgg 60
 a atg gtg agt ttt agg cga gaa aaa ttt gtc atc aaa gga ggc cct gat 109
 Met Val Ser Phe Arg Arg Glu Lys Phe Val Ile Lys Gly Gly Pro Asp
 1 5 10 15

ggg ggc gat gga ggc gat gga ggc gat gtg tat ttt gaa gtg gat aac 157
 Gly Gly Asp Gly Gly Asp Gly Gly Asp Val Tyr Phe Glu Val Asp Asn
 20 25 30

aat acc gac act cta gcg agt ttt aga ggc acc aaa cac cat aag gct 205
 Asn Thr Asp Thr Leu Ala Ser Phe Arg Gly Thr Lys His His Lys Ala
 35 40 45

aaa aat ggg gct cca gga ggt aca cga aat tgc gcg ggc aaa aag ggc 253
 Lys Asn Gly Ala Pro Gly Gly Thr Arg Asn Cys Ala Gly Lys Lys Gly
 50 55 60

gaa gac aag atc att gtc gtg cca cca gga acg cag gtt ttt gta ggt 301
 Glu Asp Lys Ile Ile Val Val Pro Pro Gly Thr Gln Val Phe Val Gly
 65 70 75 80

gat gag ttg tgg ctt gat tta gtg gaa cct aaa gaa agg gtg tta gcc 349
 Asp Glu Leu Trp Leu Asp Leu Val Glu Pro Lys Glu Arg Val Leu Ala
 85 90 95

tta aaa ggg ggc aag ggg ggg tta ggg aat gca cat ttt aaa agc gcg 397
 Leu Lys Gly Gly Lys Gly Gly Leu Gly Asn Ala His Phe Lys Ser Ala
 100 105 110

act aaa caa caa ccc act tac gcg caa aaa ggc tta gag ggg gtt gaa 445
 Thr Lys Gln Gln Pro Thr Tyr Ala Gln Lys Gly Leu Glu Gly Val Glu
 115 120 125

aaa tgc gtg cgt ttg gaa tta aaa ctc atc gct gat ata ggg tta gtg Lys Cys Val Arg Leu Glu Leu Lys Leu Ile Ala Asp Ile Gly Leu Val 130 135 140	493
ggc ttc cct aat gcg ggt aaa tcc acg ctc att tcc acc atc tct aac Gly Phe Pro Asn Ala Gly Lys Ser Thr Leu Ile Ser Thr Ile Ser Asn 145 150 155 160	541
gct aag cct aaa atc gct aac tat gaa ttt acg act cta gtg cct aat Ala Lys Pro Lys Ile Ala Asn Tyr Glu Phe Thr Thr Leu Val Pro Asn 165 170 175	589
tta ggg gtt gtg agc gtg gat gaa aaa agc gga ttt cta atg gcg gat Leu Gly Val Val Ser Val Asp Glu Lys Ser Gly Phe Leu Met Ala Asp 180 185 190	637
att cct ggc att att gaa ggg gct agc gag gga aag ggc tta ggg att Ile Pro Gly Ile Ile Glu Gly Ala Ser Glu Gly Lys Gly Leu Gly Ile 195 200 205	685
agc ttt tta aag cat att gaa cgc acc aaa gtt cta gct ttt gtt tta Ser Phe Leu Lys His Ile Glu Arg Thr Lys Val Leu Ala Phe Val Leu 210 215 220	733
gac gct tcc agg ctg gat tta ggc att aaa gag caa tac caa cgc ttg Asp Ala Ser Arg Leu Asp Leu Gly Ile Lys Glu Gln Tyr Gln Arg Leu 225 230 235 240	781
agg ttg gag ttg gaa aaa ttt tca tcc gct ttg gcc aat aag cct ttt Arg Leu Glu Leu Glu Lys Phe Ser Ser Ala Leu Ala Asn Lys Pro Phe 245 250 255	829
ggg gtg ttg ctc aat aaa tgc gat gtt gta gaa aac att gat gag atg Gly Val Leu Leu Asn Lys Cys Asp Val Val Glu Asn Ile Asp Glu Met 260 265 270	877
act aag gat ttt tgt gcc ttt tta aat ttg gga gcg cag aaa tta aac Thr Lys Asp Phe Cys Ala Phe Leu Asn Leu Gly Ala Gln Lys Leu Asn 275 280 285	925
gag ttt ggt tta gag ccg tat tta ggg ttt ttg cac ccc cat tta acc Glu Phe Gly Leu Glu Pro Tyr Leu Gly Phe Leu His Pro His Leu Thr 290 295 300	973
aat gat ttt gaa aat aac cct aat gag caa tca gcg ctc ttt gtc ttg Asn Asp Phe Glu Asn Asn Pro Asn Glu Gln Ser Ala Leu Phe Val Leu 305 310 315 320	1021
ccc ctt tca gcg gtt agc gct ctt aat gtg cat gca ctc aaa ttt gtg Pro Leu Ser Ala Val Ser Ala Leu Asn Val His Ala Leu Lys Phe Val 325 330 335	1069
ttg ttg gaa gcg tta ccc taaaacgcta tttttaaaat aatccattaa Leu Leu Glu Ala Leu Pro 340	1117
aataaaggcg aggaatgaaa agat	1141

<210> 534
 <211> 342
 <212> PRT
 <213> Helicobacter pylori

<400> 534
 Met Val Ser Phe Arg Arg Glu Lys Phe Val Ile Lys Gly Gly Pro Asp
 1 5 10 15
 Gly Gly Asp Gly Gly Asp Gly Gly Asp Val Tyr Phe Glu Val Asp Asn
 20 25 30
 Asn Thr Asp Thr Leu Ala Ser Phe Arg Gly Thr Lys His His Lys Ala
 35 40 45
 Lys Asn Gly Ala Pro Gly Gly Thr Arg Asn Cys Ala Gly Lys Lys Gly
 50 55 60
 Glu Asp Lys Ile Ile Val Val Pro Pro Gly Thr Gln Val Phe Val Gly
 65 70 75 80
 Asp Glu Leu Trp Leu Asp Leu Val Glu Pro Lys Glu Arg Val Leu Ala
 85 90 95
 Leu Lys Gly Gly Lys Gly Gly Leu Gly Asn Ala His Phe Lys Ser Ala
 100 105 110
 Thr Lys Gln Gln Pro Thr Tyr Ala Gln Lys Gly Leu Glu Gly Val Glu
 115 120 125
 Lys Cys Val Arg Leu Glu Leu Lys Leu Ile Ala Asp Ile Gly Leu Val
 130 135 140
 Gly Phe Pro Asn Ala Gly Lys Ser Thr Leu Ile Ser Thr Ile Ser Asn
 145 150 155 160
 Ala Lys Pro Lys Ile Ala Asn Tyr Glu Phe Thr Thr Leu Val Pro Asn
 165 170 175
 Leu Gly Val Val Ser Val Asp Glu Lys Ser Gly Phe Leu Met Ala Asp
 180 185 190
 Ile Pro Gly Ile Ile Glu Gly Ala Ser Glu Gly Lys Gly Leu Gly Ile
 195 200 205
 Ser Phe Leu Lys His Ile Glu Arg Thr Lys Val Leu Ala Phe Val Leu
 210 215 220
 Asp Ala Ser Arg Leu Asp Leu Gly Ile Lys Glu Gln Tyr Gln Arg Leu
 225 230 235 240
 Arg Leu Glu Leu Glu Lys Phe Ser Ser Ala Leu Ala Asn Lys Pro Phe
 245 250 255
 Gly Val Leu Leu Asn Lys Cys Asp Val Val Glu Asn Ile Asp Glu Met
 260 265 270
 Thr Lys Asp Phe Cys Ala Phe Leu Asn Leu Gly Ala Gln Lys Leu Asn
 275 280 285
 Glu Phe Gly Leu Glu Pro Tyr Leu Gly Phe Leu His Pro His Leu Thr
 290 295 300
 Asn Asp Phe Glu Asn Asn Pro Asn Glu Gln Ser Ala Leu Phe Val Leu
 305 310 315 320
 Pro Leu Ser Ala Val Ser Ala Leu Asn Val His Ala Leu Lys Phe Val
 325 330 335
 Leu Leu Glu Ala Leu Pro
 340

<210> 535
 <211> 621
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS

<222> (16)...(567)

<400> 535

```
attaaaggat aatga atg aaa aaa atg gtt ttg gta tcg gtt tta cta gca 51
          Met Lys Lys Met Val Leu Val Ser Val Leu Leu Ala
              1              5              10

ggg ttt ttg caa gcg gtg aat ttg gat tta tct tcg gct aag cta aca 99
Gly Phe Leu Gln Ala Val Asn Leu Asp Leu Ser Ser Ala Lys Leu Thr
          15              20              25

tgg aca gcc ttt aaa act aag gct aaa aca cca gta aat ggg agt ttt 147
Trp Thr Ala Phe Lys Thr Lys Ala Lys Thr Pro Val Asn Gly Ser Phe
          30              35              40

gaa agc atc acc tat aaa ttg ggt aaa tct caa gat agt tta aaa acc 195
Glu Ser Ile Thr Tyr Lys Leu Gly Lys Ser Gln Asp Ser Leu Lys Thr
          45              50              55              60

ctt tta gag gga gcg agc gcg agc atg gat agc ttg aaa gtc aat tta 243
Leu Leu Glu Gly Ala Ser Ala Ser Met Asp Ser Leu Lys Val Asn Leu
          65              70              75

ggc gat gaa ttg aaa aac aaa aat gtg aaa gaa gct ttt ttc gct ctt 291
Gly Asp Glu Leu Lys Asn Lys Asn Val Lys Glu Ala Phe Phe Ala Leu
          80              85              90

ttt aaa aac act aac atc aaa gta act ttc agg aat gtg ata gaa ggc 339
Phe Lys Asn Thr Asn Ile Lys Val Thr Phe Arg Asn Val Ile Glu Gly
          95              100              105

gat cat gca ggt tct ctt acg gct tat gtg aga atg aat gaa aag ctg 387
Asp His Ala Gly Ser Leu Thr Ala Tyr Val Arg Met Asn Glu Lys Leu
          110              115              120

gtg aaa gtg cct atg caa tac acg att gct gag gat aag atc gtg gtt 435
Val Lys Val Pro Met Gln Tyr Thr Ile Ala Glu Asp Lys Ile Val Val
          125              130              135              140

aaa ggg gtt ttg gat tta ttg aat ttt ggc ttg aaa aac gaa tta gcc 483
Lys Gly Val Leu Asp Leu Leu Asn Phe Gly Leu Lys Asn Glu Leu Ala
          145              150              155

agc ttg gcc aaa cga tgc gaa agc ttt cat gag ggc ttg act tgg tcg 531
Ser Leu Ala Lys Arg Cys Glu Ser Phe His Glu Gly Leu Thr Trp Ser
          160              165              170

caa gtg gaa atc caa ttt gaa agc atg atc aag gga taatgtaaaa 577
Gln Val Glu Ile Gln Phe Glu Ser Met Ile Lys Gly
          175              180

tcatggagtt gttgcacagc attaatgatt tcaatgaagc taag 621
```

<210> 536

<211> 184

<212> PRT

<213> *Helicobacter pylori*

<400> 536

Met	Lys	Lys	Met	Val	Leu	Val	Ser	Val	Leu	Leu	Ala	Gly	Phe	Leu	Gln
1				5					10					15	
Ala	Val	Asn	Leu	Asp	Leu	Ser	Ser	Ala	Lys	Leu	Thr	Trp	Thr	Ala	Phe
		20						25					30		
Lys	Thr	Lys	Ala	Lys	Thr	Pro	Val	Asn	Gly	Ser	Phe	Glu	Ser	Ile	Thr
		35					40					45			
Tyr	Lys	Leu	Gly	Lys	Ser	Gln	Asp	Ser	Leu	Lys	Thr	Leu	Leu	Glu	Gly
	50					55					60				
Ala	Ser	Ala	Ser	Met	Asp	Ser	Leu	Lys	Val	Asn	Leu	Gly	Asp	Glu	Leu
65					70					75					80
Lys	Asn	Lys	Asn	Val	Lys	Glu	Ala	Phe	Phe	Ala	Leu	Phe	Lys	Asn	Thr
			85						90					95	
Asn	Ile	Lys	Val	Thr	Phe	Arg	Asn	Val	Ile	Glu	Gly	Asp	His	Ala	Gly
		100						105					110		
Ser	Leu	Thr	Ala	Tyr	Val	Arg	Met	Asn	Glu	Lys	Leu	Val	Lys	Val	Pro
		115					120					125			
Met	Gln	Tyr	Thr	Ile	Ala	Glu	Asp	Lys	Ile	Val	Val	Lys	Gly	Val	Leu
	130					135					140				
Asp	Leu	Leu	Asn	Phe	Gly	Leu	Lys	Asn	Glu	Leu	Ala	Ser	Leu	Ala	Lys
145					150					155					160
Arg	Cys	Glu	Ser	Phe	His	Glu	Gly	Leu	Thr	Trp	Ser	Gln	Val	Glu	Ile
				165					170					175	
Gln	Phe	Glu	Ser	Met	Ile	Lys	Gly								
			180												

<210> 537
 <211> 1406
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (49)...(1338)
 <223>

<400> 537																
caagtggaaa	tc	caatttga	aagcatgatc	aagggataat	gt	aaaatc	atg	gag	ttg						57	
							Met	Glu	Leu							
							1									
ttg	cac	agc	att	aat	gat	ttc	aat	gaa	gct	aag	cag	gtg	atc	gct	ggg	105
Leu	His	Ser	Ile	Asn	Asp	Phe	Asn	Glu	Ala	Lys	Gln	Val	Ile	Ala	Gly	
	5					10					15					
ggg	gtc	aat	tca	cct	gtt	agg	gcg	ttt	aag	agc	gtt	aaa	ggc	act	ccc	153
Gly	Val	Asn	Ser	Pro	Val	Arg	Ala	Phe	Lys	Ser	Val	Lys	Gly	Thr	Pro	
	20				25				30					35		
ccc	ttt	att	tta	aaa	ggc	aag	ggg	gcg	tat	ctt	tat	gat	gtg	gat	aac	201
Pro	Phe	Ile	Leu	Lys	Gly	Lys	Gly	Ala	Tyr	Leu	Tyr	Asp	Val	Asp	Asn	
				40				45						50		
aac	cat	tat	ata	gat	ttt	gtg	caa	agc	tgg	ggg	cct	ttg	att	ttt	ggg	249
Asn	His	Tyr	Ile	Asp	Phe	Val	Gln	Ser	Trp	Gly	Pro	Leu	Ile	Phe	Gly	
			55					60					65			
cat	gct	gat	gaa	gag	att	gaa	gaa	aat	att	att	aat	gca	tta	aaa	aaa	297
His	Ala	Asp	Glu	Glu	Ile	Glu	Glu	Asn	Ile	Ile	Asn	Ala	Leu	Lys	Lys	

70				75				80								
ggc	act	tct	ttt	ggc	gct	ccc	aca	gaa	tta	gaa	acc	act	tta	gct	aag	345
Gly	Thr	Ser	Phe	Gly	Ala	Pro	Thr	Glu	Leu	Glu	Thr	Thr	Leu	Ala	Lys	
	85					90					95					
gaa	atc	att	tct	tgt	tat	gaa	ggc	tta	gat	aag	gtg	cgt	tta	gtc	agt	393
Glu	Ile	Ile	Ser	Cys	Tyr	Glu	Gly	Leu	Asp	Lys	Val	Arg	Leu	Val	Ser	
100				105						110					115	
agc	ggc	aca	gaa	gcg	acc	atg	agc	gcg	ata	cga	ctc	gct	aga	gct	tat	441
Ser	Gly	Thr	Glu	Ala	Thr	Met	Ser	Ala	Ile	Arg	Leu	Ala	Arg	Ala	Tyr	
				120					125					130		
agc	caa	aaa	gat	gat	ttg	atc	aag	ttt	gaa	ggg	tgc	tac	cat	ggg	cat	489
Ser	Gln	Lys	Asp	Asp	Leu	Ile	Lys	Phe	Glu	Gly	Cys	Tyr	His	Gly	His	
			135					140					145			
agc	gac	tcc	tta	ttg	gtg	aaa	gcg	ggg	agc	ggg	tgt	gct	act	ttt	gga	537
Ser	Asp	Ser	Leu	Leu	Val	Lys	Ala	Gly	Ser	Gly	Cys	Ala	Thr	Phe	Gly	
	150						155					160				
tcg	cct	tct	tct	tta	ggc	gtg	ccg	aac	gat	ttt	agc	aaa	cac	act	cta	585
Ser	Pro	Ser	Ser	Leu	Gly	Val	Pro	Asn	Asp	Phe	Ser	Lys	His	Thr	Leu	
	165					170					175					
gtg	gct	cgt	tat	aac	gat	tta	aac	tcc	aca	gaa	gaa	tgc	ttt	aaa	aaa	633
Val	Ala	Arg	Tyr	Asn	Asp	Leu	Asn	Ser	Thr	Glu	Glu	Cys	Phe	Lys	Lys	
180				185						190					195	
ggc	aat	gtg	ggg	tgc	gtc	atc	att	gaa	ccc	att	gcc	ggg	aat	atg	ggc	681
Gly	Asn	Val	Gly	Cys	Val	Ile	Ile	Glu	Pro	Ile	Ala	Gly	Asn	Met	Gly	
				200					205					210		
tta	gtg	ccg	gct	caa	aaa	gag	ttt	tta	ttg	ggc	tta	aag	gcc	ttg	tgt	729
Leu	Val	Pro	Ala	Gln	Lys	Glu	Phe	Leu	Leu	Gly	Leu	Lys	Ala	Leu	Cys	
			215					220					225			
gaa	aaa	tac	caa	gcg	gtg	ctg	att	tta	gat	gaa	gtg	atg	agc	ggg	ttt	777
Glu	Lys	Tyr	Gln	Ala	Val	Leu	Ile	Leu	Asp	Glu	Val	Met	Ser	Gly	Phe	
		230					235					240				
aga	gcg	agc	ttg	agc	ggg	tcg	caa	gaa	ttt	tat	ggc	gtg	gtg	ccg	gat	825
Arg	Ala	Ser	Leu	Ser	Gly	Ser	Gln	Glu	Phe	Tyr	Gly	Val	Val	Pro	Asp	
	245					250					255					
ttg	gta	acc	ttt	ggg	aag	gtg	ata	ggg	gct	ggg	ctt	cct	ttg	gcg	tgt	873
Leu	Val	Thr	Phe	Gly	Lys	Val	Ile	Gly	Ala	Gly	Leu	Pro	Leu	Ala	Cys	
260				265						270					275	
ttt	gga	ggg	cgt	gca	gaa	att	atg	gac	ttg	ctt	tcg	ccc	att	gga	agc	921
Phe	Gly	Gly	Arg	Ala	Glu	Ile	Met	Asp	Leu	Leu	Ser	Pro	Ile	Gly	Ser	
				280				285						290		
gtg	tat	caa	gca	ggc	act	ttg	agc	ggg	aac	ccc	cta	gcg	gtg	tgc	gcg	969
Val	Tyr	Gln	Ala	Gly	Thr	Leu	Ser	Gly	Asn	Pro	Leu	Ala	Val	Cys	Ala	
			295					300					305			
ggg	ttg	agt	gcg	ctt	tat	aaa	atc	aaa	aga	gac	aaa	acc	ctt	tat	act	1017

Gly Leu Ser Ala Leu Tyr Lys Ile Lys Arg Asp Lys Thr Leu Tyr Thr
 310 315 320

cgc tta gac gct tta gct att cgt ttg act caa ggc tta caa aag agc 1065
 Arg Leu Asp Ala Leu Ala Ile Arg Leu Thr Gln Gly Leu Gln Lys Ser
 325 330 335

gct caa aac tat aac atc gct tta gag acg ctt aac atg ggg agc atg 1113
 Ala Gln Asn Tyr Asn Ile Ala Leu Glu Thr Leu Asn Met Gly Ser Met
 340 345 350 355

ttt ggc ttt ttc ttt aac gaa aat gcg gtg cac gat ttt gat gac gct 1161
 Phe Gly Phe Phe Phe Asn Glu Asn Ala Val His Asp Phe Asp Asp Ala
 360 365 370

tta aaa agc gat acg gag atg ttt gca aaa ttc cac caa aaa atg ctc 1209
 Leu Lys Ser Asp Thr Glu Met Phe Ala Lys Phe His Gln Lys Met Leu
 375 380 385

ttt aag ggc gtg tat ttg gcg tgc tca agc ttt gaa acc ggc ttt att 1257
 Phe Lys Gly Val Tyr Leu Ala Cys Ser Ser Phe Glu Thr Gly Phe Ile
 390 395 400

tgt gag cct atg act gaa gag atg att gat tta acg atc gca aaa gcc 1305
 Cys Glu Pro Met Thr Glu Glu Met Ile Asp Leu Thr Ile Ala Lys Ala
 405 410 415

gat gaa agt ttt gat gaa atc ata aaa ggt gtg tgaatttttt gaaaaagcca 1358
 Asp Glu Ser Phe Asp Glu Ile Ile Lys Gly Val
 420 425 430

aagtattata aattcataga gggggcgaat tatttgaact tggggcctt 1406

<210> 538

<211> 430

<212> PRT

<213> Helicobacter pylori

<400> 538

Met Glu Leu Leu His Ser Ile Asn Asp Phe Asn Glu Ala Lys Gln Val
 1 5 10 15
 Ile Ala Gly Gly Val Asn Ser Pro Val Arg Ala Phe Lys Ser Val Lys
 20 25 30
 Gly Thr Pro Pro Phe Ile Leu Lys Gly Lys Gly Ala Tyr Leu Tyr Asp
 35 40 45
 Val Asp Asn Asn His Tyr Ile Asp Phe Val Gln Ser Trp Gly Pro Leu
 50 55 60
 Ile Phe Gly His Ala Asp Glu Glu Ile Glu Glu Asn Ile Ile Asn Ala
 65 70 75 80
 Leu Lys Lys Gly Thr Ser Phe Gly Ala Pro Thr Glu Leu Glu Thr Thr
 85 90 95
 Leu Ala Lys Glu Ile Ile Ser Cys Tyr Glu Gly Leu Asp Lys Val Arg
 100 105 110
 Leu Val Ser Ser Gly Thr Glu Ala Thr Met Ser Ala Ile Arg Leu Ala
 115 120 125
 Arg Ala Tyr Ser Gln Lys Asp Asp Leu Ile Lys Phe Glu Gly Cys Tyr
 130 135 140
 His Gly His Ser Asp Ser Leu Leu Val Lys Ala Gly Ser Gly Cys Ala
 145 150 155 160

ggt caa gcc gct ttg gat cag cgc atc tta agc gtt caa tat tgc ggt	257
Gly Gln Ala Ala Leu Asp Gln Arg Ile Leu Ser Val Gln Tyr Cys Gly	
45 50 55	
gaa aaa atg ctc tat ctt aac gca ggg tgc gtg tgt tgc aac aaa cgc	305
Glu Lys Met Leu Tyr Leu Asn Ala Gly Cys Val Cys Cys Asn Lys Arg	
60 65 70	
ttg gat tta gtg gag tct cta aaa gcc acg ctc aac aac tat gaa tgg	353
Leu Asp Leu Val Glu Ser Leu Lys Ala Thr Leu Asn Asn Tyr Glu Trp	
75 80 85	
cac ggc gaa att cta agg cgc atc atc att gaa act acc ggt tta gcc	401
His Gly Glu Ile Leu Arg Arg Ile Ile Ile Glu Thr Thr Gly Leu Ala	
90 95 100	
aac ccg gca ccg att tta tgg acg att ttg agc gac act ttt tta gga	449
Asn Pro Ala Pro Ile Leu Trp Thr Ile Leu Ser Asp Thr Phe Leu Gly	
105 110 115 120	
gtg cat ttt gag att caa agc gtg gtg gct tgc gtg gat gca ttg aat	497
Val His Phe Glu Ile Gln Ser Val Val Ala Cys Val Asp Ala Leu Asn	
125 130 135	
gct aga gag cat tta acc aac aat gaa gct aaa gag caa atc gtt ttt	545
Ala Arg Glu His Leu Thr Asn Asn Glu Ala Lys Glu Gln Ile Val Phe	
140 145 150	
gct gat agc gtt tta ttg acc aaa acg gat tta caa aac gat agc gcg	593
Ala Asp Ser Val Leu Leu Thr Lys Thr Asp Leu Gln Asn Asp Ser Ala	
155 160 165	
gct tta aca aaa cta aaa gag agg ata caa gcc ctt aac cct agt gca	641
Ala Leu Thr Lys Leu Lys Glu Arg Ile Gln Ala Leu Asn Pro Ser Ala	
170 175 180	
gaa att ttt gac aag agg gcg ata gac tat gag agc ctc ttt tca cgc	689
Glu Ile Phe Asp Lys Arg Ala Ile Asp Tyr Glu Ser Leu Phe Ser Arg	
185 190 195 200	
aaa aat agg gcg cga aat ttt atg cca aga atg cca aaa gat tcg cac	737
Lys Asn Arg Ala Arg Asn Phe Met Pro Arg Met Pro Lys Asp Ser His	
205 210 215	
tcg caa ggc ttt gag act tta agc att aat ttt gaa ggc acg atg gag	785
Ser Gln Gly Phe Glu Thr Leu Ser Ile Asn Phe Glu Gly Thr Met Glu	
220 225 230	
tgg agc gcg ttt ggg att tgg ctg agt ttg tta ttg cat caa tac ggc	833
Trp Ser Ala Phe Gly Ile Trp Leu Ser Leu Leu Leu His Gln Tyr Gly	
235 240 245	
aca cag att tta cgc atc aag ggg att att gac att gga agc ggc ttt	881
Thr Gln Ile Leu Arg Ile Lys Gly Ile Ile Asp Ile Gly Ser Gly Phe	
250 255 260	
ttg gtg agt att aac ggc gtg atg cat gtc att tac ccg cct aag cat	929
Leu Val Ser Ile Asn Gly Val Met His Val Ile Tyr Pro Pro Lys His	
265 270 275 280	

att tta aag gat caa aac ggc tct aac ctc gtt ttt atc atg cgc cat 977
 Ile Leu Lys Asp Gln Asn Gly Ser Asn Leu Val Phe Ile Met Arg His
 285 290 295

tta gag cgt gaa aaa atc tta aat tcc tta aag ggt ttt aag gat ttt 1025
 Leu Glu Arg Glu Lys Ile Leu Asn Ser Leu Lys Gly Phe Lys Asp Phe
 300 305 310

ctc ggc atc aag ggt ttt gaa acc caa taatttttct atttatggat 1072
 Leu Gly Ile Lys Gly Phe Glu Thr Gln
 315 320

agctgtttgc attttgatgg ggaaaaga 1100

<210> 540
 <211> 321
 <212> PRT
 <213> Helicobacter pylori

<400> 540
 Met Pro Lys Ile Pro Ile Thr Leu Ile Thr Gly Phe Leu Gly Ser Gly
 1 5 10 15
 Lys Thr Ser Phe Leu Ser Glu Tyr Leu Asn Gln Thr Asp His Gln Gly
 20 25 30
 Val Ala Leu Ile Ile Asn Glu Ile Gly Gln Ala Ala Leu Asp Gln Arg
 35 40 45
 Ile Leu Ser Val Gln Tyr Cys Gly Glu Lys Met Leu Tyr Leu Asn Ala
 50 55 60
 Gly Cys Val Cys Cys Asn Lys Arg Leu Asp Leu Val Glu Ser Leu Lys
 65 70 75 80
 Ala Thr Leu Asn Asn Tyr Glu Trp His Gly Glu Ile Leu Arg Arg Ile
 85 90 95
 Ile Ile Glu Thr Thr Gly Leu Ala Asn Pro Ala Pro Ile Leu Trp Thr
 100 105 110
 Ile Leu Ser Asp Thr Phe Leu Gly Val His Phe Glu Ile Gln Ser Val
 115 120 125
 Val Ala Cys Val Asp Ala Leu Asn Ala Arg Glu His Leu Thr Asn Asn
 130 135 140
 Glu Ala Lys Glu Gln Ile Val Phe Ala Asp Ser Val Leu Leu Thr Lys
 145 150 155 160
 Thr Asp Leu Gln Asn Asp Ser Ala Ala Leu Thr Lys Leu Lys Glu Arg
 165 170 175
 Ile Gln Ala Leu Asn Pro Ser Ala Glu Ile Phe Asp Lys Arg Ala Ile
 180 185 190
 Asp Tyr Glu Ser Leu Phe Ser Arg Lys Asn Arg Ala Arg Asn Phe Met
 195 200 205
 Pro Arg Met Pro Lys Asp Ser His Ser Gln Gly Phe Glu Thr Leu Ser
 210 215 220
 Ile Asn Phe Glu Gly Thr Met Glu Trp Ser Ala Phe Gly Ile Trp Leu
 225 230 235 240
 Ser Leu Leu Leu His Gln Tyr Gly Thr Gln Ile Leu Arg Ile Lys Gly
 245 250 255
 Ile Ile Asp Ile Gly Ser Gly Phe Leu Val Ser Ile Asn Gly Val Met
 260 265 270
 His Val Ile Tyr Pro Pro Lys His Ile Leu Lys Asp Gln Asn Gly Ser
 275 280 285
 Asn Leu Val Phe Ile Met Arg His Leu Glu Arg Glu Lys Ile Leu Asn
 290 295 300

gta tgg ctc gct tac aga gaa cat gtt tta aaa gaa agc gta act tac	580
Val Trp Leu Ala Tyr Arg Glu His Val Leu Lys Glu Ser Val Thr Tyr	
170 175 180 185	
cca gaa gtc ttt tac aaa ggc gaa tac atc att gaa atc gct aaa aag	628
Pro Glu Val Phe Tyr Lys Gly Glu Tyr Ile Ile Glu Ile Ala Lys Lys	
190 195 200	
gcg aac aac gat tta gaa cca agc ctt tta aaa gaa aac gaa gaa acg	676
Ala Asn Asn Asp Leu Glu Pro Ser Leu Leu Lys Glu Asn Glu Glu Thr	
205 210 215	
att att gaa gtt tta agc ggc tat gct agg gat cta atg ctt tta gaa	724
Ile Ile Glu Val Leu Ser Gly Tyr Ala Arg Asp Leu Met Leu Leu Glu	
220 225 230	
att aaa gat aat tta gac gct tta ggc att cat ttt gat tcc tat gcg	772
Ile Lys Asp Asn Leu Asp Ala Leu Gly Ile His Phe Asp Ser Tyr Ala	
235 240 245	
agc gaa aaa gaa gtt ttt aaa cat aaa gat gcg gtg ttt gaa caa tta	820
Ser Glu Lys Glu Val Phe Lys His Lys Asp Ala Val Phe Glu Gln Leu	
250 255 260 265	
gaa aaa gcg aac gcc ctt tat gaa aag gat tct aaa atc tgg ctc aaa	868
Glu Lys Ala Asn Ala Leu Tyr Glu Lys Asp Ser Lys Ile Trp Leu Lys	
270 275 280	
tct tca ctc tac cag gat gaa agc gat cgg gtg ctc att aaa gaa gat	916
Ser Ser Leu Tyr Gln Asp Glu Ser Asp Arg Val Leu Ile Lys Glu Asp	
285 290 295	
aaa agc tac act tat tta gcg ggc gat att gtc tat cat gat gaa aaa	964
Lys Ser Tyr Thr Tyr Leu Ala Gly Asp Ile Val Tyr His Asp Glu Lys	
300 305 310	
ttc aag caa gat tat acc aaa tac atc aac att tgg ggg gca gac cac	1012
Phe Lys Gln Asp Tyr Thr Lys Tyr Ile Asn Ile Trp Gly Ala Asp His	
315 320 325	
cac ggc tat atc gct aga gtg aaa gcc agc ctt gag ttt ttg ggc tat	1060
His Gly Tyr Ile Ala Arg Val Lys Ala Ser Leu Glu Phe Leu Gly Tyr	
330 335 340 345	
gat tcc aac aag ctt gaa gtc ttg ctc gct caa atg gtg cgc ttg ctc	1108
Asp Ser Asn Lys Leu Glu Val Leu Leu Ala Gln Met Val Arg Leu Leu	
350 355 360	
aaa gat aac gag cct tac aag atg agt aaa aga gcg ggt aat ttt att	1156
Lys Asp Asn Glu Pro Tyr Lys Met Ser Lys Arg Ala Gly Asn Phe Ile	
365 370 375	
ttg att aaa gat gtg gtt gat gat gtg ggt aag gac gct ttg agg ttt	1204
Leu Ile Lys Asp Val Val Asp Asp Val Gly Lys Asp Ala Leu Arg Phe	
380 385 390	
att ttt ttg agc aaa cgg ctt gac act cat tta gaa ttt gat gtc aat	1252
Ile Phe Leu Ser Lys Arg Leu Asp Thr His Leu Glu Phe Asp Val Asn	

395	400	405	
act tta aaa aag caa gac agc tca aac ccc att tac tat atc cat tac			1300
Thr Leu Lys Lys Gln Asp Ser Ser Asn Pro Ile Tyr Tyr Ile His Tyr			
410	415	420	425
gct aat tcg cgc atc cac acc atg cta gaa aaa tcg ccc ttt tct aaa			1348
Ala Asn Ser Arg Ile His Thr Met Leu Glu Lys Ser Pro Phe Ser Lys			
	430	435	440
gaa gag gtt ttg caa acc cct tta acc aat tta aac gct gaa gaa aaa			1396
Glu Glu Val Leu Gln Thr Pro Leu Thr Asn Leu Asn Ala Glu Glu Lys			
	445	450	455
tac ttg ctt ttt agc gct tta agc ttg cct aaa gca att gaa tcc tct			1444
Tyr Leu Leu Phe Ser Ala Leu Ser Leu Pro Lys Ala Ile Glu Ser Ser			
	460	465	470
ttt gaa gaa tac ggc ttg caa aaa atg tgc gaa tac gca aaa acc ctc			1492
Phe Glu Glu Tyr Gly Leu Gln Lys Met Cys Glu Tyr Ala Lys Thr Leu			
	475	480	485
gca tca gaa ttc cac cgc ttc tat aac gct ggc aaa atc tta gac acc			1540
Ala Ser Glu Phe His Arg Phe Tyr Asn Ala Gly Lys Ile Leu Asp Thr			
	490	495	500
cct aaa gct aaa gag ctt tta aaa att tgt tta ata gta agc ttg agc			1588
Pro Lys Ala Lys Glu Leu Leu Lys Ile Cys Leu Ile Val Ser Leu Ser			
	510	515	520
tta agc aac gct ttt aaa ctt tta ggc ata gag ata aag acc aaa att			1636
Leu Ser Asn Ala Phe Lys Leu Leu Gly Ile Glu Ile Lys Thr Lys Ile			
	525	530	535
tcc gct aga gat taagccaata ttttaattttt tggtataaca ttcccccttat			1688
Ser Ala Arg Asp			
	540		
tttttgaaac taaggagaat attat			1713

<210> 542
 <211> 541
 <212> PRT
 <213> Helicobacter pylori

<400> 542

Met His Thr Leu Ile Lys Gly Ile Leu Glu Glu Ile Leu Glu Glu Glu	
1 5 10 15	
Val Ile Val Glu Tyr Pro Lys Asp Arg Glu His Gly His Tyr Ala Thr	
20 25 30	
Pro Ile Ala Phe Asn Leu Ala Lys Val Phe Lys Lys Ser Pro Leu Ala	
35 40 45	
Ile Ala Glu Glu Leu Ala Leu Lys Ile Ser Thr His Glu Lys Thr Gln	
50 55 60	
Gly Leu Phe Asp Ser Val Val Ala Cys Lys Gly Tyr Ile Asn Phe Thr	
65 70 75 80	
Leu Ser Leu Asp Phe Leu Glu Arg Phe Thr Gln Lys Ala Leu Glu Leu	
85 90 95	
Lys Glu Lys Phe Gly Ser Gln Val Lys Ser Glu Arg Ser Gln Lys Ile	

			100				105				110				
Phe	Leu	Glu	Phe	Val	Ser	Ala	Asn	Pro	Thr	Gly	Pro	Leu	His	Ile	Gly
		115					120					125			
His	Ala	Arg	Gly	Ala	Val	Phe	Gly	Asp	Ser	Leu	Ala	Lys	Ile	Ala	Arg
	130					135					140				
Phe	Leu	Gly	His	Glu	Val	Leu	Cys	Glu	Tyr	Tyr	Val	Asn	Asp	Met	Gly
145					150					155					160
Ser	Gln	Ile	Arg	Leu	Gly	Leu	Ser	Val	Trp	Leu	Ala	Tyr	Arg	Glu	
				165				170						175	
His	Val	Leu	Lys	Glu	Ser	Val	Thr	Tyr	Pro	Glu	Val	Phe	Tyr	Lys	Gly
		180						185					190		
Glu	Tyr	Ile	Ile	Glu	Ile	Ala	Lys	Lys	Ala	Asn	Asn	Asp	Leu	Glu	Pro
	195						200					205			
Ser	Leu	Leu	Lys	Glu	Asn	Glu	Glu	Thr	Ile	Ile	Glu	Val	Leu	Ser	Gly
	210				215						220				
Tyr	Ala	Arg	Asp	Leu	Met	Leu	Leu	Glu	Ile	Lys	Asp	Asn	Leu	Asp	Ala
225					230					235					240
Leu	Gly	Ile	His	Phe	Asp	Ser	Tyr	Ala	Ser	Glu	Lys	Glu	Val	Phe	Lys
				245				250						255	
His	Lys	Asp	Ala	Val	Phe	Glu	Gln	Leu	Glu	Lys	Ala	Asn	Ala	Leu	Tyr
		260					265						270		
Glu	Lys	Asp	Ser	Lys	Ile	Trp	Leu	Lys	Ser	Ser	Leu	Tyr	Gln	Asp	Glu
	275					280					285				
Ser	Asp	Arg	Val	Leu	Ile	Lys	Glu	Asp	Lys	Ser	Tyr	Thr	Tyr	Leu	Ala
	290				295					300					
Gly	Asp	Ile	Val	Tyr	His	Asp	Glu	Lys	Phe	Lys	Gln	Asp	Tyr	Thr	Lys
305					310				315						320
Tyr	Ile	Asn	Ile	Trp	Gly	Ala	Asp	His	His	Gly	Tyr	Ile	Ala	Arg	Val
		325						330					335		
Lys	Ala	Ser	Leu	Glu	Phe	Leu	Gly	Tyr	Asp	Ser	Asn	Lys	Leu	Glu	Val
	340						345					350			
Leu	Leu	Ala	Gln	Met	Val	Arg	Leu	Lys	Asp	Asn	Glu	Pro	Tyr	Lys	
	355						360				365				
Met	Ser	Lys	Arg	Ala	Gly	Asn	Phe	Ile	Leu	Ile	Lys	Asp	Val	Val	Asp
	370				375					380					
Asp	Val	Gly	Lys	Asp	Ala	Leu	Arg	Phe	Ile	Phe	Leu	Ser	Lys	Arg	Leu
385					390				395						400
Asp	Thr	His	Leu	Glu	Phe	Asp	Val	Asn	Thr	Leu	Lys	Lys	Gln	Asp	Ser
		405						410					415		
Ser	Asn	Pro	Ile	Tyr	Tyr	Ile	His	Tyr	Ala	Asn	Ser	Arg	Ile	His	Thr
	420						425						430		
Met	Leu	Glu	Lys	Ser	Pro	Phe	Ser	Lys	Glu	Glu	Val	Leu	Gln	Thr	Pro
	435				440						445				
Leu	Thr	Asn	Leu	Asn	Ala	Glu	Glu	Lys	Tyr	Leu	Leu	Phe	Ser	Ala	Leu
	450				455					460					
Ser	Leu	Pro	Lys	Ala	Ile	Glu	Ser	Ser	Phe	Glu	Glu	Tyr	Gly	Leu	Gln
465					470				475						480
Lys	Met	Cys	Glu	Tyr	Ala	Lys	Thr	Leu	Ala	Ser	Glu	Phe	His	Arg	Phe
		485						490					495		
Tyr	Asn	Ala	Gly	Lys	Ile	Leu	Asp	Thr	Pro	Lys	Ala	Lys	Glu	Leu	Leu
	500						505					510			
Lys	Ile	Cys	Leu	Ile	Val	Ser	Leu	Ser	Leu	Ser	Asn	Ala	Phe	Lys	Leu
	515					520					525				
Leu	Gly	Ile	Glu	Ile	Lys	Thr	Lys	Ile	Ser	Ala	Arg	Asp			
	530					535					540				

<210> 543

<211> 896

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (38)...(835)

<400> 543

```
aagtagagat tatattacct agatagtgaa tcaacga atg aaa agc cac ttc caa 55
                                     Met Lys Ser His Phe Gln
                                     1           5

tac agc acg cta gaa aat atc cct aaa gcc ttt gac att ctc aaa gac 103
Tyr Ser Thr Leu Glu Asn Ile Pro Lys Ala Phe Asp Ile Leu Lys Asp
                10                15                20

ccc cct aaa aaa ctc tat tgt gtg ggc gat acc aag ctt ttg gac acg 151
Pro Pro Lys Lys Leu Tyr Cys Val Gly Asp Thr Lys Leu Leu Asp Thr
                25                30                35

cct tta aaa gtg gcg atc ata ggc aca aga aga ccc acc cct tac agc 199
Pro Leu Lys Val Ala Ile Ile Gly Thr Arg Arg Pro Thr Pro Tyr Ser
                40                45                50

aag caa cac acg atc act cta gct aga gag ctt gct aaa aat ggc gcg 247
Lys Gln His Thr Ile Thr Leu Ala Arg Glu Leu Ala Lys Asn Gly Ala
    55                60                65                70

gtt att gtg agt ggg gga gcg tta ggc gtg gat att atc gct caa gaa 295
Val Ile Val Ser Gly Gly Ala Leu Gly Val Asp Ile Ile Ala Gln Glu
                75                80                85

aac gcc ttg cca aaa acg atc atg ctt tgc cct tgc agt ttg gat ttc 343
Asn Ala Leu Pro Lys Thr Ile Met Leu Ser Pro Cys Ser Leu Asp Phe
                90                95                100

atc tat cct acg aac aat cat aaa gtg atc caa gaa atc gcg caa aac 391
Ile Tyr Pro Thr Asn Asn His Lys Val Ile Gln Glu Ile Ala Gln Asn
                105                110                115

ggc ttg att tta agc gaa tat gaa aag gat ttc atg ccc att aaa ggc 439
Gly Leu Ile Leu Ser Glu Tyr Glu Lys Asp Phe Met Pro Ile Lys Gly
                120                125                130

tct ttt ttg gcg aga aac cgc ctg gtg atc gct tta agc gat gtg gtg 487
Ser Phe Leu Ala Arg Asn Arg Leu Val Ile Ala Leu Ser Asp Val Val
                135                140                145                150

att atc ccc caa gcg gat tta aaa agc ggc tct atg agc agc gcg aga 535
Ile Ile Pro Gln Ala Asp Leu Lys Ser Gly Ser Met Ser Ser Ala Arg
                155                160                165

tta gcc cag aaa tac caa aag cct tta ttt gtt tta ccc caa cgc ctg 583
Leu Ala Gln Lys Tyr Gln Lys Pro Leu Phe Val Leu Pro Gln Arg Leu
                170                175                180

aat gag agc gat ggc act aat gag ctt tta gaa aaa ggg cag gct caa 631
Asn Glu Ser Asp Gly Thr Asn Glu Leu Leu Glu Lys Gly Gln Ala Gln
                185                190                195
```

ggg ata ttt aat att caa aat ttt ata aac acc ctt tta aaa gac tac 679
 Gly Ile Phe Asn Ile Gln Asn Phe Ile Asn Thr Leu Leu Lys Asp Tyr
 200 205 210

cat tta aaa gaa atg cct gaa atg gaa gat gaa ttt tta gaa tat tgt 727
 His Leu Lys Glu Met Pro Glu Met Glu Asp Glu Phe Leu Glu Tyr Cys
 215 220 225 230

gcc aaa aac ccg agc tat gaa gaa gcg tat ctc aaa ttt ggg gat aac 775
 Ala Lys Asn Pro Ser Tyr Glu Glu Ala Tyr Leu Lys Phe Gly Asp Lys
 235 240 245

ctt tta gaa tac gag ctg ttg ggt aag atc aag cgc atc aat cac att 823
 Leu Leu Glu Tyr Glu Leu Leu Gly Lys Ile Lys Arg Ile Asn His Ile
 250 255 260

gtg gtg tta gcg tgattttggc atgcgatgtg gggttaaaac gcattggcat 875
 Val Val Leu Ala
 265

cgctgcgctt ttaaattggcg t 896

<210> 544

<211> 266

<212> PRT

<213> Helicobacter pylori

<400> 544

Met Lys Ser His Phe Gln Tyr Ser Thr Leu Glu Asn Ile Pro Lys Ala
 1 5 10 15
 Phe Asp Ile Leu Lys Asp Pro Pro Lys Lys Leu Tyr Cys Val Gly Asp
 20 25 30
 Thr Lys Leu Leu Asp Thr Pro Leu Lys Val Ala Ile Ile Gly Thr Arg
 35 40 45
 Arg Pro Thr Pro Tyr Ser Lys Gln His Thr Ile Thr Leu Ala Arg Glu
 50 55 60
 Leu Ala Lys Asn Gly Ala Val Ile Val Ser Gly Gly Ala Leu Gly Val
 65 70 75 80
 Asp Ile Ile Ala Gln Glu Asn Ala Leu Pro Lys Thr Ile Met Leu Ser
 85 90 95
 Pro Cys Ser Leu Asp Phe Ile Tyr Pro Thr Asn Asn His Lys Val Ile
 100 105 110
 Gln Glu Ile Ala Gln Asn Gly Leu Ile Leu Ser Glu Tyr Glu Lys Asp
 115 120 125
 Phe Met Pro Ile Lys Gly Ser Phe Leu Ala Arg Asn Arg Leu Val Ile
 130 135 140
 Ala Leu Ser Asp Val Val Ile Ile Pro Gln Ala Asp Leu Lys Ser Gly
 145 150 155 160
 Ser Met Ser Ser Ala Arg Leu Ala Gln Lys Tyr Gln Lys Pro Leu Phe
 165 170 175
 Val Leu Pro Gln Arg Leu Asn Glu Ser Asp Gly Thr Asn Glu Leu Leu
 180 185 190
 Glu Lys Gly Gln Ala Gln Gly Ile Phe Asn Ile Gln Asn Phe Ile Asn
 195 200 205
 Thr Leu Leu Lys Asp Tyr His Leu Lys Glu Met Pro Glu Met Glu Asp
 210 215 220
 Glu Phe Leu Glu Tyr Cys Ala Lys Asn Pro Ser Tyr Glu Glu Ala Tyr
 225 230 235 240

Leu Lys Phe Gly Asp Lys Leu Leu Glu Tyr Glu Leu Leu Gly Lys Ile
 245 250 255
 Lys Arg Ile Asn His Ile Val Val Leu Ala
 260 265

<210> 545
 <211> 459
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (82)...(408)

<400> 545
 taaaacgctc ttgaaagggt gagcgtggaa ttgcttcta tcgtttggtt gctcatagtc 60
 aatattctga tttttattct c atg ctg gtg gat aaa aat tcg gct gat caa 111
 Met Leu Val Asp Lys Asn Ser Ala Asp Gln
 1 5 10

 aaa atg tgg cgt att cct gaa aaa gct ttg tgg gtt tta tcg ctc ctt 159
 Lys Met Trp Arg Ile Pro Glu Lys Ala Leu Trp Val Leu Ser Leu Leu
 15 20 25

 ggc ggg tct gtc ggg ttt ttg gtc gct atg gtt gtg tcc cac cat aag 207
 Gly Gly Ser Val Gly Phe Leu Val Ala Met Val Val Ser His His Lys
 30 35 40

 atc tta aag cct gag ttt aaa tac ggc gtt tcg ctc att tac ttg ata 255
 Ile Leu Lys Pro Glu Phe Lys Tyr Gly Val Ser Leu Ile Tyr Leu Ile
 45 50 55

 gag agc aca atc ctt tac ttt gtc agc aaa gat ctt tct tgg ata gta 303
 Glu Ser Thr Ile Leu Tyr Phe Val Ser Lys Asp Leu Ser Trp Ile Val
 60 65 70

 gcg cta acg ata ttc tca cta tct ttg ata ctg gta gcg ttt aag atc 351
 Ala Leu Thr Ile Phe Ser Leu Ser Leu Ile Leu Val Ala Phe Lys Ile
 75 80 85 90

 ttc ctc ctt aaa gac aac cct aac aaa cgc ttc aaa aac aac aag agc 399
 Phe Leu Leu Lys Asp Asn Pro Asn Lys Arg Phe Lys Asn Asn Lys Arg
 95 100 105

 gat aaa aaa taatgtctta tttttttaaa atcattctgg gcacaagcgt 448
 Asp Lys Lys

 gatcgtgggg g 459

<210> 546
 <211> 109
 <212> PRT
 <213> Helicobacter pylori

<400> 546
 Met Leu Val Asp Lys Asn Ser Ala Asp Gln Lys Met Trp Arg Ile Pro
 1 5 10 15

Glu	Lys	Ala	Leu	Trp	Val	Leu	Ser	Leu	Leu	Gly	Gly	Ser	Val	Gly	Phe
			20					25					30		
Leu	Val	Ala	Met	Val	Val	Ser	His	His	Lys	Ile	Leu	Lys	Pro	Glu	Phe
		35					40					45			
Lys	Tyr	Gly	Val	Ser	Leu	Ile	Tyr	Leu	Ile	Glu	Ser	Thr	Ile	Leu	Tyr
	50				55					60					
Phe	Val	Ser	Lys	Asp	Leu	Ser	Trp	Ile	Val	Ala	Leu	Thr	Ile	Phe	Ser
65					70				75						80
Leu	Ser	Leu	Ile	Leu	Val	Ala	Phe	Lys	Ile	Phe	Leu	Leu	Lys	Asp	Asn
			85					90					95		
Pro	Asn	Lys	Arg	Phe	Lys	Asn	Asn	Lys	Arg	Asp	Lys	Lys			
			100					105							

<210> 547

<211> 399

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (47)...(379)

<400> 547

agcgctcaaa	tcatttattg	gttatcaaaa	tatttttagga	gtgagt	atg	gaa	aat	55
							Met Glu Asn	
							1	

gat	gtt	aaa	gaa	gat	cta	gag	caa	gca	aga	cca	aag	tta	gag	cca	gaa	103
Asp	Val	Lys	Glu	Asp	Leu	Glu	Gln	Ala	Arg	Pro	Lys	Leu	Glu	Pro	Glu	
	5					10					15					

aag	caa	aag	caa	gag	cca	gag	gaa	cag	aaa	caa	gaa	aaa	caa	gac	aaa	151
Lys	Gln	Lys	Gln	Glu	Pro	Glu	Glu	Gln	Lys	Gln	Glu	Lys	Gln	Asp	Lys	
	20				25				30					35		

caa	gag	cag	aag	cca	aag	caa	gaa	aaa	gaa	gag	tca	aag	agc	aag	gaa	199
Gln	Glu	Gln	Lys	Pro	Lys	Gln	Glu	Lys	Glu	Glu	Ser	Lys	Ser	Lys	Glu	
			40					45						50		

caa	gaa	gaa	aac	aaa	aaa	caa	aag	aga	tct	agc	tat	att	ttt	tgg	gga	247
Gln	Glu	Glu	Asn	Lys	Lys	Gln	Lys	Arg	Ser	Ser	Tyr	Ile	Phe	Trp	Gly	
			55					60					65			

tgt	att	att	ggt	ttg	tgt	ata	gtt	gtt	att	att	gcc	aaa	att	att	gcg	295
Cys	Ile	Ile	Gly	Leu	Cys	Ile	Val	Val	Ile	Ile	Ala	Lys	Ile	Ile	Ala	
		70					75					80				

ttt	ggc	gga	tct	agt	gag	gag	gca	aaa	gca	gac	aaa	cca	aaa	aac	tct	343
Phe	Gly	Gly	Ser	Ser	Glu	Glu	Ala	Lys	Ala	Asp	Lys	Pro	Lys	Asn	Ser	
	85					90					95					

tta	agt	atg	ctg	aaa	aac	ttt	tac	cta	ccg	ata	tta	taaaagataa				389
Leu	Ser	Met	Leu	Lys	Asn	Phe	Tyr	Leu	Pro	Ile	Leu					
100					105					110						

tcttaataac																399
------------	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	-----

<210> 548

<211> 111
 <212> PRT
 <213> Helicobacter pylori

<400> 548
 Met Glu Asn Asp Val Lys Glu Asp Leu Glu Gln Ala Arg Pro Lys Leu
 1 5 10 15
 Glu Pro Glu Lys Gln Lys Glu Pro Glu Glu Gln Lys Gln Glu Lys
 20 25 30
 Gln Asp Lys Gln Glu Gln Lys Pro Lys Gln Glu Lys Glu Glu Ser Lys
 35 40 45
 Ser Lys Glu Gln Glu Glu Asn Lys Lys Gln Lys Arg Ser Ser Tyr Ile
 50 55 60
 Phe Trp Gly Cys Ile Ile Gly Leu Cys Ile Val Val Ile Ile Ala Lys
 65 70 75 80
 Ile Ile Ala Phe Gly Gly Ser Ser Glu Glu Ala Lys Ala Asp Lys Pro
 85 90 95
 Lys Asn Ser Leu Ser Met Leu Lys Asn Phe Tyr Leu Pro Ile Leu
 100 105 110

<210> 549
 <211> 1627
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (21)...(1568)

<400> 549
 tctaaatcct aatctaacaa atg aaa caa aag ctt aaa gct caa atc aaa gag 53
 Met Lys Gln Lys Leu Lys Ala Gln Ile Lys Glu
 1 5 10
 cgc atg gct tct atc gct tat aat gaa aaa ggg ttt cct agc ccc ttt 101
 Arg Met Ala Ser Ile Ala Tyr Asn Glu Lys Gly Phe Pro Ser Pro Phe
 15 20 25
 tta ttt aaa gac ttg aaa aaa gcc gcg ctc aaa atc ata gaa gcc atg 149
 Leu Phe Lys Asp Leu Lys Lys Ala Ala Leu Lys Ile Ile Glu Ala Met
 30 35 40
 cgc aca aac aca gaa att tta gtg gtg ggc gat tat gac gct gac ggc 197
 Arg Thr Asn Thr Glu Ile Leu Val Val Gly Asp Tyr Asp Ala Asp Gly
 45 50 55
 gtg att agc tct gct atc atg gca aaa ttt ttt gaa agc ctg aac tat 245
 Val Ile Ser Ser Ala Ile Met Ala Lys Phe Phe Glu Ser Leu Asn Tyr
 60 65 70 75
 aag cat gtc cgc att gca atc cct aat cgc ttc atg gat ggc tat ggc 293
 Lys His Val Arg Ile Ala Ile Pro Asn Arg Phe Met Asp Gly Tyr Gly
 80 85 90
 att tct aaa aaa ttt tta gaa aaa cac cac gcc cct tta atc atc acg 341
 Ile Ser Lys Lys Phe Leu Glu Lys His His Ala Pro Leu Ile Ile Thr
 95 100 105

gtg gat aac ggg att aac gcc ttt gaa gcc gcg cga ttt tgt aaa gaa	389
Val Asp Asn Gly Ile Asn Ala Phe Glu Ala Ala Arg Phe Cys Lys Glu	
110 115 120	
aaa aat tac acc ctt atc atc aca gat cac cat tgc tta cac cat gat	437
Lys Asn Tyr Thr Leu Ile Ile Thr Asp His His Cys Leu His His Asp	
125 130 135	
gaa gtc cca gac gct tat gcg gtg atc aac ccc aag caa ccg gat tgt	485
Glu Val Pro Asp Ala Tyr Ala Val Ile Asn Pro Lys Gln Pro Asp Cys	
140 145 150 155	
gat ttt atc caa aag gaa gtg tgc ggg gcg ttg gta gcg ttt tat ttg	533
Asp Phe Ile Gln Lys Glu Val Cys Gly Ala Leu Val Ala Phe Tyr Leu	
160 165 170	
tgc tat ggg atc cat cag ctt tta gga aaa gaa aaa agc cat tct agt	581
Cys Tyr Gly Ile His Gln Leu Leu Gly Lys Glu Lys Ser His Ser Ser	
175 180 185	
gag tta tta tgt tta gcg ggc gtg gcg act att gct gac atg atg cct	629
Glu Leu Leu Cys Leu Ala Gly Val Ala Thr Ile Ala Asp Met Met Pro	
190 195 200	
ttg act ttt ttt aac cgc ttt tta gtt tct aaa gcc ttg tat ttt ttg	677
Leu Thr Phe Phe Asn Arg Phe Leu Val Ser Lys Ala Leu Tyr Phe Leu	
205 210 215	
caa aaa gaa tcc tta ggg gcg atg ggt ttt ttg cgc caa aga gaa gtt	725
Gln Lys Glu Ser Leu Gly Ala Met Gly Phe Leu Arg Gln Arg Glu Val	
220 225 230 235	
ttt aga aaa cgc tct tta aaa gcg agt gat att tct ttt aat atc gcc	773
Phe Arg Lys Arg Ser Leu Lys Ala Ser Asp Ile Ser Phe Asn Ile Ala	
240 245 250	
ccc tta atc aac tcc gca ggg cgc atg caa gat gcg aaa atg gct tta	821
Pro Leu Ile Asn Ser Ala Gly Arg Met Gln Asp Ala Lys Met Ala Leu	
255 260 265	
gat ttt tta agc gcg aat aat tct caa gat ggc tat tct ttg tat gaa	869
Asp Phe Leu Ser Ala Asn Asn Ser Gln Asp Gly Tyr Ser Leu Tyr Glu	
270 275 280	
cgc ttg aaa gca tgc aat ttg aag cgt aaa atg atc caa cag cag gtt	917
Arg Leu Lys Ala Cys Asn Leu Lys Arg Lys Met Ile Gln Gln Gln Val	
285 290 295	
ttt gaa gaa gct ttt aag cat gcg atg gtt gga gaa aaa att atc gtc	965
Phe Glu Glu Ala Phe Lys His Ala Met Val Gly Glu Lys Ile Ile Val	
300 305 310 315	
gct ttt aag gac aat tgg cat gag gga gtg ctg ggg att gtg gct tca	1013
Ala Phe Lys Asp Asn Trp His Glu Gly Val Leu Gly Ile Val Ala Ser	
320 325 330	
aaa tta gtg gaa gcc act caa aag cca agc ctg gtt ttt acc ttt aaa	1061
Lys Leu Val Glu Ala Thr Gln Lys Pro Ser Leu Val Phe Thr Phe Lys	
335 340 345	

gaa ggg gtg tat aaa ggg agc gct cgt agc tct tca aac att gac ttg 1109
 Glu Gly Val Tyr Lys Gly Ser Ala Arg Ser Ser Ser Asn Ile Asp Leu
 350 355 360

att gac gct ttg aat ggg gtt tct tct tta ttg ctc ggc tat gga ggc 1157
 Ile Asp Ala Leu Asn Gly Val Ser Ser Leu Leu Leu Gly Tyr Gly Gly
 365 370 375

cat agg caa gct tgc ggg ttg agc gtt gaa aaa aac aat atc atc tcg 1205
 His Arg Gln Ala Cys Gly Leu Ser Val Glu Lys Asn Asn Ile Ile Ser
 380 385 390 395

ctc ttt gaa act tta gaa aat ttt gat ttt aaa gtt tta cct ttt tgt 1253
 Leu Phe Glu Thr Leu Glu Asn Phe Asp Phe Lys Val Leu Pro Phe Cys
 400 405 410

aaa aca gag ccc cct tta acg ctc aaa tta aaa gac att gac aga gag 1301
 Lys Thr Glu Pro Pro Leu Thr Leu Lys Leu Lys Asp Ile Asp Arg Glu
 415 420 425

ctt tta gag att ata gaa atg ggc gaa cct tat ggg caa gaa aac cct 1349
 Leu Leu Glu Ile Ile Glu Met Gly Glu Pro Tyr Gly Gln Glu Asn Pro
 430 435 440

gaa ccc cta ttc caa gca aaa aat tta gaa gtc ata gaa gaa aaa atc 1397
 Glu Pro Leu Phe Gln Ala Lys Asn Leu Glu Val Ile Glu Glu Lys Ile
 445 450 455

att aaa gaa agc cac cag gtt ttg cgt ttt aag gat aaa gaa tgc gtc 1445
 Ile Lys Glu Ser His Gln Val Leu Arg Phe Lys Asp Lys Glu Cys Val
 460 465 470 475

aaa gag gct att tat ttt agc gct gag cgg ttt ttg aaa gcg ggc gaa 1493
 Lys Glu Ala Ile Tyr Phe Ser Ala Glu Arg Phe Leu Lys Ala Gly Glu
 480 485 490

aag gtg agc gtg ctt ttt agc gtg gaa tta gat gag tgt tct aat gag 1541
 Lys Val Ser Val Leu Phe Ser Val Glu Leu Asp Glu Cys Ser Asn Glu
 495 500 505

cct aaa atg ttt gtt aaa agt ttg ttg tagtgccttt tgttgaagaa 1588
 Pro Lys Met Phe Val Lys Ser Leu Leu
 510 515

gaatttgaaa ttttaaaacc caccaaagcc ttgtttttt 1627

<210> 550

<211> 516

<212> PRT

<213> Helicobacter pylori

<400> 550

Met Lys Gln Lys Leu Lys Ala Gln Ile Lys Glu Arg Met Ala Ser Ile
 1 5 10 15
 Ala Tyr Asn Glu Lys Gly Phe Pro Ser Pro Phe Leu Phe Lys Asp Leu
 20 25 30
 Lys Lys Ala Ala Leu Lys Ile Ile Glu Ala Met Arg Thr Asn Thr Glu
 35 40 45

Ile	Leu	Val	Val	Gly	Asp	Tyr	Asp	Ala	Asp	Gly	Val	Ile	Ser	Ser	Ala
50						55					60				
Ile	Met	Ala	Lys	Phe	Phe	Glu	Ser	Leu	Asn	Tyr	Lys	His	Val	Arg	Ile
65					70					75					80
Ala	Ile	Pro	Asn	Arg	Phe	Met	Asp	Gly	Tyr	Gly	Ile	Ser	Lys	Lys	Phe
				85					90					95	
Leu	Glu	Lys	His	His	Ala	Pro	Leu	Ile	Ile	Thr	Val	Asp	Asn	Gly	Ile
			100					105						110	
Asn	Ala	Phe	Glu	Ala	Ala	Arg	Phe	Cys	Lys	Glu	Lys	Asn	Tyr	Thr	Leu
		115					120					125			
Ile	Ile	Thr	Asp	His	His	Cys	Leu	His	His	Asp	Glu	Val	Pro	Asp	Ala
130						135					140				
Tyr	Ala	Val	Ile	Asn	Pro	Lys	Gln	Pro	Asp	Cys	Asp	Phe	Ile	Gln	Lys
145					150					155					160
Glu	Val	Cys	Gly	Ala	Leu	Val	Ala	Phe	Tyr	Leu	Cys	Tyr	Gly	Ile	His
				165					170					175	
Gln	Leu	Leu	Gly	Lys	Glu	Lys	Ser	His	Ser	Ser	Glu	Leu	Leu	Cys	Leu
			180					185						190	
Ala	Gly	Val	Ala	Thr	Ile	Ala	Asp	Met	Met	Pro	Leu	Thr	Phe	Phe	Asn
		195					200					205			
Arg	Phe	Leu	Val	Ser	Lys	Ala	Leu	Tyr	Phe	Leu	Gln	Lys	Glu	Ser	Leu
	210					215					220				
Gly	Ala	Met	Gly	Phe	Leu	Arg	Gln	Arg	Glu	Val	Phe	Arg	Lys	Arg	Ser
225					230					235					240
Leu	Lys	Ala	Ser	Asp	Ile	Ser	Phe	Asn	Ile	Ala	Pro	Leu	Ile	Asn	Ser
				245					250					255	
Ala	Gly	Arg	Met	Gln	Asp	Ala	Lys	Met	Ala	Leu	Asp	Phe	Leu	Ser	Ala
			260					265					270		
Asn	Asn	Ser	Gln	Asp	Gly	Tyr	Ser	Leu	Tyr	Glu	Arg	Leu	Lys	Ala	Cys
		275					280					285			
Asn	Leu	Lys	Arg	Lys	Met	Ile	Gln	Gln	Gln	Val	Phe	Glu	Glu	Ala	Phe
	290					295					300				
Lys	His	Ala	Met	Val	Gly	Glu	Lys	Ile	Ile	Val	Ala	Phe	Lys	Asp	Asn
305					310					315					320
Trp	His	Glu	Gly	Val	Leu	Gly	Ile	Val	Ala	Ser	Lys	Leu	Val	Glu	Ala
				325					330					335	
Thr	Gln	Lys	Pro	Ser	Leu	Val	Phe	Thr	Phe	Lys	Glu	Gly	Val	Tyr	Lys
			340					345					350		
Gly	Ser	Ala	Arg	Ser	Ser	Ser	Asn	Ile	Asp	Leu	Ile	Asp	Ala	Leu	Asn
		355					360					365			
Gly	Val	Ser	Ser	Leu	Leu	Leu	Gly	Tyr	Gly	Gly	His	Arg	Gln	Ala	Cys
	370					375					380				
Gly	Leu	Ser	Val	Glu	Lys	Asn	Asn	Ile	Ile	Ser	Leu	Phe	Glu	Thr	Leu
385					390					395					400
Glu	Asn	Phe	Asp	Phe	Lys	Val	Leu	Pro	Phe	Cys	Lys	Thr	Glu	Pro	Pro
				405					410					415	
Leu	Thr	Leu	Lys	Leu	Lys	Asp	Ile	Asp	Arg	Glu	Leu	Leu	Glu	Ile	Ile
			420					425					430		
Glu	Met	Gly	Glu	Pro	Tyr	Gly	Gln	Glu	Asn	Pro	Glu	Pro	Leu	Phe	Gln
		435					440					445			
Ala	Lys	Asn	Leu	Glu	Val	Ile	Glu	Glu	Lys	Ile	Ile	Lys	Glu	Ser	His
	450					455					460				
Gln	Val	Leu	Arg	Phe	Lys	Asp	Lys	Glu	Cys	Val	Lys	Glu	Ala	Ile	Tyr
465					470					475					480
Phe	Ser	Ala	Glu	Arg	Phe	Leu	Lys	Ala	Gly	Glu	Lys	Val	Ser	Val	Leu
				485					490					495	
Phe	Ser	Val	Glu	Leu	Asp	Glu	Cys	Ser	Asn	Glu	Pro	Lys	Met	Phe	Val
			500					505					510		
Lys	Ser	Leu	Leu												

```
<220>
<221> CDS
<222> (51) ... (908)
```

-659-

165	170	175	
cct tat ttc acc cct tta cac	ccc ttg tta aaa gat	aaa agc tct aac	632
Pro Tyr Phe Thr Pro Leu His	Pro Leu Leu Lys Asp	Lys Ser Ser Asn	
180	185	190	
cac ctt tat cct att tta atg	cac caa aaa ttt ttt	aca tgc aaa aaa	680
His Leu Tyr Pro Ile Leu Met	His Gln Lys Phe Phe	Thr Cys Lys Lys	
195	200	205 210	
ctc att tta gaa agt ttg	cac aag cgt ggc att tta	gcc caa gtg cat	728
Leu Ile Leu Glu Ser Leu His	Lys Arg Gly Ile Leu	Ala Gln Val His	
215	220	225	
tac aag ccc att tat caa tac	caa ttg tac caa cag	ctc ttc aat aca	776
Tyr Lys Pro Ile Tyr Gln Tyr	Gln Leu Tyr Gln Gln	Leu Phe Asn Thr	
230	235	240	
gcc cca tta aaa agc gca gag	gat ttc tat cac gct	gaa att tcc ttg	824
Ala Pro Leu Lys Ser Ala Glu	Asp Phe Tyr His Ala	Glu Ile Ser Leu	
245	250	255	
cct tgt cat gcg aat tta aat	tta gag agc gtt caa	aac atc gct cat	872
Pro Cys His Ala Asn Leu Asn	Leu Glu Ser Val Gln	Asn Ile Ala His	
260	265	270	
agc gtt tta aaa act ttt gag	agt ttt aaa ata gaa	tgagtttcat	918
Ser Val Leu Lys Thr Phe Glu	Ser Phe Lys Ile Glu		
275	280	285	
ttagggccttc aaatcttaat	cattaagaat ggtgcggaag	aaa	961

<210> 552

<211> 286

<212> PRT

<213> Helicobacter pylori

<400> 552

Met Leu Leu Glu Ser Gly Tyr Thr Pro Val Phe Ala Gly Ile Lys Asn	
1 5 10 15	
Asp Gly Asn Ile Asp Glu Leu Ala Leu Glu Lys Leu Ile Asn Glu Arg	
20 25 30	
Thr Lys Ala Ile Val Ser Val Asp Tyr Ala Gly Lys Ser Val Glu Val	
35 40 45	
Glu Ser Val Gln Lys Leu Cys Lys Lys His Ser Leu Ser Phe Leu Ser	
50 55 60	
Asp Ser Ser His Ala Leu Gly Ser Glu Tyr Gln Asn Lys Lys Val Gly	
65 70 75 80	
Gly Phe Ala Leu Ala Ser Val Phe Ser Phe His Ala Ile Lys Pro Ile	
85 90 95	
Thr Thr Ala Glu Gly Gly Ala Val Val Thr Asn Asp Ser Glu Leu His	
100 105 110	
Glu Lys Met Lys Leu Phe Arg Ser His Gly Met Leu Lys Lys Asp Phe	
115 120 125	
Phe Glu Gly Glu Val Lys Ser Ile Gly His Asn Phe Arg Leu Asn Glu	
130 135 140	
Ile Gln Ser Ala Leu Gly Leu Ser Gln Leu Lys Lys Ala Pro Phe Leu	
145 150 155 160	
Met Gln Lys Arg Glu Glu Ala Ala Leu Thr Tyr Asp Arg Ile Phe Lys	

				165					170					175			
Asp	Asn	Pro	Tyr	Phe	Thr	Pro	Leu	His	Pro	Leu	Leu	Lys	Asp	Lys	Ser		
			180					185					190				
Ser	Asn	His	Leu	Tyr	Pro	Ile	Leu	Met	His	Gln	Lys	Phe	Phe	Thr	Cys		
		195					200					205					
Lys	Lys	Leu	Ile	Leu	Glu	Ser	Leu	His	Lys	Arg	Gly	Ile	Leu	Ala	Gln		
	210					215					220						
Val	His	Tyr	Lys	Pro	Ile	Tyr	Gln	Tyr	Gln	Leu	Tyr	Gln	Gln	Leu	Phe		
225					230					235					240		
Asn	Thr	Ala	Pro	Leu	Lys	Ser	Ala	Glu	Asp	Phe	Tyr	His	Ala	Glu	Ile		
			245					250						255			
Ser	Leu	Pro	Cys	His	Ala	Asn	Leu	Asn	Leu	Glu	Ser	Val	Gln	Asn	Ile		
		260					265						270				
Ala	His	Ser	Val	Leu	Lys	Thr	Phe	Glu	Ser	Phe	Lys	Ile	Glu				
		275					280						285				

<210> 553
 <211> 728
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (15)...(692)
 <221> misc_feature
 <222> 528
 <223> n = A,T,C or G

<400> 553
 taatgggcct ttga atg cgt ttt gtc tat cac cct tta gcc aaa gag cct 50
 Met Arg Phe Val Tyr His Pro Leu Ala Lys Glu Pro
 1 5 10

gtt tta aaa ata gaa ggc gag agt tat acg cat tta tac cga tca agc 98
 Val Leu Lys Ile Glu Gly Glu Ser Tyr Thr His Leu Tyr Arg Ser Arg
 15 20 25

cgt gtc aaa agt gcg agt cgt ttg gat ttg aga aat tta aaa gac ggc 146
 Arg Val Lys Ser Ala Ser Arg Leu Asp Leu Arg Asn Leu Lys Asp Gly
 30 35 40

ttt tta tac acc tat gag cat gca gaa atc act aaa aaa cac gcc ctt 194
 Phe Leu Tyr Thr Tyr Glu His Ala Glu Ile Thr Lys Lys His Ala Leu
 45 50 55 60

tta aag cta gtg ggc gcg cga tta tta gag gtt atg gcc agt aaa aaa 242
 Leu Lys Leu Val Gly Ala Arg Leu Leu Glu Val Met Ala Ser Lys Lys
 65 70 75

acg cat ttg att tta agc gtg att gaa atc aaa aac att gaa aaa atc 290
 Thr His Leu Ile Leu Ser Val Ile Glu Ile Lys Asn Ile Glu Lys Ile
 80 85 90

cta ccc ttt tta aat cag tta ggc gtg agc aag ttg agt tta ttc tat 338
 Leu Pro Phe Leu Asn Gln Leu Gly Val Ser Lys Leu Ser Leu Phe Tyr
 95 100 105

gcg gat ttt agc caa cgc aat gaa aaa ata gac atc gct aaa tta gag	386
Ala Asp Phe Ser Gln Arg Asn Glu Lys Ile Asp Ile Ala Lys Leu Glu	
110 115 120	

cgc ttt caa aag att ttg atc cat tct tgc gag cag tgt ggt agg agt	434
Arg Phe Gln Lys Ile Leu Ile His Ser Cys Glu Gln Cys Gly Arg Ser	
125 130 135 140	

gct tta atg gaa ttg gaa gtg ttt tca aac act aaa gag gcg cta aaa	482
Ala Leu Met Glu Leu Glu Val Phe Ser Asn Thr Lys Glu Ala Leu Lys	
145 150 155	

gcc tat cct aag gcg agc gtt ttg gat ttt aag ggc gaa acc tta ncc	530
Ala Tyr Pro Lys Ala Ser Val Leu Asp Phe Lys Gly Glu Thr Leu Xaa	
160 165 170	

gca agc gcg gat ttt gaa aag ggc gtt atc ata ggg cct gag ggg ggc	578
Ala Ser Ala Asp Phe Glu Lys Gly Val Ile Ile Gly Pro Glu Gly Gly	
175 180 185	

ttt agc gaa cca gaa aga ggg tat ttt aaa gag cgt gaa att tat cgc	626
Phe Ser Glu Pro Glu Arg Gly Tyr Phe Lys Glu Arg Glu Ile Tyr Arg	
190 195 200	

atc ccg tta gat atg gtg cta aag tct gag agt gca tgc gtg ttt gta	674
Ile Pro Leu Asp Met Val Leu Lys Ser Glu Ser Ala Cys Val Phe Val	
205 210 215 220	

gcg agt atc gca caa gtt tagggggggtta ttgggggattt taaatcctaa	722
Ala Ser Ile Ala Gln Val	
225	

aaaatc	728
--------	-----

<210> 554
 <211> 226
 <212> PRT
 <213> Helicobacter pylori

 <220>
 <221> VARIANT
 <222> 172
 <223> Xaa = Any Amino Acid

<400> 554	
Met Arg Phe Val Tyr His Pro Leu Ala Lys Glu Pro Val Leu Lys Ile	
1 5 10 15	
Glu Gly Glu Ser Tyr Thr His Leu Tyr Arg Ser Arg Arg Val Lys Ser	
20 25 30	
Ala Ser Arg Leu Asp Leu Arg Asn Leu Lys Asp Gly Phe Leu Tyr Thr	
35 40 45	
Tyr Glu His Ala Glu Ile Thr Lys Lys His Ala Leu Leu Lys Leu Val	
50 55 60	
Gly Ala Arg Leu Leu Glu Val Met Ala Ser Lys Lys Thr His Leu Ile	
65 70 75 80	
Leu Ser Val Ile Glu Ile Lys Asn Ile Glu Lys Ile Leu Pro Phe Leu	
85 90 95	
Asn Gln Leu Gly Val Ser Lys Leu Ser Leu Phe Tyr Ala Asp Phe Ser	
100 105 110	

Gln	Arg	Asn	Glu	Lys	Ile	Asp	Ile	Ala	Lys	Leu	Glu	Arg	Phe	Gln	Lys
		115					120					125			
Ile	Leu	Ile	His	Ser	Cys	Glu	Gln	Cys	Gly	Arg	Ser	Ala	Leu	Met	Glu
	130					135					140				
Leu	Glu	Val	Phe	Ser	Asn	Thr	Lys	Glu	Ala	Leu	Lys	Ala	Tyr	Pro	Lys
145					150					155					160
Ala	Ser	Val	Leu	Asp	Phe	Lys	Gly	Glu	Thr	Leu	Xaa	Ala	Ser	Ala	Asp
			165						170					175	
Phe	Glu	Lys	Gly	Val	Ile	Ile	Gly	Pro	Glu	Gly	Gly	Phe	Ser	Glu	Pro
			180					185					190		
Glu	Arg	Gly	Tyr	Phe	Lys	Glu	Arg	Glu	Ile	Tyr	Arg	Ile	Pro	Leu	Asp
	195						200					205			
Met	Val	Leu	Lys	Ser	Glu	Ser	Ala	Cys	Val	Phe	Val	Ala	Ser	Ile	Ala
	210					215					220				
Gln	Val														
225															

<210> 555
 <211> 888
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (13)...(840)

<400> 555
 ttatgaaatt ga atg acc ctt tcg caa gcc cta aac aaa gcc aaa aaa gga 51
 Met Thr Leu Ser Gln Ala Leu Asn Lys Ala Lys Lys Gly
 1 5 10

tta tcg caa aaa ggt ttt agg ggg ggc tta gaa tct gaa att tta tta 99
 Leu Ser Gln Lys Gly Phe Arg Gly Gly Leu Glu Ser Glu Ile Leu Leu
 15 20 25

ggc ttt gtc ttg caa aaa gaa agg gtt ttt ttg cac acg cat gcc tat 147
 Gly Phe Val Leu Gln Lys Glu Arg Val Phe Leu His Thr His Ala Tyr
 30 35 40 45

tta gag tta aac cac gaa gaa gag gtg cgt ttt ttt gaa ttg gta gaa 195
 Leu Glu Leu Asn His Glu Glu Glu Val Arg Phe Phe Glu Leu Val Glu
 50 55 60

aag cgc ttg aat aac tgc ccc ata gag tat tta tta gaa agc tgt gat 243
 Lys Arg Leu Asn Asn Cys Pro Ile Glu Tyr Leu Leu Glu Ser Cys Asp
 65 70 75

ttt tat ggg cgc tct ttt ttt gtg aat gag cat gtt tta atc cca cga 291
 Phe Tyr Gly Arg Ser Phe Phe Val Asn Glu His Val Leu Ile Pro Arg
 80 85 90

cct gaa acc gag att ttg gtc caa aaa gcc ctt gat att att tct caa 339
 Pro Glu Thr Glu Ile Leu Val Gln Lys Ala Leu Asp Ile Ile Ser Gln
 95 100 105

tac cat tta aaa gag ata ggc gaa atc ggc ata ggg agc gga tgc gtg 387
 Tyr His Leu Lys Glu Ile Gly Glu Ile Gly Ile Gly Ser Gly Cys Val
 110 115 120 125

tct gtg agt ttg gct tta gaa aac cct aat ctc tct att tat gcg agc 435
Ser Val Ser Leu Ala Leu Glu Asn Pro Asn Leu Ser Ile Tyr Ala Ser
130 135 140
gat att tca cca aac gct tta gaa gtg gcg tcc aaa aat att gag cac 483
Asp Ile Ser Pro Asn Ala Leu Glu Val Ala Ser Lys Asn Ile Glu His
145 150 155
ttt tgt cta aaa gag cgt gtt ttt tta aaa caa aca cgc ctt tgg gat 531
Phe Cys Leu Lys Glu Arg Val Phe Leu Lys Gln Thr Arg Leu Trp Asp
160 165 170
cat atg ccc atg ata gaa atg ctt gtc tct aac ccg ccc tat atc gct 579
His Met Pro Met Ile Glu Met Leu Val Ser Asn Pro Pro Tyr Ile Ala
175 180 185
aga aat tat cct ttg gaa aaa tcc gtc ctc aaa gaa ccg cat gaa gcc 627
Arg Asn Tyr Pro Leu Glu Lys Ser Val Leu Lys Glu Pro His Glu Ala
190 195 200 205
ctt ttt ggg ggg gtt aaa ggc gat gag atc tta aaa gaa atc gtt ttt 675
Leu Phe Gly Gly Val Lys Gly Asp Glu Ile Leu Lys Glu Ile Val Phe
210 215 220
tta gcc gct aaa tta aaa atc cct ttt ttg gtt tgt gaa atg ggg tat 723
Leu Ala Ala Lys Leu Lys Ile Pro Phe Leu Val Cys Glu Met Gly Tyr
225 230 235
gac cag ttg aaa agc ttg aaa gaa tgc ttg gaa ttt tgc ggt tat gat 771
Asp Gln Leu Lys Ser Leu Lys Glu Cys Leu Glu Phe Cys Gly Tyr Asp
240 245 250
gca gag ttt tac aag gat ttg agc ggc ttt gat aga ggg ttt gtg gcc 819
Ala Glu Phe Tyr Lys Asp Leu Ser Gly Phe Asp Arg Gly Phe Val Gly
255 260 265
gtt tta aaa agt ttt tta aga taaattaa cttaattacc ctttttagtgt 870
Val Leu Lys Ser Phe Leu Arg
270 275
tacaataaaa acacttaa 888

<210> 556

<211> 276

<212> PRT

<213> *Helicobacter pylori*

<400> 556

Met Thr Leu Ser Gln Ala Leu Asn Lys Ala Lys Lys Gly Leu Ser Gln
1 5 10 15
Lys Gly Phe Arg Gly Gly Leu Glu Ser Glu Ile Leu Leu Gly Phe Val
20 25 30
Leu Gln Lys Glu Arg Val Phe Leu His Thr His Ala Tyr Leu Glu Leu
35 40 45
Asn His Glu Glu Glu Val Arg Phe Phe Glu Leu Val Glu Lys Arg Leu
50 55 60
Asn Asn Cys Pro Ile Glu Tyr Leu Leu Glu Ser Cys Asp Phe Tyr Gly
65 70 75 80

Arg	Ser	Phe	Phe	Val	Asn	Glu	His	Val	Leu	Ile	Pro	Arg	Pro	Glu	Thr
				85					90					95	
Glu	Ile	Leu	Val	Gln	Lys	Ala	Leu	Asp	Ile	Ile	Ser	Gln	Tyr	His	Leu
			100					105					110		
Lys	Glu	Ile	Gly	Glu	Ile	Gly	Ile	Gly	Ser	Gly	Cys	Val	Ser	Val	Ser
		115					120					125			
Leu	Ala	Leu	Glu	Asn	Pro	Asn	Leu	Ser	Ile	Tyr	Ala	Ser	Asp	Ile	Ser
	130					135					140				
Pro	Asn	Ala	Leu	Glu	Val	Ala	Ser	Lys	Asn	Ile	Glu	His	Phe	Cys	Leu
145					150					155					160
Lys	Glu	Arg	Val	Phe	Leu	Lys	Gln	Thr	Arg	Leu	Trp	Asp	His	Met	Pro
			165						170					175	
Met	Ile	Glu	Met	Leu	Val	Ser	Asn	Pro	Pro	Tyr	Ile	Ala	Arg	Asn	Tyr
		180						185					190		
Pro	Leu	Glu	Lys	Ser	Val	Leu	Lys	Glu	Pro	His	Glu	Ala	Leu	Phe	Gly
	195						200					205			
Gly	Val	Lys	Gly	Asp	Glu	Ile	Leu	Lys	Glu	Ile	Val	Phe	Leu	Ala	Ala
	210					215					220				
Lys	Leu	Lys	Ile	Pro	Phe	Leu	Val	Cys	Glu	Met	Gly	Tyr	Asp	Gln	Leu
225					230					235					240
Lys	Ser	Leu	Lys	Glu	Cys	Leu	Glu	Phe	Cys	Gly	Tyr	Asp	Ala	Glu	Phe
			245						250					255	
Tyr	Lys	Asp	Leu	Ser	Gly	Phe	Asp	Arg	Gly	Phe	Val	Gly	Val	Leu	Lys
		260						265					270		
Ser	Phe	Leu	Arg												
		275													

<210> 557
 <211> 1026
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (28)...(960)

<400> 557
 ccattctcaaaa ataaggacgc ctaaattc atg gca gaa aaa aca gct aac gat tta 54
 Met Ala Glu Lys Thr Ala Asn Asp Leu
 1 5

aaa cta agt gag ata gaa ctc gtg gat ttt cgt att tat ggc atg caa 102
 Lys Leu Ser Glu Ile Glu Leu Val Asp Phe Arg Ile Tyr Gly Met Gln
 10 15 20 25

gag ggc gtc cct tat gag ggg att tat ggt atc aat gtg gct aaa gtc 150
 Glu Gly Val Pro Tyr Glu Gly Ile Tyr Gly Ile Asn Val Ala Lys Val
 30 35 40

caa gaa atc atc ccc atg ccc acc ctt ttt gaa tac ccc acg aat ttg 198
 Gln Glu Ile Ile Pro Met Pro Thr Leu Phe Glu Tyr Pro Thr Asn Leu
 45 50 55

gat tac att atc ggc gtg ttt gat ttg cgc tcc ata atc att ccg ctt 246
 Asp Tyr Ile Ile Gly Val Phe Asp Leu Arg Ser Ile Ile Ile Pro Leu
 60 65 70

ata gac ttg gct aaa tgg ata ggg att atc cca gat aaa agc aag gaa 294

Ile	Asp	Leu	Ala	Lys	Trp	Ile	Gly	Ile	Ile	Pro	Asp	Lys	Ser	Lys	Glu		
	75					80					85						
aac	gaa	aaa	atc	gtc	att	atc	act	gaa	ttt	aac	aac	gtt	aaa	atg	ggt	342	
Asn	Glu	Lys	Ile	Val	Ile	Ile	Thr	Glu	Phe	Asn	Asn	Val	Lys	Met	Gly	105	
	90				95					100							
ttt	tta	gtc	cat	tcg	gct	agg	cgt	atc	agg	cgc	att	agc	tggt	aaa	gat	390	
Phe	Leu	Val	His	Ser	Ala	Arg	Arg	Ile	Arg	Arg	Ile	Ser	Trp	Lys	Asp	120	
				110					115								
gtg	gag	cct	gca	tcc	ttt	agc	gcc	tct	aat	agc	atc	aat	aaa	gaa	aat	438	
Val	Glu	Pro	Ala	Ser	Phe	Ser	Ala	Ser	Asn	Ser	Ile	Asn	Lys	Glu	Asn		
			125				130						135				
att	acc	ggc	acg	aca	cgc	att	gaa	aac	gac	aaa	acc	ctg	ctc	att	ttg	486	
Ile	Thr	Gly	Thr	Thr	Arg	Ile	Glu	Asn	Asp	Lys	Thr	Leu	Leu	Ile	Leu		
	140						145					150					
gat	tta	gaa	agc	att	tta	gac	gat	tta	aag	ctt	aat	gaa	gac	gct	aaa	534	
Asp	Leu	Glu	Ser	Ile	Leu	Asp	Asp	Leu	Lys	Leu	Asn	Glu	Asp	Ala	Lys		
	155					160					165						
aac	gct	aaa	gat	acc	cat	aaa	gag	cgt	ttt	gaa	ggc	gaa	gtg	ttg	ttt	582	
Asn	Ala	Lys	Asp	Thr	His	Lys	Glu	Arg	Phe	Glu	Gly	Glu	Val	Leu	Phe		
	170				175					180					185		
tta	gac	gat	agc	aag	acc	gca	aga	aaa	acc	tta	aaa	aac	cat	ttg	agc	630	
Leu	Asp	Asp	Ser	Lys	Thr	Ala	Arg	Lys	Thr	Leu	Lys	Asn	His	Leu	Ser		
				190					195					200			
aaa	tta	ggt	ttt	agc	atc	act	gaa	gct	gtg	gat	ggg	gaa	gac	ggg	ttc	678	
Lys	Leu	Gly	Phe	Ser	Ile	Thr	Glu	Ala	Val	Asp	Gly	Glu	Asp	Gly	Leu		
			205					210					215				
aac	aaa	tta	gaa	atg	tta	ttc	aaa	aaa	tac	ggg	gac	gat	ttg	aga	aag	726	
Asn	Lys	Leu	Glu	Met	Leu	Phe	Lys	Lys	Tyr	Gly	Asp	Asp	Leu	Arg	Lys		
		220					225					230					
cat	ttg	aaa	ttc	att	att	tca	gat	gtt	gaa	atg	cct	aaa	atg	gat	gac	774	
His	Leu	Lys	Phe	Ile	Ile	Ser	Asp	Val	Glu	Met	Pro	Lys	Met	Asp	Gly		
	235					240					245						
tat	cat	ttc	tta	ttc	aag	ctc	caa	aaa	gac	cct	agg	ttt	gct	tat	att	822	
Tyr	His	Phe	Leu	Phe	Lys	Leu	Gln	Lys	Asp	Pro	Arg	Phe	Ala	Tyr	Ile		
	250				255					260					265		
cct	gtg	att	ttt	aat	tct	tct	att	tgc	gat	aat	tac	agc	gct	gaa	agg	870	
Pro	Val	Ile	Phe	Asn	Ser	Ser	Ile	Cys	Asp	Asn	Tyr	Ser	Ala	Glu	Arg		
				270					275					280			
gct	aaa	gaa	atg	ggg	gct	gta	gcg	tat	tta	gtc	aag	ttt	gac	gca	gaa	918	
Ala	Lys	Glu	Met	Gly	Ala	Val	Ala	Tyr	Leu	Val	Lys	Phe	Asp	Ala	Glu		
			285					290					295				
aaa	ttc	acc	gaa	gaa	att	tct	aag	att	tta	gac	aag	aat	gcc			960	
Lys	Phe	Thr	Glu	Glu	Ile	Ser	Lys	Ile	Leu	Asp	Lys	Asn	Ala				
		300					305					310					

taattctttt tataaaattg taaaatactc ttatctcaaa cgctaaaaaag gggtttttaa 1020
 tggatg 1026

<210> 558
 <211> 311
 <212> PRT
 <213> Helicobacter pylori

<400> 558
 Met Ala Glu Lys Thr Ala Asn Asp Leu Lys Leu Ser Glu Ile Glu Leu
 1 5 10 15
 Val Asp Phe Arg Ile Tyr Gly Met Gln Glu Gly Val Pro Tyr Glu Gly
 20 25 30
 Ile Tyr Gly Ile Asn Val Ala Lys Val Gln Glu Ile Ile Pro Met Pro
 35 40 45
 Thr Leu Phe Glu Tyr Pro Thr Asn Leu Asp Tyr Ile Ile Gly Val Phe
 50 55 60
 Asp Leu Arg Ser Ile Ile Ile Pro Leu Ile Asp Leu Ala Lys Trp Ile
 65 70 75 80
 Gly Ile Ile Pro Asp Lys Ser Lys Glu Asn Glu Lys Ile Val Ile Ile
 85 90 95
 Thr Glu Phe Asn Asn Val Lys Met Gly Phe Leu Val His Ser Ala Arg
 100 105 110
 Arg Ile Arg Arg Ile Ser Trp Lys Asp Val Glu Pro Ala Ser Phe Ser
 115 120 125
 Ala Ser Asn Ser Ile Asn Lys Glu Asn Ile Thr Gly Thr Thr Arg Ile
 130 135 140
 Glu Asn Asp Lys Thr Leu Leu Ile Leu Asp Leu Glu Ser Ile Leu Asp
 145 150 155 160
 Asp Leu Lys Leu Asn Glu Asp Ala Lys Asn Ala Lys Asp Thr His Lys
 165 170 175
 Glu Arg Phe Glu Gly Glu Val Leu Phe Leu Asp Asp Ser Lys Thr Ala
 180 185 190
 Arg Lys Thr Leu Lys Asn His Leu Ser Lys Leu Gly Phe Ser Ile Thr
 195 200 205
 Glu Ala Val Asp Gly Glu Asp Gly Leu Asn Lys Leu Glu Met Leu Phe
 210 215 220
 Lys Lys Tyr Gly Asp Asp Leu Arg Lys His Leu Lys Phe Ile Ile Ser
 225 230 235 240
 Asp Val Glu Met Pro Lys Met Asp Gly Tyr His Phe Leu Phe Lys Leu
 245 250 255
 Gln Lys Asp Pro Arg Phe Ala Tyr Ile Pro Val Ile Phe Asn Ser Ser
 260 265 270
 Ile Cys Asp Asn Tyr Ser Ala Glu Arg Ala Lys Glu Met Gly Ala Val
 275 280 285
 Ala Tyr Leu Val Lys Phe Asp Ala Glu Lys Phe Thr Glu Glu Ile Ser
 290 295 300
 Lys Ile Leu Asp Lys Asn Ala
 305 310

<210> 559
 <211> 753
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (32)...(697)

<400> 559

```
gatctataaa gaatagccat aaagaagaat t atg tta gat tat cgc caa aaa 52
                               Met Leu Asp Tyr Arg Gln Lys
                               1                               5

att gat gct ctc atc acc aaa ata gaa aag gct cgc acc gcc tat tca 100
Ile Asp Ala Leu Ile Thr Lys Ile Glu Lys Ala Arg Thr Ala Tyr Ser
          10          15          20

agg cac cac att gtc aaa atc gtg gct gtt tca aaa aac gct tcc cca 148
Arg His His Ile Val Lys Ile Val Ala Val Ser Lys Asn Ala Ser Pro
          25          30          35

gaa gct atc caa cat tat tat aac tgc tct caa agg gct ttt gga gaa 196
Glu Ala Ile Gln His Tyr Tyr Asn Cys Ser Gln Arg Ala Phe Gly Glu
          40          45          50          55

aat aaa gtt caa gat tta aaa act aaa atg cat tct tta gag cat ttg 244
Asn Lys Val Gln Asp Leu Lys Thr Lys Met His Ser Leu Glu His Leu
          60          65          70

ccc ctt gaa tgg cac atg ata ggc tct tta caa gaa aat aaa atc aat 292
Pro Leu Glu Trp His Met Ile Gly Ser Leu Gln Glu Asn Lys Ile Asn
          75          80          85

gcg ctt ttg agt tta aag ccc gct ctt ttg cat tct tta gac tct tta 340
Ala Leu Leu Ser Leu Lys Pro Ala Leu Leu His Ser Leu Asp Ser Leu
          90          95          100

aaa ctc gct ttg aaa ata gaa aag cgt tgc gaa ata ttg ggc gtc aat 388
Lys Leu Ala Leu Lys Ile Glu Lys Arg Cys Glu Ile Leu Gly Val Asn
          105          110          115

tta aac gct ctt tta cag gtt aat agc gcg tat gag gaa agt aaa agc 436
Leu Asn Ala Leu Leu Gln Val Asn Ser Ala Tyr Glu Glu Ser Lys Ser
          120          125          130          135

ggg gtg gtg cct gaa gaa gcg cta gaa att tat tct caa atc agt gaa 484
Gly Val Val Pro Glu Glu Ala Leu Glu Ile Tyr Ser Gln Ile Ser Glu
          140          145          150

act tgc aag cac ctc aag ctt aag ggg ctt atg tgt ata ggg gca cac 532
Thr Cys Lys His Leu Lys Leu Lys Gly Leu Met Cys Ile Gly Ala His
          155          160          165

aca gat gat gaa aag gaa att gaa aaa tcc ttt atc acc acc aaa aag 580
Thr Asp Asp Glu Lys Glu Ile Glu Lys Ser Phe Ile Thr Thr Lys Lys
          170          175          180

ctt ttt gac caa ata aag aat gcg agc gtt ctt tca atg ggc atg agt 628
Leu Phe Asp Gln Ile Lys Asn Ala Ser Val Leu Ser Met Gly Met Ser
          185          190          195

gat gat ttt gaa tta gcg att gct tgc ggg gcg aat ctt tta agg att 676
Asp Asp Phe Glu Leu Ala Ile Ala Cys Gly Ala Asn Leu Leu Arg Ile
          200          205          210          215

ggc tct ttt ttg ttc aaa gag taagatgcta gaaacttatg cacttaaaaa 727
Gly Ser Phe Leu Phe Lys Glu
```


tggggctggtt tttatctctg atgcgc

753

<210> 560

<211> 222

<212> PRT

<213> Helicobacter pylori

<400> 560

```

Met Leu Asp Tyr Arg Gln Lys Ile Asp Ala Leu Ile Thr Lys Ile Glu
 1          5          10          15
Lys Ala Arg Thr Ala Tyr Ser Arg His His Ile Val Lys Ile Val Ala
          20          25          30
Val Ser Lys Asn Ala Ser Pro Glu Ala Ile Gln His Tyr Tyr Asn Cys
          35          40          45
Ser Gln Arg Ala Phe Gly Glu Asn Lys Val Gln Asp Leu Lys Thr Lys
          50          55          60
Met His Ser Leu Glu His Leu Pro Leu Glu Trp His Met Ile Gly Ser
          65          70          75          80
Leu Gln Glu Asn Lys Ile Asn Ala Leu Leu Ser Leu Lys Pro Ala Leu
          85          90          95
Leu His Ser Leu Asp Ser Leu Lys Leu Ala Leu Lys Ile Glu Lys Arg
          100          105          110
Cys Glu Ile Leu Gly Val Asn Leu Asn Ala Leu Leu Gln Val Asn Ser
          115          120          125
Ala Tyr Glu Glu Ser Lys Ser Gly Val Val Pro Glu Glu Ala Leu Glu
          130          135          140
Ile Tyr Ser Gln Ile Ser Glu Thr Cys Lys His Leu Lys Leu Lys Gly
          145          150          155          160
Leu Met Cys Ile Gly Ala His Thr Asp Asp Glu Lys Glu Ile Glu Lys
          165          170          175
Ser Phe Ile Thr Thr Lys Lys Leu Phe Asp Gln Ile Lys Asn Ala Ser
          180          185          190
Val Leu Ser Met Gly Met Ser Asp Asp Phe Glu Leu Ala Ile Ala Cys
          195          200          205
Gly Ala Asn Leu Leu Arg Ile Gly Ser Phe Leu Phe Lys Glu
          210          215          220

```

<210> 561

<211> 1633

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (22)...(1593)

<400> 561

```

ttttaaatc aaaggataaa a atg tat caa gta gcc att tgc gac ccc atc      51
                        Met Tyr Gln Val Ala Ile Cys Asp Pro Ile
                        1          5          10

cat gct aaa ggc att caa att tta gaa gct caa aaa gac att gtc ttg      99
His Ala Lys Gly Ile Gln Ile Leu Glu Ala Gln Lys Asp Ile Val Leu
          15          20          25

cat gat tat tcc aaa tgc cct aaa aag gag ctt tta gaa aaa ctc aci     147

```

His	Asp	Tyr	Ser	Lys	Cys	Pro	Lys	Lys	Glu	Leu	Leu	Glu	Lys	Leu	Thr		
			30					35					40				
ccc	atg	gat	gcg	ctc	atc	act	cgc	agc	atg	acc	cct	atc	aca	agc	gat	195	
Pro	Met	Asp	Ala	Leu	Ile	Thr	Arg	Ser	Met	Thr	Pro	Ile	Thr	Ser	Asp		
		45					50				55						
ttt	tta	aag	ccc	tta	acc	cac	tta	aaa	tcc	atc	gtg	aga	gcg	ggc	gtc	243	
Phe	Leu	Lys	Pro	Leu	Thr	His	Leu	Lys	Ser	Ile	Val	Arg	Ala	Gly	Val		
	60					65					70						
gga	gtg	gat	aat	att	gat	tta	gaa	agc	tgc	tct	caa	aaa	ggg	att	gta	291	
Gly	Val	Asp	Asn	Ile	Asp	Leu	Glu	Ser	Cys	Ser	Gln	Lys	Gly	Ile	Val		
	75				80					85					90		
gtg	atg	aat	atc	cct	acc	gct	aac	acg	att	gcc	gct	gtg	gaa	ttg	acc	339	
Val	Met	Asn	Ile	Pro	Thr	Ala	Asn	Thr	Ile	Ala	Ala	Val	Glu	Leu	Thr		
				95					100					105			
atg	gcg	cat	ttg	atc	aat	gca	gtg	cgt	tcg	ttc	cct	tgt	gca	aac	gat	387	
Met	Ala	His	Leu	Ile	Asn	Ala	Val	Arg	Ser	Phe	Pro	Cys	Ala	Asn	Asp		
			110					115					120				
caa	atc	aaa	cac	caa	agg	tta	tgg	aaa	aga	gaa	gat	tgg	tat	ggc	acg	435	
Gln	Ile	Lys	His	Gln	Arg	Leu	Trp	Lys	Arg	Glu	Asp	Trp	Tyr	Gly	Thr		
		125					130					135					
gaa	ttg	aaa	aat	aaa	aag	ctg	gcc	atc	att	ggt	ttt	ggg	aat	att	ggc	483	
Glu	Leu	Lys	Asn	Lys	Lys	Leu	Gly	Ile	Ile	Gly	Phe	Gly	Asn	Ile	Gly		
	140					145					150						
tct	agg	gtg	ggc	att	aga	gca	aaa	gcc	ttt	gaa	atg	gaa	gtt	cta	gcc	531	
Ser	Arg	Val	Gly	Ile	Arg	Ala	Lys	Ala	Phe	Glu	Met	Glu	Val	Leu	Ala		
	155				160					165					170		
tat	gat	cct	tat	atc	cct	tct	tca	aaa	gcc	act	gat	tta	gga	gtc	att	579	
Tyr	Asp	Pro	Tyr	Ile	Pro	Ser	Ser	Lys	Ala	Thr	Asp	Leu	Gly	Val	Ile		
				175					180					185			
tac	acg	aaa	aat	ttt	gaa	gac	att	ttg	caa	tgc	gat	atg	atc	act	atc	627	
Tyr	Thr	Lys	Asn	Phe	Glu	Asp	Ile	Leu	Gln	Cys	Asp	Met	Ile	Thr	Ile		
			190					195					200				
cac	acc	cct	aaa	aat	aaa	gaa	acg	att	aac	atg	ata	ggt	gct	aaa	gag	675	
His	Thr	Pro	Lys	Asn	Lys	Glu	Thr	Ile	Asn	Met	Ile	Gly	Ala	Lys	Glu		
		205					210					215					
att	gag	cgc	atg	aaa	aaa	ggg	gtt	att	ttg	ctc	aat	tgc	gct	agg	ggt	723	
Ile	Glu	Arg	Met	Lys	Lys	Gly	Val	Ile	Leu	Leu	Asn	Cys	Ala	Arg	Gly		
	220					225					230						
ggg	ctt	tat	aat	gaa	gac	gct	ctt	tat	gag	gct	tta	gaa	acc	aaa	aaa	771	
Gly	Leu	Tyr	Asn	Glu	Asp	Ala	Leu	Tyr	Glu	Ala	Leu	Glu	Thr	Lys	Lys		
	235				240					245					250		
gtg	cgt	tgg	ctt	ggc	att	gat	gtc	ttt	tct	aaa	gag	cct	ggc	att	cac	819	
Val	Arg	Trp	Leu	Gly	Ile	Asp	Val	Phe	Ser	Lys	Glu	Pro	Gly	Ile	His		
				255					260					265			

aac aag ctt tta gac ttg ccc aat gtt tat gcg acc ccc cat att ggc	867
Asn Lys Leu Leu Asp Leu Pro Asn Val Tyr Ala Thr Pro His Ile Gly	
270 275 280	
gca aac act tta gaa tcc caa gaa gaa att tcc aaa caa gcc gct caa	915
Ala Asn Thr Leu Glu Ser Gln Glu Glu Ile Ser Lys Gln Ala Ala Gln	
285 290 295	
ggg gtt atg gaa tct tta agg ggt tca agc cac ccg cat gct ttg aat	963
Gly Val Met Glu Ser Leu Arg Gly Ser Ser His Pro His Ala Leu Asn	
300 305 310	
tta ccc atg caa gct ttt gac gcg agc gca aaa gcc tac ttg aat tta	1011
Leu Pro Met Gln Ala Phe Asp Ala Ser Ala Lys Ala Tyr Leu Asn Leu	
315 320 325 330	
gcg caa aaa ttg ggt tat ttt tcc agt caa atc cat aag ggc gtg tgc	1059
Ala Gln Lys Leu Gly Tyr Phe Ser Ser Gln Ile His Lys Gly Val Cys	
335 340 345	
caa aaa att gag ctc agt ctt tgt ggg gag atc aac caa ttt aaa gac	1107
Gln Lys Ile Glu Leu Ser Leu Cys Gly Glu Ile Asn Gln Phe Lys Asp	
350 355 360	
gct ctt gta gcc ttt atg tta gtg ggg gtg tta aaa cct gtt gta ggc	1155
Ala Leu Val Ala Phe Met Leu Val Gly Val Leu Lys Pro Val Val Gly	
365 370 375	
gat aaa atc aat tac att aac gcc ccc ttt gtg gcc aaa gaa aga ggt	1203
Asp Lys Ile Asn Tyr Ile Asn Ala Pro Phe Val Ala Lys Glu Arg Gly	
380 385 390	
att gag att aag gtt agc ctt aaa gaa agc gct tcg ccc tat aag aac	1251
Ile Glu Ile Lys Val Ser Leu Lys Glu Ser Ala Ser Pro Tyr Lys Asn	
395 400 405 410	
atg ctc tct tta acc ctc aat gcg gct aat ggc aca atc agc gtg agc	1299
Met Leu Ser Leu Thr Leu Asn Ala Ala Asn Gly Thr Ile Ser Val Ser	
415 420 425	
ggc acg gtg ttt gaa gaa gat att tta aaa ctc act gag att gat ggc	1347
Gly Thr Val Phe Glu Glu Asp Ile Leu Lys Leu Thr Glu Ile Asp Gly	
430 435 440	
ttt cat att gat ata gag cca aag ggt aaa atg ctt tta ttc agg aat	1395
Phe His Ile Asp Ile Glu Pro Lys Gly Lys Met Leu Leu Phe Arg Asn	
445 450 455	
acg gat att cca gcc gtt att ggg agt gtg ggc aat gcg ttc gct agc	1443
Thr Asp Ile Pro Gly Val Ile Gly Ser Val Gly Asn Ala Phe Ala Arg	
460 465 470	
cat ggc att aac atc gct gat ttt cgt ttg ggg cgt aac acg caa aaa	1491
His Gly Ile Asn Ile Ala Asp Phe Arg Leu Gly Arg Asn Thr Gln Lys	
475 480 485 490	
gaa gcc cta gca ctc att att gta gat gaa gaa gtt tct ttg gaa gtt	1539
Glu Ala Leu Ala Leu Ile Ile Val Asp Glu Glu Val Ser Leu Val	
495 500 505	

tta gaa gag ctt aaa aac att cct gcg tgc tta agc gtt cat tat gtg	1587
Leu Glu Glu Leu Lys Asn Ile Pro Ala Cys Leu Ser Val His Tyr Val	
510 515 520	

gtt att taaggtagtt ggatgcgaga ttttttaaaaa cttttaaaaa	1633
Val Ile	

<210> 562
 <211> 524
 <212> PRT
 <213> Helicobacter pylori

<400> 562

Met Tyr Gln Val Ala Ile Cys Asp Pro Ile His Ala Lys Gly Ile Gln	
1 5 10 15	
Ile Leu Glu Ala Gln Lys Asp Ile Val Leu His Asp Tyr Ser Lys Cys	
20 25 30	
Pro Lys Lys Glu Leu Leu Glu Lys Leu Thr Pro Met Asp Ala Leu Ile	
35 40 45	
Thr Arg Ser Met Thr Pro Ile Thr Ser Asp Phe Leu Lys Pro Leu Thr	
50 55 60	
His Leu Lys Ser Ile Val Arg Ala Gly Val Gly Val Asp Asn Ile Asp	
65 70 75 80	
Leu Glu Ser Cys Ser Gln Lys Gly Ile Val Val Met Asn Ile Pro Thr	
85 90 95	
Ala Asn Thr Ile Ala Ala Val Glu Leu Thr Met Ala His Leu Ile Asn	
100 105 110	
Ala Val Arg Ser Phe Pro Cys Ala Asn Asp Gln Ile Lys His Gln Arg	
115 120 125	
Leu Trp Lys Arg Glu Asp Trp Tyr Gly Thr Glu Leu Lys Asn Lys Lys	
130 135 140	
Leu Gly Ile Ile Gly Phe Gly Asn Ile Gly Ser Arg Val Gly Ile Arg	
145 150 155 160	
Ala Lys Ala Phe Glu Met Glu Val Leu Ala Tyr Asp Pro Tyr Ile Pro	
165 170 175	
Ser Ser Lys Ala Thr Asp Leu Gly Val Ile Tyr Thr Lys Asn Phe Glu	
180 185 190	
Asp Ile Leu Gln Cys Asp Met Ile Thr Ile His Thr Pro Lys Asn Lys	
195 200 205	
Glu Thr Ile Asn Met Ile Gly Ala Lys Glu Ile Glu Arg Met Lys Lys	
210 215 220	
Gly Val Ile Leu Leu Asn Cys Ala Arg Gly Gly Leu Tyr Asn Glu Asp	
225 230 235 240	
Ala Leu Tyr Glu Ala Leu Glu Thr Lys Lys Val Arg Trp Leu Gly Ile	
245 250 255	
Asp Val Phe Ser Lys Glu Pro Gly Ile His Asn Lys Leu Leu Asp Leu	
260 265 270	
Pro Asn Val Tyr Ala Thr Pro His Ile Gly Ala Asn Thr Leu Glu Ser	
275 280 285	
Gln Glu Glu Ile Ser Lys Gln Ala Ala Gln Gly Val Met Glu Ser Leu	
290 295 300	
Arg Gly Ser Ser His Pro His Ala Leu Asn Leu Pro Met Gln Ala Phe	
305 310 315 320	
Asp Ala Ser Ala Lys Ala Tyr Leu Asn Leu Ala Gln Lys Leu Gly Tyr	
325 330 335	
Phe Ser Ser Gln Ile His Lys Gly Val Cys Gln Lys Ile Glu Leu Ser	

tcc gaa aaa ggt gaa cac cct agc gtt tcc tac aaa aag gcc att tcc	342
Ser Glu Lys Gly Glu His Pro Ser Val Ser Tyr Lys Lys Ala Ile Ser	
90 95 100	
caa caa aag att caa gct aaa att gaa gaa tta ggc gaa aac tat gaa	390
Gln Gln Lys Ile Gln Ala Lys Ile Glu Glu Leu Gly Glu Asn Tyr Glu	
105 110 115	
aac gcc att att gaa ggc aag att gta ggc aag aat aaa ggg ggt tat	438
Asn Ala Ile Ile Glu Gly Lys Ile Val Gly Lys Asn Lys Gly Gly Tyr	
120 125 130 135	
atc gtg gag tct caa ggc gtg gag tat ttc ctc tcc cgc tcg cac tct	486
Ile Val Glu Ser Gln Gly Val Glu Tyr Phe Leu Ser Arg Ser His Ser	
140 145 150	
tct tta aag aat gac gca aac cat atc ggc aaa cgc gtt aaa gcg tgc	534
Ser Leu Lys Asn Asp Ala Asn His Ile Gly Lys Arg Val Lys Ala Cys	
155 160 165	
atc att cgt gtg gat aag gaa aac cat tct atc aat att tct cgc aaa	582
Ile Ile Arg Val Asp Lys Glu Asn His Ser Ile Asn Ile Ser Arg Lys	
170 175 180	
cga ttc ttt gaa gtc aat gac aaa cga caa ctt gag gtt tct aag gaa	630
Arg Phe Phe Glu Val Asn Asp Lys Arg Gln Leu Glu Val Ser Lys Glu	
185 190 195	
ttg tta gaa gcc aca gag ccg gtg tta ggg gtt gtg cgc cag atc acc	678
Leu Leu Glu Ala Thr Glu Pro Val Leu Gly Val Val Arg Gln Ile Thr	
200 205 210 215	
cct ttt ggc att ttt gta gaa gct aag ggg att gag ggc ttg gtc cat	726
Pro Phe Gly Ile Phe Val Glu Ala Lys Gly Ile Glu Gly Leu Val His	
220 225 230	
tat tct gaa atc agc cat aag gca cca gtc aat cct gaa aaa tac tac	774
Tyr Ser Glu Ile Ser His Lys Gly Pro Val Asn Pro Glu Lys Tyr Tyr	
235 240 245	
aaa gag ggc gat gaa gtc tat gtc aaa gcc atc gct tat gat gca gaa	822
Lys Glu Gly Asp Glu Val Tyr Val Lys Ala Ile Ala Tyr Asp Ala Glu	
250 255 260	
aaa aga cgc ctt tca ctc tcc ata aaa gcg act ata gaa gac cca tgg	870
Lys Arg Arg Leu Ser Leu Ser Ile Lys Ala Thr Ile Glu Asp Pro Trp	
265 270 275	
gaa gag att caa gac aag cta aaa ccc gga tac gcc att aag gta gtc	918
Glu Glu Ile Gln Asp Lys Leu Lys Pro Gly Tyr Ala Ile Lys Val Val	
280 285 290 295	
gtg agc aac att gaa cat tat ggg gtg ttt gtg gat att ggt aat gat	966
Val Ser Asn Ile Glu His Tyr Gly Val Phe Val Asp Ile Gly Asn Asp	
300 305 310	
att gaa ggc ttt ttg cat gtt tct gaa atc tct tgg gat aaa aat gtc	1014
Ile Glu Gly Phe Leu His Val Ser Glu Ile Ser Trp Asp Lys Asn Val	
315 320 325	

agc	cac	cct	aac	aat	tac	ttg	agc	gtg	ggg	caa	gag	att	gat	gtg	aaa	1062
Ser	His	Pro	Asn	Asn	Tyr	Leu	Ser	Val	Gly	Gln	Glu	Ile	Asp	Val	Lys	
		330					335					340				
atc	att	gac	att	gat	cca	aaa	aat	cgc	cgc	tta	agg	gtt	tct	tta	aac	1110
Ile	Ile	Asp	Ile	Asp	Pro	Lys	Asn	Arg	Arg	Leu	Arg	Val	Ser	Leu	Lys	
	345					350					355					
caa	ctc	act	aac	agg	cct	ttt	gat	gtt	ttt	gaa	tct	aaa	cac	caa	gtc	1158
Gln	Leu	Thr	Asn	Arg	Pro	Phe	Asp	Val	Phe	Glu	Ser	Lys	His	Gln	Val	
360					365					370					375	
ggg	gat	gtt	tta	gaa	ggc	aaa	gtg	gcg	act	tta	acg	gat	ttt	ggg	gcg	1206
Gly	Asp	Val	Leu	Glu	Gly	Lys	Val	Ala	Thr	Leu	Thr	Asp	Phe	Gly	Ala	
				380					385					390		
ttt	tta	aat	ctg	ggt	ggg	gtg	gat	ggt	ttg	ctc	cac	aat	cac	gac	gct	1254
Phe	Leu	Asn	Leu	Gly	Gly	Val	Asp	Gly	Leu	Leu	His	Asn	His	Asp	Ala	
		395						400					405			
ttt	tgg	gat	aaa	gat	aaa	aaa	tgc	aaa	gac	cac	tat	aaa	att	ggc	gat	1302
Phe	Trp	Asp	Lys	Asp	Lys	Lys	Cys	Lys	Asp	His	Tyr	Lys	Ile	Gly	Asp	
		410					415					420				
gtg	atc	aaa	gtg	aaa	atc	ctt	aaa	atc	aac	aaa	aaa	gat	aaa	aag	att	1350
Val	Ile	Lys	Val	Lys	Ile	Leu	Lys	Ile	Asn	Lys	Lys	Asp	Lys	Lys	Ile	
	425					430						435				
tct	ttg	agc	gcg	aag	cac	ttg	gtg	act	tcc	cct	aca	gaa	gaa	ttc	gct	1398
Ser	Leu	Ser	Ala	Lys	His	Leu	Val	Thr	Ser	Pro	Thr	Glu	Glu	Phe	Ala	
440					445					450					455	
caa	aag	cat	aaa	aca	gac	agc	gtg	att	caa	ggc	aaa	gtg	gtg	agt	att	1446
Gln	Lys	His	Lys	Thr	Asp	Ser	Val	Ile	Gln	Gly	Lys	Val	Val	Ser	Ile	
				460					465					470		
aag	gat	ttt	ggc	gtt	ttc	att	aat	gct	gat	ggc	att	gat	gtg	ctg	atc	1494
Lys	Asp	Phe	Gly	Val	Phe	Ile	Asn	Ala	Asp	Gly	Ile	Asp	Val	Leu	Ile	
		475						480					485			
aaa	aat	gaa	gat	ttg	aac	ccc	ttg	aaa	aaa	gat	gaa	att	aaa	ata	ggc	1542
Lys	Asn	Glu	Asp	Leu	Asn	Pro	Leu	Lys	Lys	Asp	Glu	Ile	Lys	Ile	Gly	
		490					495					500				
caa	gaa	atc	aca	tgc	gtg	gtg	gtt	gcg	att	gaa	aaa	tct	aac	aac	aac	1590
Gln	Glu	Ile	Thr	Cys	Val	Val	Val	Ala	Ile	Glu	Lys	Ser	Asn	Asn	Lys	
	505					510					515					
gtg	cgt	gct	tct	gtg	cat	agg	tta	gag	cgc	aaa	aaa	gaa	aaa	gaa	gaa	1638
Val	Arg	Ala	Ser	Val	His	Arg	Leu	Glu	Arg	Lys	Lys	Glu	Lys	Glu	Glu	
520					525					530					535	
ttg	caa	gct	ttt	aac	acg	agc	gat	gat	aaa	atg	act	tta	ggg	gat	att	1686
Leu	Gln	Ala	Phe	Asn	Thr	Ser	Asp	Asp	Lys	Met	Thr	Leu	Gly	Asp	Ile	
				540					545					550		
ctt	aaa	gaa	aaa	ctc	taa	agagtga	ttttaaaaagc	atgagaatgg	catgagattt							1741
Leu	Lys	Glu	Lys	Leu												

aagggtc

1748

<210> 564

<211> 556

<212> PRT

<213> *Helicobacter pylori*

<400> 564

```

Met Ser Lys Ile Ala Asp Asp Gln Asn Phe Asn Asp Glu Glu Glu Asn
 1      5      10      15
Phe Ala Lys Leu Phe Lys Lys Glu Leu Glu Lys Glu Glu Thr Leu Glu
 20      25      30
Lys Gly Thr Ile Lys Glu Gly Leu Val Val Ser Ile Asn Glu Asn Asp
 35      40      45
Gly Tyr Ala Met Val Ser Val Gly Gly Lys Thr Glu Gly Arg Leu Ala
 50      55      60
Leu Asn Glu Ile Thr Asp Glu Lys Gly Gln Leu Leu Tyr Gln Lys Asn
 65      70      75      80
Asp Pro Ile Ile Val His Val Ser Glu Lys Gly Glu His Pro Ser Val
 85      90      95
Ser Tyr Lys Lys Ala Ile Ser Gln Gln Lys Ile Gln Ala Lys Ile Glu
 100     105     110
Glu Leu Gly Glu Asn Tyr Glu Asn Ala Ile Ile Glu Gly Lys Ile Val
 115     120     125
Gly Lys Asn Lys Gly Gly Tyr Ile Val Glu Ser Gln Gly Val Glu Tyr
 130     135     140
Phe Leu Ser Arg Ser His Ser Ser Leu Lys Asn Asp Ala Asn His Ile
 145     150     155     160
Gly Lys Arg Val Lys Ala Cys Ile Ile Arg Val Asp Lys Glu Asn His
 165     170     175
Ser Ile Asn Ile Ser Arg Lys Arg Phe Phe Glu Val Asn Asp Lys Arg
 180     185     190
Gln Leu Glu Val Ser Lys Glu Leu Leu Glu Ala Thr Glu Pro Val Leu
 195     200     205
Gly Val Val Arg Gln Ile Thr Pro Phe Gly Ile Phe Val Glu Ala Lys
 210     215     220
Gly Ile Glu Gly Leu Val His Tyr Ser Glu Ile Ser His Lys Gly Pro
 225     230     235     240
Val Asn Pro Glu Lys Tyr Tyr Lys Glu Gly Asp Glu Val Tyr Val Lys
 245     250     255
Ala Ile Ala Tyr Asp Ala Glu Lys Arg Arg Leu Ser Leu Ser Ile Lys
 260     265     270
Ala Thr Ile Glu Asp Pro Trp Glu Glu Ile Gln Asp Lys Leu Lys Pro
 275     280     285
Gly Tyr Ala Ile Lys Val Val Val Ser Asn Ile Glu His Tyr Gly Val
 290     295     300
Phe Val Asp Ile Gly Asn Asp Ile Glu Gly Phe Leu His Val Ser Glu
 305     310     315     320
Ile Ser Trp Asp Lys Asn Val Ser His Pro Asn Asn Tyr Leu Ser Val
 325     330     335
Gly Gln Glu Ile Asp Val Lys Ile Ile Asp Ile Asp Pro Lys Asn Arg
 340     345     350
Arg Leu Arg Val Ser Leu Lys Gln Leu Thr Asn Arg Pro Phe Asp Val
 355     360     365
Phe Glu Ser Lys His Gln Val Gly Asp Val Leu Glu Gly Lys Val Ala
 370     375     380
Thr Leu Thr Asp Phe Gly Ala Phe Leu Asn Leu Gly Gly Val Asp Gly

```


385					390					395					400
Leu	Leu	His	Asn	His	Asp	Ala	Phe	Trp	Asp	Lys	Asp	Lys	Lys	Cys	Lys
				405					410					415	
Asp	His	Tyr	Lys	Ile	Gly	Asp	Val	Ile	Lys	Val	Lys	Ile	Leu	Lys	Ile
			420					425					430		
Asn	Lys	Lys	Asp	Lys	Lys	Ile	Ser	Leu	Ser	Ala	Lys	His	Leu	Val	Thr
		435					440					445			
Ser	Pro	Thr	Glu	Glu	Phe	Ala	Gln	Lys	His	Lys	Thr	Asp	Ser	Val	Ile
	450				455						460				
Gln	Gly	Lys	Val	Val	Ser	Ile	Lys	Asp	Phe	Gly	Val	Phe	Ile	Asn	Ala
465					470					475					480
Asp	Gly	Ile	Asp	Val	Leu	Ile	Lys	Asn	Glu	Asp	Leu	Asn	Pro	Leu	Lys
			485					490						495	
Lys	Asp	Glu	Ile	Lys	Ile	Gly	Gln	Glu	Ile	Thr	Cys	Val	Val	Val	Ala
		500					505					510			
Ile	Glu	Lys	Ser	Asn	Asn	Lys	Val	Arg	Ala	Ser	Val	His	Arg	Leu	Glu
		515					520					525			
Arg	Lys	Lys	Glu	Lys	Glu	Glu	Leu	Gln	Ala	Phe	Asn	Thr	Ser	Asp	Asp
	530				535						540				
Lys	Met	Thr	Leu	Gly	Asp	Ile	Leu	Lys	Glu	Lys	Leu				
545					550					555					

<210> 565

<211> 1636

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (43)...(1584)

<400> 565

aatttggggt	gttttaacag	aatgcaagct	tgaaggagaa	tc	atg	tcc	att	tca		54						
					Met	Ser	Ile	Ser								
cgc	aga	agt	atc	cta	aca	aaa	atc	cca	atc	gcg	ctc	gct	agc	gct	aat	102
Arg	Arg	Ser	Ile	Leu	Thr	Lys	Ile	Pro	Ile	Ala	Leu	Ala	Ser	Ala	Asn	
5					10					15					20	
gtt	ttg	aaa	gct	gtt	ggg	gtt	ttt	gaa	aaa	gta	gaa	tcc	att	ccg	cat	150
Val	Leu	Lys	Ala	Val	Gly	Val	Phe	Glu	Lys	Val	Glu	Ser	Ile	Pro	His	
				25					30					35		
gca	acg	cat	ttt	ggc	ccc	ttt	atc	gca	aag	gtt	caa	aat	gga	gtg	att	198
Ala	Thr	His	Phe	Gly	Pro	Phe	Ile	Ala	Lys	Val	Gln	Asn	Gly	Val	Ile	
			40					45					50			
aaa	gat	att	gtc	ccc	caa	aaa	agc	gat	tat	aac	cct	act	atg	atg	tta	246
Lys	Asp	Ile	Val	Pro	Gln	Lys	Ser	Asp	Tyr	Asn	Pro	Thr	Met	Met	Leu	
		55					60					65				
aaa	gcg	atg	gtt	gat	agg	gtg	tat	tca	gat	agt	agg	gtg	aag	tat	cct	294
Lys	Ala	Met	Val	Asp	Arg	Val	Tyr	Ser	Asp	Ser	Arg	Val	Lys	Tyr	Prc	
	70					75					80					
tgc	gtg	cgc	aag	agc	ttc	tta	gaa	aac	aaa	aaa	aac	cac	aaa	gaa	ttc	342
Cys	Val	Arg	Lys	Ser	Phe	Leu	Glu	Asn	Lys	Lys	Asn	His	Lys	Glu	Leu	

85	90	95	100	
cgc ggg aga gaa gag ttt gtg cgt gtg agt tgg gat gtg gcg ttg gai	390			
Arg Gly Arg Glu Glu Phe Val Arg Val Ser Trp Asp Val Ala Leu Asp				
105	110	115		
tta gcg gct aaa aag ctt aaa gaa atc cct aaa gaa aac att tat aat	438			
Leu Ala Ala Lys Lys Leu Lys Glu Ile Pro Lys Glu Asn Ile Tyr Asn				
120	125	130		
gcc agt tat ggt ggc tgg ggg cat gcg ggc agc ttg cat cgt tgc cat	486			
Ala Ser Tyr Gly Gly Trp Gly His Ala Gly Ser Leu His Arg Cys His				
135	140	145		
cat tta gca tgg cgt ttt ttt aac acg act tta gga ggg gct att ggc	534			
His Leu Ala Trp Arg Phe Phe Asn Thr Thr Leu Gly Gly Ala Ile Gly				
150	155	160		
act gat ggg gaa tat agt aat ggc gcg gcc gca aga ata aac cct atc	582			
Thr Asp Gly Glu Tyr Ser Asn Gly Ala Ala Ala Arg Ile Asn Pro Met				
165	170	175	180	
att gta ggg gat atg gaa gtt tat tgc caa caa acc acg cat gaa gag	630			
Ile Val Gly Asp Met Glu Val Tyr Ser Gln Gln Thr Thr His Glu Glu				
185	190	195		
atg att aaa aat tct aag gtg tat gtc atg tgg ggg gcg gat tta ctc	678			
Met Ile Lys Asn Cys Lys Val Tyr Val Met Trp Gly Ala Asp Leu Leu				
200	205	210		
aaq tgc aac cgc att gat tat ttt gtg cca aac cat gtc aat gac agc	726			
Lys Cys Asn Arg Ile Asp Tyr Phe Val Pro Asn His Val Asn Asp Ser				
215	220	225		
tac tac ccc aag tat aaa aga gct ggt att aaa ttc att agt atc gat	774			
Tyr Tyr Pro Lys Tyr Lys Arg Ala Gly Ile Lys Phe Ile Ser Ile Asp				
230	235	240		
ccc att tat acc gaa acc gct caa gcc ttt agt gct gaa tgg ata ccc	822			
Pro Ile Tyr Thr Glu Thr Ala Gln Ala Phe Ser Ala Glu Trp Ile Pro				
245	250	255	260	
att cgc cct aac act gat gta gcg tta atg cta ggc atg atg cat tat	870			
Ile Arg Pro Asn Thr Asp Val Ala Leu Met Leu Gly Met Met His Tyr				
265	270	275		
ctt tat acg agc aat caa tat gat aaa gcg ttt atc gct aaa tac act	918			
Leu Tyr Thr Ser Asn Gln Tyr Asp Lys Ala Phe Ile Ala Lys Tyr Thr				
280	285	290		
gat ggt ttt gat aaa ttt tta ccc tat ttg cta gga gag agc gat aat	966			
Asp Gly Phe Asp Lys Phe Leu Pro Tyr Leu Leu Gly Glu Ser Asp Asn				
295	300	305		
gcg cct aag act tta gaa tgg gcg tct caa atc act gga gtg agc gca	1014			
Ala Pro Lys Thr Leu Glu Trp Ala Ser Gln Ile Thr Gly Val Ser Ala				
310	315	320		
gaa aaa atc aaa gaa tta gcg gat ttg ttt gtt tct aaa cgc act ttt	1062			

Glu 325	Lys	Ile	Lys	Glu	Leu 330	Ala	Asp	Leu	Phe	Val 335	Ser	Lys	Arg	Thr	Phe 340	
tta gcg ggt aat tgg gcc atg caa aga gct cag tat ggc gag caa ccg	1110															
Leu Ala Gly Asn Trp Ala Met Gln Arg Ala Gln Tyr Gly Glu Gln Pro																
gat tgg gcg tta att gtt tta gct agc atg att ggt caa gtg ggc tta	1158															
Asp Trp Ala Leu Ile Val Leu Ala Ser Met Ile Gly Gln Val Gly Leu																
tcg ggt ggg ggc ttt ggc ttt tct atg cat tat gga ggg aac gct caa	1206															
Ser Gly Gly Gly Phe Gly Phe Ser Met His Tyr Gly Gly Asn Ala Gln																
gca agc tca ggg gca aga att gtt cct atg att tca caa ggg cat aat	1254															
Ala Ser Ser Gly Ala Arg Ile Val Pro Met Ile Ser Gln Gly His Asn																
tct gta aaa agc gtt att cca gca tct agg gtt tct gaa gcg att tta	1302															
Ser Val Lys Ser Val Ile Pro Ala Ser Arg Val Ser Glu Ala Ile Leu																
aat ccg gat aaa gaa att gat ttt atg ggc aaa aaa ctg aaa ttg cct	1350															
Asn Pro Asp Lys Glu Ile Asp Phe Met Gly Lys Lys Leu Lys Leu Pro																
aaa atc aaa atg att tat aat tgt ggg gcg gat tta tta ggc cat gaa	1398															
Lys Ile Lys Met Ile Tyr Asn Cys Gly Ala Asp Leu Leu Gly His Glu																
act gat aca aac gag ctg att cgc gct tta agg acc tta gat tgc gtc	1446															
Thr Asp Thr Asn Glu Leu Ile Arg Ala Leu Arg Thr Leu Asp Cys Val																
atc gtg cat gag cct tgg tgg cgc cta cgc caa aat ttg ctg ata ttg	1494															
Ile Val His Glu Pro Trp Trp Arg Leu Arg Gln Asn Leu Leu Ile Leu																
tct ttg ctt cca cta gca ctg tgg aaa gag atg ata ttg ctt ttg gag	1542															
Ser Leu Leu Pro Leu Ala Leu Trp Lys Glu Met Ile Leu Leu Leu Glu																
gga gtt att cta aga atg tgg ttt atg cca tgc gta agg tgg	1584															
Gly Val Ile Leu Arg Met Trp Phe Met Pro Cys Val Arg Trp																
tagagcctgt ttatgaatct aaagacgatt atgagatttt cagacagctt gc	1636															
<210> 566																
<211> 514																
<212> PRT																
<213> Helicobacter pylori																
<400> 566																
Met 1	Ser	Ile	Ser	Arg	Arg	Ser	Ile	Leu	Thr	Lys	Ile	Pro	Ile	Ala	Leu	
Ala	Ser	Ala	Asn	Val	Leu	Lys	Ala	Val	Gly	Val	Phe	Glu	Lys	Val	Glu	

Ser	Ile	Pro	His	Ala	Thr	His	Phe	Gly	Pro	Phe	Ile	Ala	Lys	Val	Gln
	35						40					45			
Asn	Gly	Val	Ile	Lys	Asp	Ile	Val	Pro	Gln	Lys	Ser	Asp	Tyr	Asn	Pro
	50					55					60				
Thr	Met	Met	Leu	Lys	Ala	Met	Val	Asp	Arg	Val	Tyr	Ser	Asp	Ser	Arg
65					70				75						80
Val	Lys	Tyr	Pro	Cys	Val	Arg	Lys	Ser	Phe	Leu	Glu	Asn	Lys	Lys	Asn
				85					90					95	
His	Lys	Glu	Leu	Arg	Gly	Arg	Glu	Glu	Phe	Val	Arg	Val	Ser	Trp	Asp
			100					105					110		
Val	Ala	Leu	Asp	Leu	Ala	Ala	Lys	Lys	Leu	Lys	Glu	Ile	Pro	Lys	Glu
		115					120					125			
Asn	Ile	Tyr	Asn	Ala	Ser	Tyr	Gly	Gly	Trp	Gly	His	Ala	Gly	Ser	Leu
	130					135					140				
His	Arg	Cys	His	His	Leu	Ala	Trp	Arg	Phe	Phe	Asn	Thr	Thr	Leu	Gly
145					150					155					160
Gly	Ala	Ile	Gly	Thr	Asp	Gly	Glu	Tyr	Ser	Asn	Gly	Ala	Ala	Ala	Arg
				165					170					175	
Ile	Asn	Pro	Met	Ile	Val	Gly	Asp	Met	Glu	Val	Tyr	Ser	Gln	Gln	Thr
			180					185					190		
Thr	His	Glu	Glu	Met	Ile	Lys	Asn	Cys	Lys	Val	Tyr	Val	Met	Trp	Gly
	195						200					205			
Ala	Asp	Leu	Leu	Lys	Cys	Asn	Arg	Ile	Asp	Tyr	Phe	Val	Pro	Asn	His
	210					215					220				
Val	Asn	Asp	Ser	Tyr	Tyr	Pro	Lys	Tyr	Lys	Arg	Ala	Gly	Ile	Lys	Phe
225					230					235					240
Ile	Ser	Ile	Asp	Pro	Ile	Tyr	Thr	Glu	Thr	Ala	Gln	Ala	Phe	Ser	Ala
			245						250					255	
Glu	Trp	Ile	Pro	Ile	Arg	Pro	Asn	Thr	Asp	Val	Ala	Leu	Met	Leu	Gly
			260					265					270		
Met	Met	His	Tyr	Leu	Tyr	Thr	Ser	Asn	Gln	Tyr	Asp	Lys	Ala	Phe	Ile
		275					280					285			
Ala	Lys	Tyr	Thr	Asp	Gly	Phe	Asp	Lys	Phe	Leu	Pro	Tyr	Leu	Leu	Gly
	290					295					300				
Glu	Ser	Asp	Asn	Ala	Pro	Lys	Thr	Leu	Glu	Trp	Ala	Ser	Gln	Ile	Thr
305					310					315					320
Gly	Val	Ser	Ala	Glu	Lys	Ile	Lys	Glu	Leu	Ala	Asp	Leu	Phe	Val	Ser
				325					330					335	
Lys	Arg	Thr	Phe	Leu	Ala	Gly	Asn	Trp	Ala	Met	Gln	Arg	Ala	Gln	Tyr
			340					345					350		
Gly	Glu	Gln	Pro	Asp	Trp	Ala	Leu	Ile	Val	Leu	Ala	Ser	Met	Ile	Gly
			355				360					365			
Gln	Val	Gly	Leu	Ser	Gly	Gly	Gly	Phe	Gly	Phe	Ser	Met	His	Tyr	Gly
	370					375					380				
Gly	Asn	Ala	Gln	Ala	Ser	Ser	Gly	Ala	Arg	Ile	Val	Pro	Met	Ile	Ser
385					390					395					400
Gln	Gly	His	Asn	Ser	Val	Lys	Ser	Val	Ile	Pro	Ala	Ser	Arg	Val	Ser
			405						410					415	
Glu	Ala	Ile	Leu	Asn	Pro	Asp	Lys	Glu	Ile	Asp	Phe	Met	Gly	Lys	Lys
			420					425					430		
Leu	Lys	Leu	Pro	Lys	Ile	Lys	Met	Ile	Tyr	Asn	Cys	Gly	Ala	Asp	Leu
	435						440					445			
Leu	Gly	His	Glu	Thr	Asp	Thr	Asn	Glu	Leu	Ile	Arg	Ala	Leu	Arg	Thr
	450					455					460				
Leu	Asp	Cys	Val	Ile	Val	His	Glu	Pro	Trp	Trp	Arg	Leu	Arg	Gln	Asn
465					470					475					480
Leu	Leu	Ile	Leu	Ser	Leu	Leu	Pro	Leu	Ala	Leu	Trp	Lys	Glu	Met	Ile
				485					490					495	
Leu	Leu	Leu	Glu	Gly	Val	Ile	Leu	Arg	Met	Trp	Phe	Met	Pro	Cys	Val

<210> 568
 <211> 162
 <212> PRT
 <213> Helicobacter pylori

<400> 568
 Met Asn Ile Phe Gln Thr Ser Leu Lys Cys Cys Val Gly Leu Val Leu
 1 5 10 15
 Ser Val Gly Val Leu Leu Gly Asp Ser Lys Ala Phe Lys Val Arg Val
 20 25 30
 Asp Lys Ser Leu Thr Pro Pro Phe Leu Asn Val Leu Ser Leu Ala Phe
 35 40 45
 Lys Gln Asp Met Lys Lys Glu Val Ile Phe Val Ile Thr Lys Ser Asn
 50 55 60
 Lys Leu Ser Lys Lys Val Leu Cys Asp Phe Asp Ala Phe Leu Leu Pro
 65 70 75 80
 Glu Thr Leu Met Ser Gly Met Pro Lys Lys Ala Leu Phe His Lys Glu
 85 90 95
 Phe Leu Phe Gln Ser Lys Glu Asn Lys Thr Leu Tyr Ala Phe Ser Leu
 100 105 110
 Ile Asp Ser Gln Tyr Cys Ser Lys Gly Gly Asn Tyr Arg Tyr Glu Leu
 115 120 125
 Glu Lys Leu Glu Arg Trp Phe Val Gln Lys Ala Pro Glu Leu Ala Glu
 130 135 140
 Ser Tyr Arg Val Asn Tyr Lys Asn Gln Tyr Asn Lys Thr Gln Ile Ser
 145 150 155 160
 Gln Lys

<210> 569
 <211> 1572
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (25)...(1548)

<400> 569
 tctcacaaaa ataaagaatg agcg atg att tta gta tta gat ttt ggg agt 51
 Met Ile Leu Val Leu Asp Phe Gly Ser
 1 5
 caa tac aca cag ctg att gct aga aga ttg aga gag aga ggg att tat 99
 Gln Tyr Thr Gln Leu Ile Ala Arg Arg Leu Arg Glu Arg Gly Ile Tyr
 10 15 20 25
 aca gaa ata gtc cct ttt ttt gaa agc ata gaa aac att caa aaa aaa 147
 Thr Glu Ile Val Pro Phe Phe Glu Ser Ile Glu Asn Ile Gln Lys Lys
 30 35 40
 gcc ccc aaa ggt ttg att ttg agt ggg ggg cca gcg agc gtg tat gct 195
 Ala Pro Lys Gly Leu Ile Leu Ser Gly Gly Pro Ala Ser Val Tyr Ala
 45 50 55
 aaa gac gct tac aag cct agt ggg aaa atc ttt gat ttg aat gtg ccg 243

Lys	Asp	Ala	Tyr	Lys	Pro	Ser	Gly	Lys	Ile	Phe	Asp	Leu	Asn	Val	Pro		
		60					65					70					
att	tta	ggg	att	tgc	tac	ggc	atg	cag	tat	ttg	gtg	gat	ttt	ttt	ggc	291	
Ile	Leu	Gly	Ile	Cys	Tyr	Gly	Met	Gln	Tyr	Leu	Val	Asp	Phe	Phe	Gly		
	75					80					85						
ggg	gta	gtg	gtt	ggt	gcg	aat	gag	caa	gaa	ttt	ggt	aag	gct	gtt	tta	339	
Gly	Val	Val	Val	Gly	Ala	Asn	Glu	Gln	Glu	Phe	Gly	Lys	Ala	Val	Leu		
	90				95					100					105		
gaa	atc	act	caa	aat	tct	gtg	att	ttt	gaa	ggc	gtg	aag	att	aaa	agc	387	
Glu	Ile	Thr	Gln	Asn	Ser	Val	Ile	Phe	Glu	Gly	Val	Lys	Ile	Lys	Ser		
				110					115					120			
ctt	gtg	tgg	atg	agc	cat	atg	gat	aaa	gtc	ata	gaa	ctg	cct	aaa	goc	435	
Leu	Val	Trp	Met	Ser	His	Met	Asp	Lys	Val	Ile	Glu	Leu	Pro	Lys	Gly		
				125				130					135				
ttt	act	acc	ctt	gca	aaa	agc	cct	aat	tcc	ccc	cat	tgc	gcg	att	gaa	483	
Phe	Thr	Thr	Leu	Ala	Lys	Ser	Pro	Asn	Ser	Pro	His	Cys	Ala	Ile	Glu		
			140				145					150					
aac	ggc	aag	att	ttt	ggc	ttg	caa	ttc	cac	cca	gaa	gtc	gtt	caa	agc	531	
Asn	Gly	Lys	Ile	Phe	Gly	Leu	Gln	Phe	His	Pro	Glu	Val	Val	Gln	Ser		
	155					160					165						
gaa	gaa	ggg	ggt	aag	att	tta	gaa	aat	ttt	gcc	ctt	tta	gtt	tgc	goc	579	
Glu	Glu	Gly	Gly	Lys	Ile	Leu	Glu	Asn	Phe	Ala	Leu	Leu	Val	Cys	Gly		
	170				175					180					185		
tgt	gaa	aaa	act	tgg	ggg	atg	cag	cat	ttc	gct	caa	aga	gaa	atc	gca	627	
Cys	Glu	Lys	Thr	Trp	Gly	Met	Gln	His	Phe	Ala	Gln	Arg	Glu	Ile	Ala		
				190				195						200			
cga	ttg	aaa	gaa	aaa	atc	gct	aac	gct	aag	gtt	ttg	tgc	gcg	gtg	agt	675	
Arg	Leu	Lys	Glu	Lys	Ile	Ala	Asn	Ala	Lys	Val	Leu	Cys	Ala	Val	Ser		
			205				210						215				
ggg	goc	gtg	gat	tct	acg	gtg	gtc	gct	acg	ctg	ttg	cac	aga	gcc	att	725	
Gly	Gly	Val	Asp	Ser	Thr	Val	Val	Ala	Thr	Leu	Leu	His	Arg	Ala	Ile		
		220					225					230					
aag	gat	aat	ttg	atc	gct	gtt	ttt	gtg	gat	cat	ggc	ttg	ttg	cgt	aaa	771	
Lys	Asp	Asn	Leu	Ile	Ala	Val	Phe	Val	Asp	His	Gly	Leu	Leu	Arg	Lys		
	235					240					245						
aat	gaa	aaa	gaa	agg	gtg	caa	gcg	atg	ttt	aag	gac	ttg	aaa	atc	cct	819	
Asn	Glu	Lys	Glu	Arg	Val	Gln	Ala	Met	Phe	Lys	Asp	Leu	Lys	Ile	Pro		
	250				255					260					265		
tta	aac	acg	ata	gac	gct	aaa	gaa	gtc	ttt	ttg	tct	aaa	tta	aag	goc	867	
Leu	Asn	Thr	Ile	Asp	Ala	Lys	Glu	Val	Phe	Leu	Ser	Lys	Leu	Lys	Gly		
				270					275						280		
gtg	agc	gag	cct	gaa	ttg	aag	cga	aaa	atc	atc	ggc	gag	acc	ttt	att	915	
Val	Ser	Glu	Pro	Glu	Leu	Lys	Arg	Lys	Ile	Ile	Gly	Glu	Thr	Phe	Ile		
			285					290					295				

gaa gtg ttt gaa aaa gaa gcc aaa aag cac cat tta aaa ggc aaa att Glu Val Phe Glu Lys Glu Ala Lys Lys His His Leu Lys Gly Lys Ile 300 305 310	963
gaa ttt tta gcc caa ggc act tta tac cct gat gtg att gaa tcc gtg Glu Phe Leu Ala Gln Gly Thr Leu Tyr Pro Asp Val Ile Glu Ser Val 315 320 325	1011
agc gtt aaa ggg cct tca aaa gtg atc aaa acc cat cat aat gtg ggc Ser Val Lys Gly Pro Ser Lys Val Ile Lys Thr His His Asn Val Gly 330 335 340 345	1059
gga ctg cct gaa tgg atg gat ttt aaa ctc ata gag cct tta agg gag Gly Leu Pro Glu Trp Met Asp Phe Lys Leu Ile Glu Pro Leu Arg Glu 350 355 360	1107
ttg ttt aaa gat gag gtg cgc tta ctg ggt aaa gaa ttg ggc gtt agt Leu Phe Lys Asp Glu Val Arg Leu Leu Gly Lys Glu Leu Gly Val Ser 365 370 375	1155
cag gat ttt tta atg cgc cac cct ttt cca ggg cct ggg ctt gct gta Gln Asp Phe Leu Met Arg His Pro Phe Pro Gly Pro Gly Leu Ala Val 380 385 390	1203
agg att tta ggc gaa atc agt gag agt aag atc aaa cgc ttg caa gaa Arg Ile Leu Gly Glu Ile Ser Glu Ser Lys Ile Lys Arg Leu Gln Glu 395 400 405	1251
gcg gat ttt att ttt ata gag gaa ctt aaa aaa gcc aat ttg tat gac Ala Asp Phe Ile Phe Ile Glu Glu Leu Lys Lys Ala Asn Leu Tyr Asp 410 415 420 425	1299
aag ctt tgc caa gct ttt tgc gtg ctg ttg aat gtc aat tct gtg ggc Lys Val Trp Gln Ala Phe Cys Val Leu Leu Asn Val Asn Ser Val Gly 430 435 440	1347
gtt atg ggg gat aac cgc act tat gaa aac gct att tgc tta aga gcg Val Met Gly Asp Asn Arg Thr Tyr Glu Asn Ala Ile Cys Leu Arg Ala 445 450 455	1395
gta aat gcg agc gat ggc atg acg gcg agc ttt tca ttt tta gag cat Val Asn Ala Ser Asp Gly Met Thr Ala Ser Phe Ser Phe Leu Glu His 460 465 470	1443
tct ttt tta gaa aag gtt tct aac cgt atc act aat gaa gtg agc ggt Ser Phe Leu Glu Lys Val Ser Asn Arg Ile Thr Asn Glu Val Ser Gly 475 480 485	1491
atc aat agg gtg gtg tat gac att acc tct aaa cca cca gga acg att Ile Asn Arg Val Val Tyr Asp Ile Thr Ser Lys Pro Pro Gly Thr Ile 490 495 500 505	1539
gaa tgg gaa tgattatctt aaaaaatagc acta Glu Trp Glu	1572

<210> 570

<211> 506

<212> PRT

<213> Helicobacter pylori

<400> 570

Met	Ile	Leu	Val	Leu	Asp	Phe	Gly	Ser	Gln	Tyr	Thr	Gln	Leu	Ile	Ala
1				5					10					15	
Arg	Arg	Leu	Arg	Glu	Arg	Gly	Ile	Tyr	Thr	Glu	Ile	Val	Pro	Phe	Phe
		20						25					30		
Glu	Ser	Ile	Glu	Asn	Ile	Gln	Lys	Lys	Ala	Pro	Lys	Gly	Leu	Ile	Leu
		35					40					45			
Ser	Gly	Gly	Pro	Ala	Ser	Val	Tyr	Ala	Lys	Asp	Ala	Tyr	Lys	Pro	Ser
	50					55					60				
Gly	Lys	Ile	Phe	Asp	Leu	Asn	Val	Pro	Ile	Leu	Gly	Ile	Cys	Tyr	Gly
65					70					75					80
Met	Gln	Tyr	Leu	Val	Asp	Phe	Phe	Gly	Gly	Val	Val	Val	Gly	Ala	Asn
				85					90					95	
Glu	Gln	Glu	Phe	Gly	Lys	Ala	Val	Leu	Glu	Ile	Thr	Gln	Asn	Ser	Val
			100					105					110		
Ile	Phe	Glu	Gly	Val	Lys	Ile	Lys	Ser	Leu	Val	Trp	Met	Ser	His	Met
	115						120					125			
Asp	Lys	Val	Ile	Glu	Leu	Pro	Lys	Gly	Phe	Thr	Thr	Leu	Ala	Lys	Ser
	130					135					140				
Pro	Asn	Ser	Pro	His	Cys	Ala	Ile	Glu	Asn	Gly	Lys	Ile	Phe	Gly	Leu
145					150					155					160
Gln	Phe	His	Pro	Glu	Val	Val	Gln	Ser	Glu	Glu	Gly	Gly	Lys	Ile	Leu
			165						170					175	
Glu	Asn	Phe	Ala	Leu	Leu	Val	Cys	Gly	Cys	Glu	Lys	Thr	Trp	Gly	Met
		180						185					190		
Gln	His	Phe	Ala	Gln	Arg	Glu	Ile	Ala	Arg	Leu	Lys	Glu	Lys	Ile	Ala
	195					200						205			
Asn	Ala	Lys	Val	Leu	Cys	Ala	Val	Ser	Gly	Gly	Val	Asp	Ser	Thr	Val
210					215						220				
Val	Ala	Thr	Leu	Leu	His	Arg	Ala	Ile	Lys	Asp	Asn	Leu	Ile	Ala	Val
225					230					235					240
Phe	Val	Asp	His	Gly	Leu	Leu	Arg	Lys	Asn	Glu	Lys	Glu	Arg	Val	Gln
			245						250					255	
Ala	Met	Phe	Lys	Asp	Leu	Lys	Ile	Pro	Leu	Asn	Thr	Ile	Asp	Ala	Lys
		260						265					270		
Glu	Val	Phe	Leu	Ser	Lys	Leu	Lys	Gly	Val	Ser	Glu	Pro	Glu	Leu	Lys
	275						280					285			
Arg	Lys	Ile	Ile	Gly	Glu	Thr	Phe	Ile	Glu	Val	Phe	Glu	Lys	Glu	Ala
	290					295					300				
Lys	Lys	His	His	Leu	Lys	Gly	Lys	Ile	Glu	Phe	Leu	Ala	Gln	Gly	Thr
305				310						315					320
Leu	Tyr	Pro	Asp	Val	Ile	Glu	Ser	Val	Ser	Val	Lys	Gly	Pro	Ser	Lys
			325						330					335	
Val	Ile	Lys	Thr	His	His	Asn	Val	Gly	Gly	Leu	Pro	Glu	Trp	Met	Asp
		340						345					350		
Phe	Lys	Leu	Ile	Glu	Pro	Leu	Arg	Glu	Leu	Phe	Lys	Asp	Glu	Val	Arg
	355						360					365			
Leu	Leu	Gly	Lys	Glu	Leu	Gly	Val	Ser	Gln	Asp	Phe	Leu	Met	Arg	His
	370					375					380				
Pro	Phe	Pro	Gly	Pro	Gly	Leu	Ala	Val	Arg	Ile	Leu	Gly	Glu	Ile	Ser
385					390					395					400
Glu	Ser	Lys	Ile	Lys	Arg	Leu	Gln	Glu	Ala	Asp	Phe	Ile	Phe	Ile	Glu
			405						410					415	
Glu	Leu	Lys	Lys	Ala	Asn	Leu	Tyr	Asp	Lys	Val	Trp	Gln	Ala	Phe	Cys
			420					425					430		
Val	Leu	Leu	Asn	Val	Asn	Ser	Val	Gly	Val	Met	Gly	Asp	Asn	Arg	Thr

140	145	150	
aaa ggg gag ctg gtg ttg gat acc tta atc att gat tcg ccc tta gac			532
Lys Gly Glu Leu Val Leu Asp Thr Leu Ile Ile Asp Ser Pro Leu Asp			
155	160	165	
atc gcc ctt tgc cct aaa aaa act tat gct aaa atg aaa aat gtt tat			580
Ile Ala Leu Cys Pro Lys Lys Thr Tyr Ala Lys Met Lys Asn Val Tyr			
170	175	180	185
ttt atc ccc agt gtt agc gcg tta aaa ggg tgg tgc gaa agg gta ggg			628
Phe Ile Pro Ser Val Ser Ala Leu Lys Gly Trp Cys Glu Arg Val Gly			
	190	195	200
ttt gaa aat ttt gag att ctt agc gtt tta aag acc acg cct aaa gaa			676
Phe Glu Asn Phe Glu Ile Leu Ser Val Leu Lys Thr Thr Pro Lys Glu			
	205	210	215
cag cgt aaa acg gat ttt att ttg ggg cag agt ttg gaa gat ttt ttg			724
Gln Arg Lys Thr Asp Phe Ile Leu Gly Gln Ser Leu Glu Asp Phe Leu			
	220	225	230
gat aaa aca gat ccc tct aaa act tta gag ggg tat gac gcc cct tta			772
Asp Lys Thr Asp Pro Ser Lys Thr Leu Glu Gly Tyr Asp Ala Pro Leu			
	235	240	245
agg ggg tat ttt aaa atg ctt aaa cca agc aag cgt taaataaagg			818
Arg Gly Tyr Phe Lys Met Leu Lys Pro Ser Lys Arg			
250	255	260	

attaagatag tgcaag 834

<210> 572

<211> 261

<212> PRT

<213> Helicobacter pylori

<400> 572

Met Leu Ile Cys Asn Asp Lys Ser Asn Pro Lys Thr Leu Leu Glu Glu			
1	5	10	15
Ile Met Ala Leu Arg Pro Trp Arg Lys Gly Pro Phe Glu Ile Ser Gln			
	20	25	30
Ile Lys Ile Asp Ser Glu Trp Asp Ser Ser Ile Lys Trp Asp Leu Val			
	35	40	45
Lys Asn Ala Thr Pro Leu Lys Asp Lys Val Val Ala Asp Val Gly Cys			
	50	55	60
Asn Asn Gly Tyr Tyr Leu Phe Lys Met Leu Glu His Gly Pro Lys Ser			
65	70	75	80
Leu Val Gly Phe Asp Pro Gly Val Leu Val Lys Lys Gln Phe Glu Phe			
	85	90	95
Leu Ala Pro Phe Phe Asp Lys Glu Lys Lys Ile Ile Tyr Glu Ser Leu			
	100	105	110
Gly Val Glu Asp Leu His Glu Lys Tyr Pro Asn Ala Phe Asp Val Ile			
	115	120	125
Phe Cys Leu Gly Val Leu Tyr His Arg Lys Ser Pro Leu Glu Ala Leu			
	130	135	140
Lys Ala Leu Tyr His Ala Leu Lys Ile Lys Gly Glu Leu Val Leu Asp			
145	150	155	160
Thr Leu Ile Ile Asp Ser Pro Leu Asp Ile Ala Leu Cys Pro Lys Lys			

				165					170					175			
Thr	Tyr	Ala	Lys	Met	Lys	Asn	Val	Tyr	Phe	Ile	Pro	Ser	Val	Ser	Ala		
			180					185					190				
Leu	Lys	Gly	Trp	Cys	Glu	Arg	Val	Gly	Phe	Glu	Asn	Phe	Glu	Ile	Leu		
		195					200					205					
Ser	Val	Leu	Lys	Thr	Thr	Pro	Lys	Glu	Gln	Arg	Lys	Thr	Asp	Phe	Ile		
	210					215					220						
Leu	Gly	Gln	Ser	Leu	Glu	Asp	Phe	Leu	Asp	Lys	Thr	Asp	Pro	Ser	Lys		
225					230					235					240		
Thr	Leu	Glu	Gly	Tyr	Asp	Ala	Pro	Leu	Arg	Gly	Tyr	Phe	Lys	Met	Leu		
			245					250						255			
Lys	Pro	Ser	Lys	Arg													
			260														

<210> 573

<211> 1224

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (31)...(1197)

<400> 573

ttaaattcaa	ttttaaagaa	gagtagttaa	atg gtt att gtt tta gtc gtg gat	54
			Met Val Ile Val Leu Val Val Asp	
			1 5	
agt ttt aaa gac acc agt aat ggc act tct atg aca gcg ttt cgt ttt	102			
Ser Phe Lys Asp Thr Ser Asn Gly Thr Ser Met Thr Ala Phe Arg Phe				
10 15 20				
ttt gaa gcg ctg aaa aaa aga ggg cat gtg atg aga gtg gtc gcc cct	150			
Phe Glu Ala Leu Lys Lys Arg Gly His Val Met Arg Val Val Ala Pro				
25 30 35 40				
cat gtg gat aat tta ggg agt gaa gaa gag ggg tat tac aac ctt aaa	198			
His Val Asp Asn Leu Gly Ser Glu Glu Glu Gly Tyr Tyr Asn Leu Lys				
45 50 55				
gag cgc tac atc ccc cta gtt aca gaa att tca cac aaa caa cac atc	246			
Glu Arg Tyr Ile Pro Leu Val Thr Glu Ile Ser His Lys Gln His Ile				
60 65 70				
ctt ttt gct aaa ccc gat gaa aaa atc tta aga aag gct ttt aag gga	294			
Leu Phe Ala Lys Pro Asp Glu Lys Ile Leu Arg Lys Ala Phe Lys Gly				
75 80 85				
gcg gat atg atc cat act tat ttg cct ttt ttg cta gaa aaa aca gcc	342			
Ala Asp Met Ile His Thr Tyr Leu Pro Phe Leu Leu Glu Lys Thr Ala				
90 95 100				
gta aaa atc gcg cga gaa atg caa gtg cct tat att ggc tct ttc cat	390			
Val Lys Ile Ala Arg Glu Met Gln Val Pro Tyr Ile Gly Ser Phe His				
105 110 115 120				
tta cag cca gag cat att tct tat aac atg aaa ttg ggg tgg ttt tct	438			
Leu Gln Pro Glu His Ile Ser Tyr Asn Met Lys Leu Gly Trp Phe Ser				

125							130							135							
tgg	ttc	aac	atg	atg	ctt	ttt	tcg	tgg	ttt	aaa	tct	tcg	cat	tac	cgc	486					
Trp	Phe	Asn	Met	Met	Leu	Phe	Ser	Trp	Phe	Lys	Ser	Ser	His	Tyr	Arg						
		140						145					150								
tat	atc	cac	cat	atc	cat	tgc	ccg	tca	aaa	ttc	att	gta	gaa	gaa	tta	534					
Tyr	Ile	His	His	Ile	His	Cys	Pro	Ser	Lys	Phe	Ile	Val	Glu	Glu	Leu						
		155					160					165									
gaa	aaa	tac	aac	tat	gga	ggg	aaa	aaa	tac	gct	att	tct	aac	ggc	ttt	582					
Glu	Lys	Tyr	Asn	Tyr	Gly	Gly	Lys	Lys	Tyr	Ala	Ile	Ser	Asn	Gly	Phe						
	170					175					180										
gat	ccc	atg	ttt	aga	ttt	gaa	cac	ccg	caa	aaa	agc	ctt	ttt	gac	acc	630					
Asp	Pro	Met	Phe	Arg	Phe	Glu	His	Pro	Gln	Lys	Ser	Leu	Phe	Asp	Thr						
185					190				195					200							
aca	ccc	ttt	aaa	atc	gct	atg	gta	gga	cgc	tat	tct	aat	gaa	aaa	aat	678					
Thr	Pro	Phe	Lys	Ile	Ala	Met	Val	Gly	Arg	Tyr	Ser	Asn	Glu	Lys	Asn						
			205					210					215								
caa	agc	gtt	tta	atc	aaa	gcg	gtt	gct	tta	agc	aaa	tac	aaa	caa	gat	726					
Gln	Ser	Val	Leu	Ile	Lys	Ala	Val	Ala	Leu	Ser	Lys	Tyr	Lys	Gln	Asp						
		220					225					230									
att	gta	tta	ttc	ctc	aaa	ggc	aaa	ggg	cct	gat	gag	aaa	aaa	atc	aaa	774					
Ile	Val	Leu	Leu	Leu	Lys	Gly	Lys	Gly	Pro	Asp	Glu	Lys	Lys	Ile	Lys						
		235				240					245										
ctt	tta	gcc	caa	aaa	cta	ggc	gta	aaa	gcg	gag	ttt	ggc	ttt	gtc	aat	822					
Leu	Leu	Ala	Gln	Lys	Leu	Gly	Val	Lys	Ala	Glu	Phe	Gly	Phe	Val	Asn						
	250					255					260										
tcc	aat	gaa	ttg	tta	gag	atc	tta	aaa	act	tgc	acc	ctt	tat	gtg	cat	870					
Ser	Asn	Glu	Leu	Leu	Glu	Ile	Leu	Lys	Thr	Cys	Thr	Leu	Tyr	Val	His						
265					270				275					280							
gca	gcc	aat	gtg	gaa	agc	gaa	gcg	att	gcg	tgc	tta	gag	gcc	att	agc	918					
Ala	Ala	Asn	Val	Glu	Ser	Glu	Ala	Ile	Ala	Cys	Leu	Glu	Ala	Ile	Ser						
			285				290					295									
gtg	ggg	att	gtg	cct	gtt	atc	gct	aat	agc	cct	tta	agc	gcg	acc	agc	966					
Val	Gly	Ile	Val	Pro	Val	Ile	Ala	Asn	Ser	Pro	Leu	Ser	Ala	Thr	Arg						
		300					305					310									
caa	ttt	gcg	cta	gat	gaa	cga	tcg	cta	ttt	gaa	cct	aat	aac	gct	aaa	1014					
Gln	Phe	Ala	Leu	Asp	Glu	Arg	Ser	Leu	Phe	Glu	Pro	Asn	Asn	Ala	Lys						
		315					320					325									
gat	ttg	agc	gct	aaa	ata	gat	tgg	tgg	tta	gaa	aac	aag	ctt	gaa	aga	1062					
Asp	Leu	Ser	Ala	Lys	Ile	Asp	Trp	Trp	Leu	Glu	Asn	Lys	Leu	Glu	Arg						
	330					335					340										
gaa	agg	atg	caa	aac	gaa	tac	gct	aaa	agc	gct	tta	aat	tac	act	tta	1110					
Glu	Arg	Met	Gln	Asn	Glu	Tyr	Ala	Lys	Ser	Ala	Leu	Asn	Tyr	Thr	Leu						
345					350				355						360						
gaa	aat	tca	gtc	att	caa	att	gaa	aaa	gtt	tat	gaa	gaa	gcg	atc	aga	1158					

Glu Asn Ser Val Ile Gln Ile Glu Lys Val Tyr Glu Glu Ala Ile Arg
 365 370 375

gat ttt aaa aat aac ccc cat ctc ttt aaa acc tta tca taatgaaagc 1207
 Asp Phe Lys Asn Asn Pro His Leu Phe Lys Thr Leu Ser
 380 385

ataaaaaatg caagaac 1224

<210> 574

<211> 389

<212> PRT

<213> Helicobacter pylori

<400> 574

Met	Val	Ile	Val	Leu	Val	Val	Asp	Ser	Phe	Lys	Asp	Thr	Ser	Asn	Gly
1				5					10					15	
Thr	Ser	Met	Thr	Ala	Phe	Arg	Phe	Phe	Glu	Ala	Leu	Lys	Lys	Arg	Gly
			20					25					30		
His	Val	Met	Arg	Val	Val	Ala	Pro	His	Val	Asp	Asn	Leu	Gly	Ser	Glu
		35					40					45			
Glu	Glu	Gly	Tyr	Tyr	Asn	Leu	Lys	Glu	Arg	Tyr	Ile	Pro	Leu	Val	Thr
	50				55						60				
Glu	Ile	Ser	His	Lys	Gln	His	Ile	Leu	Phe	Ala	Lys	Pro	Asp	Glu	Lys
65					70					75				80	
Ile	Leu	Arg	Lys	Ala	Phe	Lys	Gly	Ala	Asp	Met	Ile	His	Thr	Tyr	Leu
				85					90					95	
Pro	Phe	Leu	Leu	Glu	Lys	Thr	Ala	Val	Lys	Ile	Ala	Arg	Glu	Met	Gln
			100					105					110		
Val	Pro	Tyr	Ile	Gly	Ser	Phe	His	Leu	Gln	Pro	Glu	His	Ile	Ser	Tyr
		115					120					125			
Asn	Met	Lys	Leu	Gly	Trp	Phe	Ser	Trp	Phe	Asn	Met	Met	Leu	Phe	Ser
	130					135					140				
Trp	Phe	Lys	Ser	Ser	His	Tyr	Arg	Tyr	Ile	His	His	Ile	His	Cys	Pro
145					150					155					160
Ser	Lys	Phe	Ile	Val	Glu	Glu	Leu	Glu	Lys	Tyr	Asn	Tyr	Gly	Gly	Lys
				165					170					175	
Lys	Tyr	Ala	Ile	Ser	Asn	Gly	Phe	Asp	Pro	Met	Phe	Arg	Phe	Glu	His
			180					185					190		
Pro	Gln	Lys	Ser	Leu	Phe	Asp	Thr	Thr	Pro	Phe	Lys	Ile	Ala	Met	Val
		195					200					205			
Gly	Arg	Tyr	Ser	Asn	Glu	Lys	Asn	Gln	Ser	Val	Leu	Ile	Lys	Ala	Val
	210					215					220				
Ala	Leu	Ser	Lys	Tyr	Lys	Gln	Asp	Ile	Val	Leu	Leu	Leu	Lys	Gly	Lys
225					230					235					240
Gly	Pro	Asp	Glu	Lys	Lys	Ile	Lys	Leu	Leu	Ala	Gln	Lys	Leu	Gly	Val
				245					250					255	
Lys	Ala	Glu	Phe	Gly	Phe	Val	Asn	Ser	Asn	Glu	Leu	Leu	Glu	Ile	Leu
			260					265					270		
Lys	Thr	Cys	Thr	Leu	Tyr	Val	His	Ala	Ala	Asn	Val	Glu	Ser	Glu	Ala
		275					280					285			
Ile	Ala	Cys	Leu	Glu	Ala	Ile	Ser	Val	Gly	Ile	Val	Pro	Val	Ile	Ala
	290					295					300				
Asn	Ser	Pro	Leu	Ser	Ala	Thr	Arg	Gln	Phe	Ala	Leu	Asp	Glu	Arg	Ser
305					310					315					320
Leu	Phe	Glu	Pro	Asn	Asn	Ala	Lys	Asp	Leu	Ser	Ala	Lys	Ile	Asp	Trp
				325					330					335	
Trp	Leu	Glu	Asn	Lys	Leu	Glu	Arg	Glu	Arg	Met	Gln	Asn	Glu	Tyr	Ala
			340					345					350		

Lys Ser Ala Leu Asn Tyr Thr Leu Glu Asn Ser Val Ile Gln Ile Glu
 355 360 365
 Lys Val Tyr Glu Glu Ala Ile Arg Asp Phe Lys Asn Asn Pro His Leu
 370 375 380
 Phe Lys Thr Leu Ser
 385

<210> 575
 <211> 947
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (16)...(903)

<400> 575
 tagaaaagggt agttt atg gag tta gaa gaa att gtt gat agt gag agg aat 51
 Met Glu Leu Glu Glu Ile Val Asp Ser Glu Arg Asn
 1 5 10

 atc cat aag act ata gaa gtt tta gga aaa ggc gga cag ggt ata gtg 99
 Ile His Lys Thr Ile Glu Val Leu Gly Lys Gly Gly Gln Gly Ile Val
 15 20 25

 tat cgc tgt ttg gat aag gat gtg gct att aag gta gta ttg agg gat 147
 Tyr Arg Cys Leu Asp Lys Asp Val Ala Ile Lys Val Val Leu Arg Asp
 30 35 40

 gga gat ttt att aaa gac aaa gaa tcc ctc aaa caa tat gaa aaa agc 195
 Gly Asp Phe Ile Lys Asp Lys Glu Ser Leu Lys Gln Tyr Glu Lys Ser
 45 50 55 60

 gtt cta aac tta tct ttt aag ccg ata gag agt cat ttc cct atg tca 243
 Val Leu Asn Leu Ser Phe Lys Pro Ile Glu Ser His Phe Pro Met Ser
 65 70 75

 att cca ctg gta act ttg aaa gaa aaa caa ggc tat gtg atg aaa atg 293
 Ile Pro Leu Val Thr Leu Lys Glu Lys Gln Gly Tyr Val Met Lys Met
 80 85 90

 gct gag ggc tat gaa cca cta aaa act ttt tta aag aag ccc agc att 339
 Ala Glu Gly Tyr Glu Pro Leu Lys Thr Phe Leu Lys Lys Pro Ser Ile
 95 100 105

 tta gaa aac gaa gaa aaa gat ggg att ttt agg atc aat aat gcc att 387
 Leu Glu Asn Glu Glu Lys Asp Gly Ile Phe Arg Ile Asn Asn Ala Ile
 110 115 120

 caa gaa ctt tgc aaa gat aac cat tat atg act tta agt tta agt tat 435
 Gln Glu Leu Cys Lys Asp Asn His Tyr Met Thr Leu Ser Leu Ser Tyr
 125 130 135 140

 tac tca caa aca caa gga ttg aga tca cga tta aaa ata ctc acc cat 483
 Tyr Ser Gln Thr Gln Gly Leu Arg Ser Arg Leu Lys Ile Leu Thr His
 145 150 155

 tta gca aaa ctt cta ttc aga ttg caa agt aag ggt ttg gtg tat ggg 531

Leu	Ala	Lys	Leu	Leu	Phe	Arg	Leu	Gln	Ser	Lys	Gly	Leu	Val	Tyr	Gly		
			160					165					170				
gac	ttg	aat	tta	aac	aat	gtt	ttt	tat	aaa	gac	aat	tca	gcg	ttt	tta	579	
Asp	Leu	Asn	Leu	Asn	Asn	Val	Phe	Tyr	Lys	Asp	Asn	Ser	Ala	Phe	Leu		
		175					180					185					
att	gat	gcg	gat	aat	gtg	cgt	tat	gag	agc	gaa	aaa	gcc	ctg	tgt	gtt	627	
Ile	Asp	Ala	Asp	Asn	Val	Arg	Tyr	Glu	Ser	Glu	Lys	Ala	Leu	Cys	Val		
	190					195					200						
att	ttt	acg	cct	aac	tat	ggg	gct	tta	gag	att	agc	caa	acc	tct	aaa	675	
Ile	Phe	Thr	Pro	Asn	Tyr	Gly	Ala	Leu	Glu	Ile	Ser	Gln	Thr	Ser	Lys		
205					210				215						220		
aat	agc	gat	aca	acc	aat	tac	aac	acc	atg	ctt	agc	gat	acc	ttt	tct	723	
Asn	Ser	Asp	Thr	Thr	Asn	Tyr	Asn	Thr	Met	Leu	Ser	Asp	Thr	Phe	Ser		
				225					230					235			
ttt	gct	atc	ata	act	tat	gaa	ctt	tta	aat	atg	gtt	cat	cct	ttt	gat	771	
Phe	Ala	Ile	Ile	Thr	Tyr	Glu	Leu	Leu	Asn	Met	Val	His	Pro	Phe	Asp		
			240				245						250				
ggg	aat	aag	gca	gat	gat	agt	gta	gaa	aat	ttt	ata	gaa	ttg	cct	tgg	819	
Gly	Asn	Lys	Ala	Asp	Asp	Ser	Val	Glu	Asn	Phe	Ile	Glu	Leu	Pro	Trp		
		255					260					265					
att	gaa	gat	aga	aag	gat	gat	agc	aat	cgt	tct	tgt	ggc	tta	ctg	cct	867	
Ile	Glu	Asp	Arg	Lys	Asp	Asp	Ser	Asn	Arg	Ser	Cys	Gly	Leu	Leu	Pro		
	270					275					280						
ttt	ttc	tta	aca	agg	gat	tta	aaa	aat	tta	tta	gcg	taatgctttg				913	
Phe	Phe	Leu	Thr	Arg	Asp	Leu	Lys	Asn	Leu	Leu	Ala						
285					290					295							
aagaaggcaa	aaaagatcct	ttgaaacgcc	ctac													947	

<210> 576

<211> 296

<212> PRT

<213> Helicobacter pylori

<400> 576

Met	Glu	Leu	Glu	Glu	Ile	Val	Asp	Ser	Glu	Arg	Asn	Ile	His	Lys	Thr		
1				5					10					15			
Ile	Glu	Val	Leu	Gly	Lys	Gly	Gly	Gln	Gly	Ile	Val	Tyr	Arg	Cys	Leu		
		20					25						30				
Asp	Lys	Asp	Val	Ala	Ile	Lys	Val	Val	Leu	Arg	Asp	Gly	Asp	Phe	Ile		
		35					40					45					
Lys	Asp	Lys	Glu	Ser	Leu	Lys	Gln	Tyr	Glu	Lys	Ser	Val	Leu	Asn	Leu		
	50					55					60						
Ser	Phe	Lys	Pro	Ile	Glu	Ser	His	Phe	Pro	Met	Ser	Ile	Pro	Leu	Val		
65					70				75						80		
Thr	Leu	Lys	Glu	Lys	Gln	Gly	Tyr	Val	Met	Lys	Met	Ala	Glu	Gly	Tyr		
			85					90						95			
Glu	Pro	Leu	Lys	Thr	Phe	Leu	Lys	Lys	Pro	Ser	Ile	Leu	Glu	Asn	Glu		
		100					105						110				
Glu	Lys	Asp	Gly	Ile	Phe	Arg	Ile	Asn	Asn	Ala	Ile	Gln	Glu	Leu	Cys		
		115					120						125				

Lys	Asp	Asn	His	Tyr	Met	Thr	Leu	Ser	Leu	Ser	Tyr	Tyr	Ser	Gln	Thr
130						135					140				
Gln	Gly	Leu	Arg	Ser	Arg	Leu	Lys	Ile	Leu	Thr	His	Leu	Ala	Lys	Leu
145					150					155					160
Leu	Phe	Arg	Leu	Gln	Ser	Lys	Gly	Leu	Val	Tyr	Gly	Asp	Leu	Asn	Leu
			165						170					175	
Asn	Asn	Val	Phe	Tyr	Lys	Asp	Asn	Ser	Ala	Phe	Leu	Ile	Asp	Ala	Asp
		180						185					190		
Asn	Val	Arg	Tyr	Glu	Ser	Glu	Lys	Ala	Leu	Cys	Val	Ile	Phe	Thr	Pro
	195						200					205			
Asn	Tyr	Gly	Ala	Leu	Glu	Ile	Ser	Gln	Thr	Ser	Lys	Asn	Ser	Asp	Thr
	210					215					220				
Thr	Asn	Tyr	Asn	Thr	Met	Leu	Ser	Asp	Thr	Phe	Ser	Phe	Ala	Ile	Ile
225					230					235					240
Thr	Tyr	Glu	Leu	Leu	Asn	Met	Val	His	Pro	Phe	Asp	Gly	Asn	Lys	Ala
				245					250					255	
Asp	Asp	Ser	Val	Glu	Asn	Phe	Ile	Glu	Leu	Pro	Trp	Ile	Glu	Asp	Arg
			260					265					270		
Lys	Asp	Asp	Ser	Asn	Arg	Ser	Cys	Gly	Leu	Leu	Pro	Phe	Phe	Leu	Thr
	275						280					285			
Arg	Asp	Leu	Lys	Asn	Leu	Leu	Ala								
	290					295									

<210> 577

<211> 509

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (44)...(469)

<400> 577

atgctttgaa	gaaggcaaaa	aagatccttt	gaaacgccct	act	atg	ccc	tta	ttt	55
					Met	Pro	Leu	Phe	
ata	gag	agc	tta	gaa	aaa	gct	agc	ttg	caa
Ile	Glu	Ser	Leu	Glu	Lys	Ala	Ser	Leu	Gln
5					10				15
gta	gag	gag	gag	gag	gag	gag	gag	gag	gag
Cys	Ser	Met	Thr	Tyr	Tyr	Asp	Arg	Asp	Tyr
			25					30	
gta	gag	gag	gag	gag	gag	gag	gag	gag	gag
Cys	Pro	Tyr	Cys	Asp	Ala	Lys	Lys	Pro	Val
			40					45	
gta	gag	gag	gag	gag	gag	gag	gag	gag	gag
Tyr	Tyr	Gln	Lys	Ser	Glu	Val	Phe	Tyr	Phe
		55					60		
cct	att	ttt	tta	ccg	aca	acc	tta	ttt	aag
Pro	Ile	Phe	Leu	Pro	Thr	Thr	Leu	Phe	Lys
	70					75			80
agc	gaa	tgg	gag	ttt	gca	gag	att	gct	aat

Ser Glu Trp Glu Phe Ala Glu Ile Ala Asn Asn Ile Leu Ile Phe His
85 90 95 100

cat gac ata caa caa gaa aag att ctc att aat aat aaa aga ttg gat 391
His Asp Ile Gln Gln Glu Lys Ile Leu Ile Asn Asn Lys Arg Leu Asp
105 110 115

cac tat agg ata gaa ata gat tta gaa aaa gaa ttg act att tca tac 439
His Tyr Arg Ile Glu Ile Asp Leu Glu Lys Glu Leu Thr Ile Ser Tyr
120 125 130

aat ggt ttt tta att aag gtt caa aaa tgc tgagttttat caaagaagat 489
Asn Gly Phe Leu Ile Lys Val Gln Lys Cys
135 140

agcatcatca aggcttataa 509

<210> 578
<211> 142
<212> PRT
<213> Helicobacter pylori

<400> 578

Met Pro Leu Phe Ile Glu Ser Leu Glu Lys Ala Ser Leu Gln Val Leu
1 5 10 15
Glu Cys Glu Asn Cys Ser Met Thr Tyr Tyr Asp Arg Asp Tyr Asn Arg
20 25 30
Glu Cys Glu Ile Cys Pro Tyr Cys Asp Ala Lys Lys Pro Val Arg Leu
35 40 45
Val Ala Thr Ser Tyr Tyr Gln Lys Ser Glu Val Phe Tyr Phe Val Ser
50 55 60
Asn Phe Thr Asp Pro Ile Phe Leu Pro Thr Thr Leu Phe Lys Gly Ile
65 70 75 80
Glu Val Val Lys Ser Glu Trp Glu Phe Ala Glu Ile Ala Asn Asn Ile
85 90 95
Leu Ile Phe His His Asp Ile Gln Gln Glu Lys Ile Leu Ile Asn Asn
100 105 110
Lys Arg Leu Asp His Tyr Arg Ile Glu Ile Asp Leu Glu Lys Glu Leu
115 120 125
Thr Ile Ser Tyr Asn Gly Phe Leu Ile Lys Val Gln Lys Cys
130 135 140

<210> 579
<211> 1260
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (27)...(1193)

<400> 579

aatggttttt taattaagggt tcaaaa atg ctg agt ttt atc aaa gaa gat agc 53
Met Leu Ser Phe Ile Lys Glu Asp Ser
1 5

atc atc aag gct tat aac ctc aat acc gca aaa cta gag cca aaa gat 101
Ile Ile Lys Ala Tyr Asn Leu Asn Thr Ala Lys Leu Glu Pro Lys Asp

10	15	20	25	
aga gaa aaa ttg gga tta tta aag att gaa aaa aat aaa ata tat ttt	149			
Arg Glu Lys Leu Gly Leu Leu Lys Ile Glu Lys Asn Lys Ile Tyr Phe				
30 35 40				
cat cta gat gaa aag cgt tat ttg aaa tta gag atc ata ggc aaa acc	197			
His Leu Asp Glu Lys Arg Tyr Leu Lys Leu Glu Ile Ile Gly Lys Thr				
45 50 55				
aaa gaa aaa gaa att aaa aac gct ttt tgc agt aat gct ttt ctt gca	245			
Lys Glu Lys Glu Ile Lys Asn Ala Phe Cys Ser Asn Ala Phe Leu Ala				
60 65 70				
gct caa gtc cta aat tta aac caa gaa aga caa gtt tta gaa ttg aag	293			
Ala Gln Val Leu Asn Leu Asn Gln Glu Arg Gln Val Leu Glu Leu Lys				
75 80 85				
tgc cat ttc ttc aag cac cct ata aaa att ctt cct gaa cca tta aac	341			
Cys His Phe Phe Lys His Pro Ile Lys Ile Leu Pro Glu Pro Leu Asn				
90 95 100 105				
att aat ttc aaa gac aca atc ata aaa aag tta cta aaa gat atg ggc	389			
Ile Asn Phe Lys Asp Thr Ile Ile Lys Lys Leu Leu Lys Asp Met Gly				
110 115 120				
aaa gat aaa aaa ata gaa gat ttt aaa gaa act tgt att tta aaa ata	437			
Lys Asp Lys Lys Ile Glu Asp Phe Lys Glu Thr Cys Ile Leu Lys Ile				
125 130 135				
gct ggt ttt act tat ttt gtg tgc gta ttg cct tat gaa tat gag aat	485			
Ala Gly Phe Thr Tyr Phe Val Cys Val Leu Pro Tyr Glu Tyr Glu Asn				
140 145 150				
aaa gag gat aaa gag aat agt gaa gag att tta aaa gaa gat ttc agc	533			
Lys Glu Asp Lys Glu Asn Ser Glu Glu Ile Leu Lys Glu Asp Phe Arg				
155 160 165				
ctg tta aat acc aag ggg gga tta agc gtt aag cgt gct ttg ata aat	581			
Leu Leu Asn Thr Lys Gly Gly Leu Ser Val Lys Arg Ala Leu Ile Asn				
170 175 180 185				
aac agg cat tct tat gaa gcg ata aaa tta aga ccc att aaa caa gag	629			
Asn Arg His Ser Tyr Glu Ala Ile Lys Leu Arg Pro Ile Lys Gln Glu				
190 195 200				
tta gtg cct ggt ttg tgt ttg ttt ttt caa ggt tca tta gaa ttt aat	677			
Leu Val Pro Gly Leu Cys Leu Phe Phe Gln Gly Ser Leu Glu Phe Asn				
205 210 215				
gat aaa acc aca aaa acc atg cga acg agc ctt tta gac cag atc cag	725			
Asp Lys Thr Thr Lys Thr Met Arg Thr Ser Leu Leu Asp Gln Ile Gln				
220 225 230				
caa gat gac aaa tct tat tta aaa att tgg gaa aaa tat ctc atc aac	773			
Gln Asp Asp Lys Ser Tyr Leu Lys Ile Trp Glu Lys Tyr Leu Ile Lys				
235 240 245				
agc gct caa aaa agt ttt aat gag gca aaa gaa gtg ggg gtt tta gag	821			

Ser Ala Gln Lys Ser Phe Asn Glu Ala Lys Glu Val Gly Val Leu Glu
 250 255 260 265
 att gaa agc gtg agt aaa gaa gga ggg aat tta aga att cgt ttt aag 869
 Ile Glu Ser Val Ser Lys Glu Gly Gly Asn Leu Arg Ile Arg Phe Lys 270 275 280
 cca gct tta ggc aag aat aaa atg gaa atc tta aag aaa tca caa ttt 917
 Pro Ala Leu Gly Lys Asn Lys Met Glu Ile Leu Lys Lys Ser Gln Phe 285 290 295
 aaa aag ggg agt gat tta ggg gtt tta gag gat tta gac cca caa aat 965
 Lys Lys Gly Ser Asp Leu Gly Val Leu Glu Asp Leu Asp Pro Gln Asn 300 305 310
 gaa gaa aat tta atc aat ctt att tct gaa caa aag aaa caa att tct 1013
 Glu Glu Asn Leu Ile Asn Lys Ile Ser Glu Gln Lys Lys Gln Ile Ser 315 320 325
 aaa aac aac agc caa tca ata atg att gaa gac att agt ggg gat gat 1061
 Lys Asn Asn Ser Gln Ser Ile Met Ile Glu Asp Ile Ser Gly Asp Asp 330 335 340 345
 ttt att ata gat tac gat ctt tcc ata aaa gag ggc gat gct ttt cat 1109
 Phe Ile Ile Asp Tyr Asp Leu Ser Ile Lys Glu Gly Asp Ala Phe His 350 355 360
 tta aat tat atg ggg gat cta aat acg ctt aaa aaa caa tat agc gca 1157
 Leu Asn Tyr Met Gly Asp Leu Asn Thr Leu Lys Lys Gln Tyr Ser Ala 365 370 375
 tta gat aag aca aag aaa ggt ttg aag cgc caa tcc taatttagga 1203
 Leu Asp Lys Thr Lys Lys Gly Leu Lys Arg Gln Ser 380 385
 ttaatttttaa acattaaaga ggataaagag aatagtgata gcgataatga tactgca 1260
 <210> 580
 <211> 389
 <212> PRT
 <213> Helicobacter pylori

<400> 580
 Met Leu Ser Phe Ile Lys Glu Asp Ser Ile Ile Lys Ala Tyr Asn Leu
 1 5 10 15
 Asn Thr Ala Lys Leu Glu Pro Lys Asp Arg Glu Lys Leu Gly Leu Leu
 20 25 30
 Lys Ile Glu Lys Asn Lys Ile Tyr Phe His Leu Asp Glu Lys Arg Tyr
 35 40 45
 Leu Lys Leu Glu Ile Ile Gly Lys Thr Lys Glu Lys Glu Ile Lys Asn
 50 55 60
 Ala Phe Cys Ser Asn Ala Phe Leu Ala Ala Gln Val Leu Asn Leu Asn
 65 70 75 80
 Gln Glu Arg Gln Val Leu Glu Leu Lys Cys His Phe Phe Lys His Pro
 85 90 95
 Ile Lys Ile Leu Pro Glu Pro Leu Asn Ile Asn Phe Lys Asp Thr Ile
 100 105 110
 Ile Lys Lys Leu Leu Lys Asp Met Gly Lys Asp Lys Lys Ile Glu Asp
 115 120 125

Phe Lys Glu Thr Cys Ile Leu Lys Ile Ala Gly Phe Thr Tyr Phe Val
130 135 140
Cys Val Leu Pro Tyr Glu Tyr Glu Asn Lys Glu Asp Lys Glu Asn Ser
145 150 155 160
Glu Glu Ile Leu Lys Glu Asp Phe Arg Leu Leu Asn Thr Lys Gly Gly
165 170 175
Leu Ser Val Lys Arg Ala Leu Ile Asn Asn Arg His Ser Tyr Glu Ala
180 185 190
Ile Lys Leu Arg Pro Ile Lys Gln Glu Leu Val Pro Gly Leu Cys Leu
195 200 205
Phe Phe Gln Gly Ser Leu Glu Phe Asn Asp Lys Thr Thr Lys Thr Met
210 215 220
Arg Thr Ser Leu Leu Asp Gln Ile Gln Gln Asp Asp Lys Ser Tyr Leu
225 230 235 240
Lys Ile Trp Glu Lys Tyr Leu Ile Lys Ser Ala Gln Lys Ser Phe Asn
245 250 255
Glu Ala Lys Glu Val Gly Val Leu Glu Ile Glu Ser Val Ser Lys Glu
260 265 270
Gly Gly Asn Leu Arg Ile Arg Phe Lys Pro Ala Leu Gly Lys Asn Lys
275 280 285
Met Glu Ile Leu Lys Lys Ser Gln Phe Lys Lys Gly Ser Asp Leu Gly
290 295 300
Val Leu Glu Asp Leu Asp Pro Gln Asn Glu Glu Asn Leu Ile Asn Leu
305 310 315 320
Ile Ser Glu Gln Lys Lys Gln Ile Ser Lys Asn Asn Ser Gln Ser Ile
325 330 335
Met Ile Glu Asp Ile Ser Gly Asp Asp Phe Ile Ile Asp Tyr Asp Leu
340 345 350
Ser Ile Lys Glu Gly Asp Ala Phe His Leu Asn Tyr Met Gly Asp Leu
355 360 365
Asn Thr Leu Lys Lys Gln Tyr Ser Ala Leu Asp Lys Thr Lys Lys Gly
370 375 380
Leu Lys Arg Gln Ser
385

<210> 581
<211> 1185
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (16)...(1113)

<400> 581
tccataggct agttg atg tca aaa aga agc gaa gtt tta gaa caa ttt cat 51
Met Ser Lys Arg Ser Glu Val Leu Glu Gln Phe His
1 5 10
ggc ggt tta aaa aat tta gaa tta caa act aaa aga cgc atg ggt ttg 99
Gly Gly Leu Lys Asn Leu Glu Leu Gln Thr Lys Arg Arg Met Gly Leu
15 20 25
tgg ggc gat cca aaa gag aat gaa gaa caa act ttg ttt tta gaa gaa 147
Trp Gly Asp Pro Lys Glu Asn Glu Glu Gln Thr Leu Phe Leu Glu Glu
30 35 40
att gaa aat gaa tta aag caa tta gaa aac aaa gaa aat ctt aaa gca 195

Ile	Glu	Asn	Glu	Leu	Lys	Gln	Leu	Glu	Asn	Lys	Glu	Asn	Leu	Lys	Ala		
45					50					55					60		
gac	aac	aac	aca	gaa	ttt	aaa	gaa	gaa	aat	caa	gac	act	aaa	gaa	aac	243	
Asp	Asn	Asn	Thr	Glu	Phe	Lys	Glu	Glu	Asn	Gln	Asp	Thr	Lys	Glu	Asn		
				65					70					75			
cag	cct	aac	gat	ttg	ttt	tct	ttg	cca	ttg	ccc	act	caa	acc	acc	atc	291	
Gln	Pro	Asn	Asp	Leu	Phe	Ser	Leu	Pro	Leu	Pro	Thr	Gln	Thr	Thr	Ile		
			80					85					90				
aat	gga	att	aaa	gaa	ttt	gta	gaa	gag	cct	gtg	ata	gaa	aca	gag	aaa	339	
Asn	Gly	Ile	Lys	Glu	Phe	Val	Glu	Glu	Pro	Val	Ile	Glu	Thr	Glu	Lys		
		95					100					105					
aaa	gaa	aca	tcc	caa	aat	gag	cca	atc	caa	gaa	aaa	aaa	gaa	aga	att	387	
Lys	Glu	Thr	Ser	Gln	Asn	Glu	Pro	Ile	Gln	Glu	Lys	Lys	Glu	Arg	Ile		
	110					115					120						
ttt	aaa	aac	ttt	ttc	tcc	aga	ata	ggc	ttt	gat	aaa	agt	att	gcc	cct	435	
Phe	Lys	Asn	Phe	Phe	Ser	Arg	Ile	Gly	Phe	Asp	Lys	Ser	Ile	Ala	Pro		
125					130					135					140		
aca	atg	ctt	ttt	gaa	gaa	gtg	aga	gat	gca	agc	gtt	atc	tat	cat	tta	483	
Thr	Met	Leu	Phe	Glu	Glu	Val	Arg	Asp	Ala	Ser	Val	Ile	Tyr	His	Leu		
				145					150					155			
gag	aaa	aaa	tta	ggc	gat	tat	atc	ttt	tat	gta	gcg	tgt	ttc	ttc	ttt	531	
Glu	Lys	Lys	Leu	Gly	Asp	Tyr	Ile	Phe	Tyr	Val	Ala	Cys	Phe	Phe	Phe		
			160					165					170				
ggc	aca	acg	gca	ttg	ctt	att	atc	tta	ctg	act	att	ctg	ttg	ccc	tta	579	
Gly	Thr	Thr	Ala	Leu	Leu	Ile	Ile	Leu	Leu	Thr	Ile	Leu	Leu	Pro	Leu		
		175					180					185					
aaa	caa	aaa	gag	ccg	tat	tta	gtg	caa	ttt	tct	aac	aat	aaa	gaa	aat	627	
Lys	Gln	Lys	Glu	Pro	Tyr	Leu	Val	Gln	Phe	Ser	Asn	Asn	Lys	Glu	Asn		
	190					195					200						
ttt	gct	tta	gtt	caa	aag	gca	gat	agc	agc	att	aca	gcc	aat	aaa	gct	675	
Phe	Ala	Leu	Val	Gln	Lys	Ala	Asp	Ser	Ser	Ile	Thr	Ala	Asn	Lys	Ala		
205					210					215					220		
ctt	att	cgt	tca	tta	gtg	gga	gcg	tat	gtg	cta	aac	agg	gaa	agc	att	723	
Leu	Ile	Arg	Ser	Leu	Val	Gly	Ala	Tyr	Val	Leu	Asn	Arg	Glu	Ser	Ile		
				225					230					235			
act	cat	att	gag	caa	cat	gaa	aaa	atg	cgt	caa	aac	acc	att	aaa	gag	771	
Thr	His	Ile	Glu	Gln	His	Glu	Lys	Met	Arg	Gln	Asn	Thr	Ile	Lys	Glu		
			240					245					250				
caa	agt	tcc	aat	gaa	gta	tgg	tat	gaa	ttt	gaa	aaa	ctc	atc	gct	cat	819	
Gln	Ser	Ser	Asn	Glu	Val	Trp	Tyr	Glu	Phe	Glu	Lys	Leu	Ile	Ala	His		
		255					260					265					
tat	gac	agc	att	tac	act	aat	cct	tta	ctc	aca	aga	aaa	gta	aag	att	867	
Tyr	Asp	Ser	Ile	Tyr	Thr	Asn	Pro	Leu	Leu	Thr	Arg	Lys	Val	Lys	Ile		
	270					275					280						

gca aat att tac tta gat aaa gat tta gcc tat att gac att gaa gtg 915
 Ala Asn Ile Tyr Leu Asp Lys Asp Leu Ala Tyr Ile Asp Ile Glu Val
 285 290 295 300
 agc ttg tat cat agt gga gaa tta gag agc ttg aag cgc tat aaa gtg 963
 Ser Leu Tyr His Ser Gly Glu Leu Glu Ser Leu Lys Arg Tyr Lys Val
 305 310 315
 gtg atg agt ttt gaa ttt aaa aaa caa gaa atc aat ttt gac tcc atg 1011
 Val Met Ser Phe Glu Phe Lys Lys Gln Glu Ile Asn Phe Asp Ser Met
 320 325 330
 tct tta aat cct aca ggc ttt atg gtt aca agt tat gat gta act gaa 1059
 Ser Leu Asn Pro Thr Gly Phe Met Val Thr Ser Tyr Asp Val Thr Glu
 335 340 345
 att gcg att gtg aat tac cca acc gct aaa gcg att ggg ctt ttt ctt 1107
 Ile Ala Ile Val Asn Tyr Pro Thr Ala Lys Ala Ile Gly Leu Phe Leu
 350 355 360
 gct tca tagctccata actagctaga tccaatatgt ttccatattt agaactaacc 1163
 Ala Ser
 365
 ccgtagagg aagctccaca ag 1185

<210> 582

<211> 366

<212> PRT

<213> Helicobacter pylori

<400> 582

Met Ser Lys Arg Ser Glu Val Leu Glu Gln Phe His Gly Gly Leu Lys
 1 5 10 15
 Asn Leu Glu Leu Gln Thr Lys Arg Arg Met Gly Leu Trp Gly Asp Pro
 20 25 30
 Lys Glu Asn Glu Glu Gln Thr Leu Phe Leu Glu Glu Ile Glu Asn Glu
 35 40 45
 Leu Lys Gln Leu Glu Asn Lys Glu Asn Leu Lys Ala Asp Asn Asn Thr
 50 55 60
 Glu Phe Lys Glu Glu Asn Gln Asp Thr Lys Glu Asn Gln Pro Asn Asp
 65 70 75 80
 Leu Phe Ser Leu Pro Leu Pro Thr Gln Thr Thr Ile Asn Gly Ile Lys
 85 90 95
 Glu Phe Val Glu Glu Pro Val Ile Glu Thr Glu Lys Lys Glu Thr Ser
 100 105 110
 Gln Asn Glu Pro Ile Gln Glu Lys Lys Glu Arg Ile Phe Lys Asn Phe
 115 120 125
 Phe Ser Arg Ile Gly Phe Asp Lys Ser Ile Ala Pro Thr Met Leu Phe
 130 135 140
 Glu Glu Val Arg Asp Ala Ser Val Ile Tyr His Leu Glu Lys Lys Leu
 145 150 155 160
 Gly Asp Tyr Ile Phe Tyr Val Ala Cys Phe Phe Phe Gly Thr Thr Ala
 165 170 175
 Leu Leu Ile Ile Leu Leu Thr Ile Leu Leu Pro Leu Lys Gln Lys Glu
 180 185 190
 Pro Tyr Leu Val Gln Phe Ser Asn Asn Lys Glu Asn Phe Ala Leu Val
 195 200 205
 Gln Lys Ala Asp Ser Ser Ile Thr Ala Asn Lys Ala Leu Ile Arg Ser

210	215	220
Leu Val Gly Ala Tyr Val	Leu Asn Arg Glu Ser	Ile Thr His Ile Glu
225	230	235
Gln His Glu Lys Met Arg	Gln Asn Thr Ile Lys	Glu Gln Ser Ser Asn
245	250	255
Glu Val Trp Tyr Glu Phe	Glu Lys Leu Ile Ala	His Tyr Asp Ser Ile
260	265	270
Tyr Thr Asn Pro Leu Leu	Thr Arg Lys Val Lys	Ile Ala Asn Ile Tyr
275	280	285
Leu Asp Lys Asp Leu Ala	Tyr Ile Asp Ile Glu	Val Ser Leu Tyr His
290	295	300
Ser Gly Glu Leu Glu Ser	Leu Lys Arg Tyr Lys	Val Val Met Ser Phe
305	310	315
Glu Phe Lys Lys Gln Glu	Ile Asn Phe Asp Ser	Met Ser Leu Asn Pro
325	330	335
Thr Gly Phe Met Val Thr	Ser Tyr Asp Val Thr	Glu Ile Ala Ile Val
340	345	350
Asn Tyr Pro Thr Ala Lys	Ala Ile Gly Leu Phe	Leu Ala Ser
355	360	365

<210> 583
 <211> 745
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (37)...(717)

<400> 583	
taagggggga tttggaaggt gttggaattg aaatta atg gga cag aag agg atc	54
Met Gly Gln Lys Arg Met	
1 5	
aat aaa tca aac aaa tta gtc att atc aat cgc gcc att cca ggt ggc	102
Asn Lys Ser Asn Lys Leu Val Ile Ile Asn Arg Ala Ile Pro Gly Gly	
10 15 20	
ggc aag acc tct ttg atc aaa cag att gaa gag ttg gca aaa agc ttg	150
Gly Lys Thr Ser Leu Ile Lys Gln Ile Glu Glu Leu Ala Lys Ser Leu	
25 30 35	
ggg cat tct att agc gtt cat tct acc gat gaa tat ttc atc caa aca	198
Gly His Ser Ile Ser Val His Ser Thr Asp Glu Tyr Phe Ile Gln Thr	
40 45 50	
gat gaa gag ggt atc agg cat tat gtt gtt gat aaa aag aaa ctc aat	246
Asp Glu Glu Gly Ile Arg His Tyr Val Val Asp Lys Lys Lys Leu Asn	
55 60 65 70	
gaa tac cac caa aac aat caa gaa gcc ttc aaa caa gct tta gaa aat	294
Glu Tyr His Gln Asn Asn Gln Glu Ala Phe Lys Gln Ala Leu Glu Asn	
75 80 85	
cgt ata gat att gta gtg tgc gat aac acc aat ttt gaa tcg tgg caa	342
Arg Ile Asp Ile Val Val Cys Asp Asn Thr Asn Phe Glu Ser Trp Gln	
90 95 100	

agc aaa cca tat aca gat atg gct aga gaa ttt ggc tat aaa att ttg 390
 Ser Lys Pro Tyr Thr Asp Met Ala Arg Glu Phe Gly Tyr Lys Ile Leu
 105 110 115

ttg att gat ttt aag aat aqa cac tta gaa acc ccc atg gat tat gga 436
 Leu Ile Asp Phe Lys Asn Arg His Leu Glu Thr Pro Met Asp Tyr Gly
 120 125 130

tgg gat gtt gcg caa tgc atc aag aag cca cga ggt att gca aag cat 486
 Trp Asp Val Ala Gln Cys Ile Lys Lys Pro Arg Gly Ile Ala Lys His
 135 140 145 150

tat gac tat gat ttt tat ttg gag agg gtt ttg gtt gag cca cag gat 534
 Tyr Asp Tyr Asp Phe Tyr Leu Glu Arg Val Leu Val Glu Pro Gln Asp
 155 160 165

tat gag aaa caa aat aga gag ttg agc tta aaa gcc tta gaa ttt ttg 582
 Tyr Glu Lys Gln Asn Arg Glu Leu Ser Leu Lys Ala Leu Glu Phe Leu
 170 175 180

aaa tac aat ttt gat ttt gat gtg att ttt tat tct ttt ggg gag caa 630
 Lys Tyr Asn Phe Asp Phe Asp Val Ile Phe Tyr Ser Phe Gly Glu Gln
 185 190 195

tta atg cct att ctt act aga atg tta gtt tct gtc tct aag tct cat 678
 Leu Met Pro Ile Leu Thr Arg Met Leu Val Ser Val Ser Lys Ser His
 200 205 210

aga aag aga ctt gaa aac tat ggc aaa gac att aaa acc taatttagat 727
 Arg Lys Arg Leu Glu Asn Tyr Gly Lys Asp Ile Lys Thr
 215 220 225

aaagatgagt taaacaca 745

<210> 584

<211> 227

<212> PRT

<213> Helicobacter pylori

<400> 584

Met Gly Gln Lys Arg Met Asn Lys Ser Asn Lys Leu Val Ile Ile Asn
 1 5 10 15
 Arg Ala Ile Pro Gly Gly Gly Lys Thr Ser Leu Ile Lys Gln Ile Glu
 20 25 30
 Glu Leu Ala Lys Ser Leu Gly His Ser Ile Ser Val His Ser Thr Asp
 35 40 45
 Glu Tyr Phe Ile Gln Thr Asp Glu Glu Gly Ile Arg His Tyr Val Val
 50 55 60
 Asp Lys Lys Lys Leu Asn Glu Tyr His Gln Asn Asn Gln Glu Ala Phe
 65 70 75 80
 Lys Gln Ala Leu Glu Asn Arg Ile Asp Ile Val Val Cys Asp Asn Thr
 85 90 95
 Asn Phe Glu Ser Trp Gln Ser Lys Pro Tyr Thr Asp Met Ala Arg Glu
 100 105 110
 Phe Gly Tyr Lys Ile Leu Leu Ile Asp Phe Lys Asn Arg His Leu Glu
 115 120 125
 Thr Pro Met Asp Tyr Gly Trp Asp Val Ala Gln Cys Ile Lys Lys Pro
 130 135 140
 Arg Gly Ile Ala Lys His Tyr Asp Tyr Asp Phe Tyr Leu Glu Arg Val

145		150		155		160									
Leu	Val	Glu	Pro	Gln	Asp	Tyr	Glu	Lys	Gln	Asn	Arg	Glu	Leu	Ser	Leu
				165					170					175	
Lys	Ala	Leu	Glu	Phe	Leu	Lys	Tyr	Asn	Phe	Asp	Phe	Asp	Val	Ile	Phe
				180				185					190		
Tyr	Ser	Phe	Gly	Glu	Gln	Leu	Met	Pro	Ile	Leu	Thr	Arg	Met	Leu	Val
		195				200						205			
Ser	Val	Ser	Lys	Ser	His	Arg	Lys	Arg	Leu	Glu	Asn	Tyr	Gly	Lys	Asp
	210					215					220				
Ile	Lys	Thr													
225															

<210> 585
 <211> 531
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (19)...(468)

<400> 585	
atttactaaa ggaaaaca atg att aaa cta atc tta cac aag aag tcc ata	51
Met Ile Lys Leu Ile Leu His Lys Lys Ser Ile	
1 5 10	
caa att gat gaa aca ttg ctg aat gta aaa gag cat tta gaa aag ttt	99
Gln Ile Asp Glu Thr Leu Leu Asn Val Lys Glu His Leu Glu Lys Phe	
15 20 25	
tat tca aat aaa gaa caa gag aca atc gct caa act tta gag aat gaa	147
Tyr Ser Asn Lys Glu Gln Glu Thr Ile Ala Gln Thr Leu Glu Asn Glu	
30 35 40	
aca gaa att tct tgt agc tat ttt tgg gac aaa gac ttc ttg ttg tta	195
Thr Glu Ile Ser Cys Ser Tyr Phe Trp Asp Lys Asp Phe Leu Leu Leu	
45 50 55	
gag caa ctt tta gaa aat rat tta ggt cat ttt acc ttt gag agc gag	243
Glu Gln Leu Leu Glu Asn Xaa Leu Gly His Phe Thr Phe Glu Ser Glu	
60 65 70 75	
ttt gcc cta cta aaa gat aaa gag act tta aac cta tct caa atc aaa	291
Phe Ala Leu Leu Lys Asp Lys Glu Thr Leu Asn Leu Ser Gln Ile Lys	
80 85 90	
caa atc ggt gtc tta aag gtt ctt acc tat gar atg ata caa acc tta	339
Gln Ile Gly Val Leu Lys Val Leu Thr Tyr Glu Met Ile Gln Thr Leu	
95 100 105	
aaa aat caa atc att cat tta gca caa gtt gtc aat gaa gaa aat tta	387
Lys Asn Gln Ile Ile His Leu Ala Gln Val Val Asn Glu Glu Asn Leu	
110 115 120	
gaa aaa gat gaa gaa ctt gtt gtc tac cac cta aat ttc acg tca cgc	435
Glu Lys Asp Glu Glu Leu Val Val Tyr His Leu Asn Phe Thr Ser Arg	
125 130 135	

aac aat ctt aca aaa tat tat cca agt tct gtg tgattaaaaa agaaagaaat 488
 Asn Asn Leu Thr Lys Tyr Tyr Pro Ser Ser Val
 140 145 150

atcgcatgaa aaaattaagt cattttagaa agcttatcgc ctt 531

<210> 586
 <211> 150
 <212> PRT
 <213> Helicobacter pylori
 <220>
 <221> VARIANT
 <222> 66, 102
 <223> Xaa = Any Amino Acid

<400> 586
 Met Ile Lys Leu Ile Leu His Lys Lys Ser Ile Gln Ile Asp Glu Thr
 1 5 10 15
 Leu Leu Asn Val Lys Glu His Leu Glu Lys Phe Tyr Ser Asn Lys Glu
 20 25 30
 Gln Glu Thr Ile Ala Gln Thr Leu Glu Asn Glu Thr Glu Ile Ser Cys
 35 40 45
 Ser Tyr Phe Trp Asp Lys Asp Phe Leu Leu Leu Glu Gln Leu Leu Glu
 50 55 60
 Asn Xaa Leu Gly His Phe Thr Phe Glu Ser Glu Phe Ala Leu Leu Lys
 65 70 75 80
 Asp Lys Glu Thr Leu Asn Leu Ser Gln Ile Lys Gln Ile Gly Val Leu
 85 90 95
 Lys Val Leu Thr Tyr Xaa Met Ile Gln Thr Leu Lys Asn Gln Ile Ile
 100 105 110
 His Leu Ala Gln Val Val Asn Glu Glu Asn Leu Glu Lys Asp Glu Glu
 115 120 125
 Leu Val Val Tyr His Leu Asn Phe Thr Ser Arg Asn Asn Leu Thr Lys
 130 135 140
 Tyr Tyr Pro Ser Ser Val
 145 150

<210> 587
 <211> 334
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (34)...(294)

<400> 587
 ctggttttatg agtattttttt aaaagaagtc ccc atg caa tta gtt ggt att tca 54
 Met Gln Leu Val Gly Ile Ser
 1 5
 gtt tct aat ctc aaa gaa atc agc tcc aaa gaa aaa ttt ctt tgg ctc 102
 Val Ser Asn Leu Lys Glu Ile Ser Ser Lys Glu Lys Phe Leu Trp Leu
 10 15 20
 aat gct aag agt ttt tta ctc tca gga ttt gtg cct ttt att atg ata 150
 Asn Ala Lys Ser Phe Leu Leu Ser Gly Phe Val Pro Phe Ile Met Ile

25	30	35	
cct tgg cta gat ata ttg aac tct ttt gtg ctt tat gtg tgc ttt ctc			198
Pro Trp Leu Asp Ile Leu Asn Ser Phe Val Leu Tyr Val Cys Phe Leu			
40	45	50	55
tta att ttt agc ata gcg gag ttc ttt gat gaa gat ata agt gac att			246
Leu Ile Phe Ser Ile Ala Glu Phe Phe Asp Glu Asp Ile Ser Asp Ile			
	60	65	70
tta atc gct cat tcc aaa att aaa acc aaa gct aat tca ttt tac gct			294
Leu Ile Ala His Ser Lys Ile Lys Thr Lys Ala Asn Ser Phe Tyr Ala			
	75	80	85
taaaaggaaa aaatatgcaa aaagaagtct tagtagaaaa			334

<210> 588
 <211> 87
 <212> PRT
 <213> Helicobacter pylori

<400> 588

Met	Gln	Leu	Val	Gly	Ile	Ser	Val	Ser	Asn	Leu	Lys	Glu	Ile	Ser	Ser
1				5					10					15	
Lys	Glu	Lys	Phe	Leu	Trp	Leu	Asn	Ala	Lys	Ser	Phe	Leu	Leu	Ser	Gly
		20						25					30		
Phe	Val	Pro	Phe	Ile	Met	Ile	Pro	Trp	Leu	Asp	Ile	Leu	Asn	Ser	Phe
		35					40					45			
Val	Leu	Tyr	Val	Cys	Phe	Leu	Leu	Ile	Phe	Ser	Ile	Ala	Glu	Phe	Phe
	50					55					60				
Asp	Glu	Asp	Ile	Ser	Asp	Ile	Leu	Ile	Ala	His	Ser	Lys	Ile	Lys	Thr
65					70					75					80
Lys	Ala	Asn	Ser	Phe	Tyr	Ala									
				85											

<210> 589
 <211> 995
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (37)...(948)

<400> 589

taaaaacacc ctaaaagaa aaagaaagtc ttctta atg tta gaa agc gcc ctt			54
	Met	Leu	Glu
	1		5
aaa tat tgc aag gaa aaa gcc ata gac ctt tta gta ggg ttt gtg cca			102
Lys Tyr Cys Lys Glu Lys Ala Ile Asp Leu Val Gly Phe Val Pro			
	10	15	20
aaa acc tat tct atg gca caa gag tgc aat att tta ggc ttg tat gat			150
Lys Thr Tyr Ser Met Ala Gln Glu Cys Asn Ile Leu Gly Leu Tyr Asp			
	25	30	35
gat gct ttc att att acc aaa caa gaa aat cta gta ggc att ata tcc			196

Asp	Ala	Phe	Ile	Ile	Thr	Lys	Gln	Glu	Asn	Leu	Val	Gly	Ile	Ile	Ser		
40						45					50						
tta	caa	gga	cta	agc	tat	tct	aat	tta	atg	caa	aaa	gac	tta	gag	ggc	246	
Leu	Gln	Gly	Leu	Ser	Tyr	Ser	Asn	Leu	Met	Gln	Lys	Asp	Leu	Glu	Gly		
55					60					65					70		
tat	ttt	gat	gct	aga	caa	aat	ggt	ctc	aac	acc	att	agt	aaa	gac	att	294	
Tyr	Phe	Asp	Ala	Arg	Gln	Asn	Val	Leu	Asn	Thr	Ile	Ser	Lys	Asp	Ile		
				75					80					85			
caa	tta	aga	att	gtg	gct	aaa	agg	cgt	aag	gaa	ttt	atc	aat	caa	agt	342	
Gln	Leu	Arg	Ile	Val	Ala	Lys	Arg	Arg	Lys	Glu	Phe	Ile	Asn	Gln	Ser		
			90					95					100				
cca	aat	att	gac	aat	att	tat	gcc	aaa	gct	att	atc	aca	caa	ttt	gaa	390	
Pro	Asn	Ile	Asp	Asn	Ile	Tyr	Ala	Lys	Ala	Ile	Ile	Thr	Gln	Phe	Glu		
	105						110					115					
agc	aag	gga	atc	tat	aaa	aca	gag	tat	ttt	tta	gtg	ttt	gaa	act	atc	438	
Ser	Lys	Gly	Ile	Tyr	Lys	Thr	Glu	Tyr	Phe	Leu	Val	Phe	Glu	Thr	Ile		
	120					125					130						
act	tct	aat	gtc	aag	tct	ttc	ttt	gaa	aaa	aag	aaa	ttg	gaa	atg	act	486	
Thr	Ser	Asn	Val	Lys	Ser	Phe	Phe	Glu	Lys	Lys	Lys	Leu	Glu	Met	Thr		
135					140					145					150		
act	tca	att	aat	gaa	gag	tta	gaa	gaa	agc	tct	aaa	gaa	gat	aaa	caa	534	
Thr	Ser	Ile	Asn	Glu	Glu	Leu	Glu	Glu	Ser	Ser	Lys	Glu	Asp	Lys	Gln		
			155						160					165			
gag	aat	gaa	aat	aac	tcc	aat	gaa	act	cat	tca	aac	aca	agc	tct	aaa	582	
Glu	Asn	Glu	Asn	Xaa	Ser	Asn	Glu	Thr	His	Ser	Asn	Thr	Ser	Ser	Lys		
			170					175					180				
aaa	gac	aag	aaa	aac	aag	ttc	aaa	aaa	aag	ata	acc	ttt	agc	acc	aaa	630	
Lys	Asp	Lys	Lys	Asn	Lys	Phe	Lys	Lys	Lys	Ile	Thr	Phe	Ser	Thr	Lys		
	185						190					195					
agt	aaa	aga	gcc	tta	ctc	att	caa	acc	ata	gaa	aga	gta	aaa	aac	gct	678	
Ser	Lys	Arg	Ala	Leu	Leu	Ile	Gln	Thr	Ile	Glu	Arg	Val	Lys	Asn	Ala		
	200					205					210						
ctt	aaa	gaa	ttt	aaa	ccc	act	tta	cta	aat	tct	aaa	gaa	gta	tta	aat	726	
Leu	Lys	Glu	Phe	Lys	Pro	Thr	Leu	Leu	Asn	Ser	Lys	Glu	Val	Leu	Asn		
215					220					225					230		
ttc	tac	gca	gaa	tac	atc	aat	ggc	aaa	tac	atc	gcc	ttt	aat	cct	aaa	774	
Phe	Tyr	Ala	Glu	Tyr	Ile	Asn	Gly	Lys	Tyr	Ile	Ala	Phe	Asn	Pro	Lys		
				235					240					245			
tta	aag	cga	tta	agc	gat	act	ata	ttg	cat	cta	atg	tgc	att	tta	aga	822	
Leu	Lys	Arg	Leu	Ser	Asp	Thr	Ile	Leu	His	Leu	Met	Cys	Ile	Leu	Arg		
			250					255					260				
aag	att	act	ttg	tca	ttg	aat	ttc	aaa	atc	aaa	aca	cct	ttt	gtg	cgt	870	
Lys	Ile	Thr	Leu	Ser	Leu	Asn	Phe	Lys	Ile	Lys	Thr	Pro	Phe	Val	Arg		
	265						270					275					

gtg tgg gga tta agg ctt atg aga gcg aag aaa ttt ctt cgc tcc cta 918
 Val Trp Gly Leu Arg Leu Met Arg Ala Lys Lys Phe Leu Arg Ser Leu
 280 285 290

tat cta ctc ttt tac aca ccc aaa ttg aac tagatttaat cttcatatc 968
 Tyr Leu Leu Phe Tyr Thr Pro Lys Leu Asn
 295 300

cgcctcttttag ggcaatttga aagcctg 995

<210> 590
 <211> 304
 <212> PRT
 <213> Helicobacter pylori

<220>
 <221> VARIANT
 <222> 171
 <223> Xaa = Any Amino Acid

<400> 590
 Met Leu Glu Ser Ala Leu Lys Tyr Cys Lys Glu Lys Ala Ile Asp Leu
 1 5 10 15
 Leu Val Gly Phe Val Pro Lys Thr Tyr Ser Met Ala Gln Glu Cys Asn
 20 25 30
 Ile Leu Gly Leu Tyr Asp Asp Ala Phe Ile Ile Thr Lys Gln Glu Asn
 35 40 45
 Leu Val Gly Ile Ile Ser Leu Gln Gly Leu Ser Tyr Ser Asn Leu Met
 50 55 60
 Gln Lys Asp Leu Glu Gly Tyr Phe Asp Ala Arg Gln Asn Val Leu Asn
 65 70 75 80
 Thr Ile Ser Lys Asp Ile Gln Leu Arg Ile Val Ala Lys Arg Arg Lys
 85 90 95
 Glu Phe Ile Asn Gln Ser Pro Asn Ile Asp Asn Ile Tyr Ala Lys Ala
 100 105 110
 Ile Ile Thr Gln Phe Glu Ser Lys Gly Ile Tyr Lys Thr Glu Tyr Phe
 115 120 125
 Leu Val Phe Glu Thr Ile Thr Ser Asn Val Lys Ser Phe Phe Glu Lys
 130 135 140
 Lys Lys Leu Glu Met Thr Thr Ser Ile Asn Glu Glu Leu Glu Glu Ser
 145 150 155 160
 Ser Lys Glu Asp Lys Gln Glu Asn Glu Asn Xaa Ser Asn Glu Thr His
 165 170 175
 Ser Asn Thr Ser Ser Lys Lys Asp Lys Lys Asn Lys Phe Lys Lys Lys
 180 185 190
 Ile Thr Phe Ser Thr Lys Ser Lys Arg Ala Leu Leu Ile Gln Thr Ile
 195 200 205
 Glu Arg Val Lys Asn Ala Leu Lys Glu Phe Lys Pro Thr Leu Leu Asn
 210 215 220
 Ser Lys Glu Val Leu Asn Phe Tyr Ala Glu Tyr Ile Asn Gly Lys Tyr
 225 230 235 240
 Ile Ala Phe Asn Pro Lys Leu Lys Arg Leu Ser Asp Thr Ile Leu His
 245 250 255
 Leu Met Cys Ile Leu Arg Lys Ile Thr Leu Ser Leu Asn Phe Lys Ile
 260 265 270
 Lys Thr Pro Phe Val Arg Val Trp Gly Leu Arg Leu Met Arg Ala Lys
 275 280 285
 Lys Phe Leu Arg Ser Leu Tyr Leu Leu Phe Tyr Thr Pro Lys Leu Asn
 290 295 300

<210> 591
 <211> 1598
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (39)...(1556)

<400> 591
 ataattatat agaattagtg caagccaatc gtttgagc atg caa gag tgt gct tta 56
 Met Gln Glu Cys Ala Leu
 1 5

aac tta gtt ata agg gct aaa agt aaa gct aaa tta gac aag tct tta 104
 Asn Leu Val Ile Arg Ala Lys Ser Lys Ala Lys Leu Asp Lys Ser Leu
 10 15 20

aaa gag att tta tcc ttg ctt aat aat gct gga cta ggc agt gtt aca 152
 Lys Glu Ile Leu Ser Leu Leu Asn Asn Ala Gly Leu Gly Ser Val Thr
 25 30 35

gaa act ata ggg cta aaa cca tct tat ttt tca ttc ttc cca aat aac 200
 Glu Thr Ile Gly Leu Lys Pro Ser Tyr Phe Ser Phe Phe Pro Asn Asn
 40 45 50

gcc aat atc aac cct aga atg aga cat caa act tcc caa gtc ata gca 248
 Ala Asn Ile Asn Pro Arg Met Arg His Gln Thr Ser Gln Val Ile Ala
 55 60 65 70

tct ttg att ttg ttt gag aaa aat aat aca ggt ttt aga gca aat tct 296
 Ser Leu Ile Leu Phe Glu Lys Asn Asn Thr Gly Phe Arg Ala Asn Ser
 75 80 85

tgg ggg gat atg ccc tta tct gtg ttt aag aac cta gac cat agc cct 344
 Trp Gly Asp Met Pro Leu Ser Val Phe Lys Asn Leu Asp His Ser Pro
 90 95 100

tat ttg ttt aat ttt cat aat caa gaa gtc aaa cat aag ggc gtg tta 392
 Tyr Leu Phe Asn Phe His Asn Gln Glu Val Lys His Lys Gly Val Leu
 105 110 115

gcc cac aat gtc gca cga gta gtg gga cat acc atg att ata gga gca 440
 Ala His Asn Val Ala Arg Val Val Gly His Thr Met Ile Ile Gly Ala
 120 125 130

aca ggt gct ggt aaa acc aca ctc att agc tat ttg atg atg agt gcc 488
 Thr Gly Ala Gly Lys Thr Thr Leu Ile Ser Tyr Leu Met Met Ser Ala
 135 140 145 150

tta aaa tat tct aac att gat att tta gct ctt gat aga cta aat ggt 536
 Leu Lys Tyr Ser Asn Ile Asp Ile Leu Ala Leu Asp Arg Leu Asn Gly
 155 160 165

ttg tat tcc ttt acc aag tat ttt gat ggg att tat aat caa ggc gaa 584
 Leu Tyr Ser Phe Thr Lys Tyr Phe Asp Gly Ile Tyr Asn Gln Gly Glu
 170 175 180

aac ttt cat att aac cct ttt tca tta gaa gat agc gca act aat aga	632
Asn Phe His Ile Asn Pro Phe Ser Leu Glu Asp Ser Ala Thr Asn Arg	
185 190 195	
gcc ttt tta ttg cat ttt tat gcc caa atg gca aaa gtg gat agt tat	680
Ala Phe Leu Leu His Phe Tyr Ala Gln Met Ala Lys Val Asp Ser Tyr	
200 205 210	
gat gac cat aag gat aaa gta gaa gat aga aca gcc ctt tta aat gct	728
Asp Asp His Lys Asp Lys Val Glu Asp Arg Thr Ala Leu Leu Asn Ala	
215 220 225 230	
att gat acg atg tat aga aat tat aac gat gaa gtc aaa caa gcc aaa	776
Ile Asp Thr Met Tyr Arg Asn Tyr Asn Asp Glu Val Lys Gln Ala Lys	
235 240 245	
ttt agc aac caa gaa tta ccc ctt cct ttt gat tta aaa gag ttt gtc	824
Phe Ser Asn Gln Glu Leu Pro Leu Phe Asp Leu Lys Glu Phe Val	
250 255 260	
aat gcc att gct aaa acc aat aca gac att tta gat agt agt ttt gaa	872
Asn Ala Ile Ala Lys Thr Asn Thr Asp Ile Leu Asp Ser Ser Phe Glu	
265 270 275	
gac tat tta aaa tct tcc tta ttt tct agc cga atg gat agt cta gat	920
Asp Tyr Leu Lys Ser Ser Leu Phe Ser Ser Arg Met Asp Ser Leu Asp	
280 285 290	
ttt aaa act cgt att agc acc ata aat acc gat agc att tta cat aat	968
Phe Lys Thr Arg Ile Ser Thr Ile Asn Thr Asp Ser Ile Leu His Asn	
295 300 305 310	
gat gat gac gct ggg ctt tta gcc tac tat gtc ttt cat aag atg att	1016
Asp Asp Asp Ala Gly Leu Leu Ala Tyr Tyr Val Phe His Lys Met Ile	
315 320 325	
gac aga gcc tta aaa atc aat cgt ggg ttt tta tgc ttt att gat gac	1064
Asp Arg Ala Leu Lys Ile Asn Arg Gly Phe Leu Cys Phe Ile Asp Glu	
330 335 340	
ttt aag tct tac gct caa aat gaa atg atg aat aaa aaa atc aat gaa	1112
Phe Lys Ser Tyr Ala Gln Asn Glu Met Met Asn Lys Lys Ile Asn Glu	
345 350 355	
atc att act caa gct aga aag gct aat ggg gtg att gtt cta gcc tta	1160
Ile Ile Thr Gln Ala Arg Lys Ala Asn Gly Val Ile Val Leu Ala Leu	
360 365 370	
caa gac att aac caa cta agc gaa gtg aca aac gct caa agc ttt ata	1208
Gln Asp Ile Asn Gln Leu Ser Glu Val Arg Asn Ala Gln Ser Phe Ile	
375 380 385 390	
aaa aat atg ggg caa ttg att ttg tat ccc caa aga aat att gat acc	1256
Lys Asn Met Gly Gln Leu Ile Leu Tyr Pro Gln Arg Asn Ile Asp Thr	
395 400 405	
aaa gat tta aac gat aaa ttt ggc att aga cta agc gat aca gaa aaa	1304
Lys Asp Leu Asn Asp Lys Phe Gly Ile Arg Leu Ser Asp Thr Glu Lys	
410 415 420	

cat	ttt	tta	gaa	aac	acc	gcc	gtt	aat	gaa	tac	aaa	gtc	tta	ctc	aaa	1352
His	Phe	Leu	Glu	Asn	Thr	Ala	Val	Asn	Glu	Tyr	Lys	Val	Leu	Leu	Lys	
		425					430					435				

aac	atg	aat	gat	ggc	tca	tct	aac	att	ata	gat	gtg	agc	cta	agt	tct	1400
Asn	Met	Asn	Asp	Gly	Ser	Ser	Asn	Ile	Ile	Asp	Val	Ser	Leu	Ser	Ser	
	440					445				450						

ttg	ggt	aat	tac	cta	caa	atc	ttt	agc	tct	aat	tct	agc	atg	gta	gaa	1448
Leu	Gly	Asn	Tyr	Leu	Gln	Ile	Phe	Ser	Ser	Asn	Ser	Ser	Met	Val	Glu	
455					460					465					470	

cac	att	gat	aat	ctc	att	aag	cat	tac	cct	aaa	act	tgg	cga	gaa	gtc	1496
His	Ile	Asp	Asn	Leu	Ile	Lys	His	Tyr	Pro	Lys	Thr	Trp	Arg	Glu	Val	
				475					480					485		

ttt	gtg	agt	aac	aaa	cac	gaa	aat	ttt	gat	gac	aaa	aaa	cac	tta	gaa	1544
Phe	Val	Ser	Asn	Lys	His	Glu	Asn	Phe	Asp	Asp	Lys	Lys	His	Leu	Glu	
			490					495					500			

aag	gtg	ctt	aaa	tgaaaaacat	catgcgttta	gtttttgtga	tagtggctat	1596
Lys	Val	Leu	Lys					
		505						

gi	1598
----	------

<210> 592

<211> 506

<212> PRT

<213> Helicobacter pylori

<400> 592

Met	Gln	Glu	Cys	Ala	Leu	Asn	Leu	Val	Ile	Arg	Ala	Lys	Ser	Lys	Ala	
1				5					10					15		
Lys	Leu	Asp	Lys	Ser	Leu	Lys	Glu	Ile	Leu	Ser	Leu	Leu	Asn	Asn	Ala	
			20					25					30			
Gly	Leu	Gly	Ser	Val	Thr	Glu	Thr	Ile	Gly	Leu	Lys	Pro	Ser	Tyr	Phe	
		35					40					45				
Ser	Phe	Phe	Pro	Asn	Asn	Ala	Asn	Ile	Asn	Pro	Arg	Met	Arg	His	Gln	
	50					55					60					
Thr	Ser	Gln	Val	Ile	Ala	Ser	Leu	Ile	Leu	Phe	Glu	Lys	Asn	Asn	Thr	
				70						75					80	
Gly	Phe	Arg	Ala	Asn	Ser	Trp	Gly	Asp	Met	Pro	Leu	Ser	Val	Phe	Lys	
				85				90						95		
Asn	Leu	Asp	His	Ser	Pro	Tyr	Leu	Phe	Asn	Phe	His	Asn	Gln	Glu	Val	
			100					105					110			
Lys	His	Lys	Gly	Val	Leu	Ala	His	Asn	Val	Ala	Arg	Val	Val	Gly	His	
		115					120					125				
Thr	Met	Ile	Ile	Gly	Ala	Thr	Gly	Ala	Gly	Lys	Thr	Thr	Leu	Ile	Ser	
	130					135					140					
Tyr	Leu	Met	Met	Ser	Ala	Leu	Lys	Tyr	Ser	Asn	Ile	Asp	Ile	Leu	Ala	
	145				150				155						160	
Leu	Asp	Arg	Leu	Asn	Gly	Leu	Tyr	Ser	Phe	Thr	Lys	Tyr	Phe	Asp	Gly	
				165				170						175		
Ile	Tyr	Asn	Gln	Gly	Glu	Asn	Phe	His	Ile	Asn	Pro	Phe	Ser	Leu	Glu	
		180					185					190				
Asp	Ser	Ala	Thr	Asn	Arg	Ala	Phe	Leu	Leu	His	Phe	Tyr	Ala	Gln	Met	
		195					200					205				

-710-

Asn Ile Lys Glu Tyr Ala Lys Cys Phe Phe Met Ser Leu Ser Met Phe
 30 35 40

 tta gaa gaa caa gaa aaa aac caa caa gaa gag ttt tta gaa caa gat 197
 Leu Glu Glu Gln Glu Lys Asn Gln Gln Glu Glu Phe Leu Glu Gln Asp
 45 50 55

 acc aaa gaa aat caa gaa gag ctc att aaa aac att caa aca agc att 245
 Thr Lys Glu Asn Gln Glu Glu Leu Ile Lys Asn Ile Gln Thr Ser Ile
 60 65 70

 gct aaa aac caa gag tta gaa aaa atc tct ttt gaa aaa tgg gag aat 293
 Ala Lys Asn Gln Glu Leu Glu Lys Ile Ser Phe Glu Lys Trp Glu Asn
 75 80 85 90

 aaa att caa gaa agg gtt ttg cct aag tta aaa cgc att gtt acg cat 341
 Lys Ile Gln Glu Arg Val Leu Pro Lys Leu Lys Arg Ile Val Thr His
 95 100 105

 aag ttg caa gaa agt atc aca tct agc ata aac acg caa tta gag agt 389
 Lys Leu Gln Glu Ser Ile Thr Ser Ser Ile Asn Thr Gln Leu Glu Ser
 110 115 120

 ttt aaa aaa gat gag tta gat tta tct agc gtg ttt gaa atc caa aga 437
 Phe Lys Lys Asp Glu Leu Asp Leu Ser Ser Val Phe Glu Ile Gln Arg
 125 130 135

 aag aac act caa ata gcg tat aga tta gct ata ggg ggg ctt ata ggt 485
 Lys Asn Thr Gln Ile Ala Tyr Arg Leu Ala Ile Gly Gly Leu Ile Gly
 140 145 150

 atc att gct tta agc tcg caa att tgattattaa ctctataactt cacgctttttt 539
 Ile Ile Ala Leu Ser Ser Gln Ile
 155 160

 agcctttgtg tgttctttttg taaa 563

 <210> 594
 <211> 162
 <212> PRT
 <213> Helicobacter pylori

<400> 594
 Met Ser Asn Leu Gln Glu Leu Arg Glu His Leu Lys Glu Leu Glu Asn
 1 5 10 15
 Ser Phe Glu Ile Gly Ser Phe Thr Lys Glu Asn Ile Lys Glu Tyr Ala
 20 25 30
 Lys Cys Phe Phe Met Ser Leu Ser Met Phe Leu Glu Glu Gln Glu Lys
 35 40 45
 Asn Gln Gln Glu Glu Phe Leu Glu Gln Asp Thr Lys Glu Asn Gln Glu
 50 55 60
 Glu Leu Ile Lys Asn Ile Gln Thr Ser Ile Ala Lys Asn Gln Glu Leu
 65 70 75 80
 Glu Lys Ile Ser Phe Glu Lys Trp Glu Asn Lys Ile Gln Glu Arg Val
 85 90 95
 Leu Pro Lys Leu Lys Arg Ile Val Thr His Lys Leu Gln Glu Ser Ile
 100 105 110
 Thr Ser Ser Ile Asn Thr Gln Leu Glu Ser Phe Lys Lys Asp Glu Leu
 115 120 125

Asp	Leu	Ser	Ser	Val	Phe	Glu	Ile	Gln	Arg	Lys	Asn	Thr	Gln	Ile	Ala
130						135					140				
Tyr	Arg	Leu	Ala	Ile	Gly	Gly	Leu	Ile	Gly	Ile	Ile	Ala	Leu	Ser	Ser
145					150					155					160
Gln	Ile														

<210> 595
 <211> 3222
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (22)...(3186)

<221> misc_feature
 <222> 642
 <223> n = A,T,C or G

ccttaa	atct	aagggg	tgtg	c	atg	cca	tac	aat	gaa	atc	aca	agg	gtt	caa	51
					Met	Pro	Tyr	Asn	Glu	Ile	Thr	Arg	Val	Gln	10
					1				5						
atc	cct	gcc	tta	atg	cat	tta	gcc	aag	ttg	ggc	tat	gat	ttt	atc	ccc
Ile	Pro	Ala	Leu	Met	His	Leu	Ala	Lys	Leu	Gly	Tyr	Asp	Phe	Ile	Pro
			15						20					25	
act	aat	tct	aaa	gaa	aat	aag	ccc	aac	cta	gac	acc	gcc	acc	aac	att
Thr	Asn	Ser	Lys	Glu	Asn	Lys	Pro	Asn	Leu	Asp	Thr	Ala	Thr	Asn	Ile
			30					35					40		
tta	acc	aat	agt	ttc	act	aaa	tcc	ttt	gag	cgg	tta	aac	ccc	act	aaa
Leu	Thr	Asn	Ser	Phe	Thr	Lys	Ser	Phe	Glu	Arg	Leu	Asn	Pro	Thr	Lys
		45					50					55			
aac	qca	caa	gaa	acg	ctt	gct	gaa	atg	aaa	aaa	cgc	ttg	aat	tgc	gat
Asn	Ala	Gln	Glu	Thr	Leu	Ala	Glu	Met	Lys	Lys	Arg	Leu	Asn	Cys	Asp
	60					65					70				
gat	ttg	ggc	aaa	agc	ttt	tat	gaa	tac	ttg	ctc	aaa	agc	gag	aat	caa
Asp	Leu	Gly	Lys	Ser	Phe	Tyr	Glu	Tyr	Leu	Leu	Lys	Ser	Glu	Asn	Gln
	75				80					85					90
atc	ata	gac	ttt	gat	aac	cct	aac	aac	aat	ctt	tat	gaa	atg	atg	act
Ile	Ile	Asp	Phe	Asp	Asn	Pro	Asn	Asn	Asn	Leu	Tyr	Glu	Met	Met	Thr
				95					100					105	
gaa	tta	ccc	tac	aaa	tct	ttt	agg	cct	gac	acc	acc	ctt	ttt	atc	aat
Glu	Leu	Pro	Tyr	Lys	Ser	Phe	Arg	Pro	Asp	Thr	Thr	Leu	Phe	Ile	Asn
			110					115					120		
ggc	ttg	cct	ttg	gtg	aat	ata	gaa	gtt	aaa	cac	cct	tac	gcc	aaa	aaa
Gly	Leu	Pro	Leu	Val	Asn	Ile	Glu	Val	Lys	Gln	Pro	Tyr	Ala	Lys	Lys
		125					130					135			
ggc	att	aaa	gaa	gaa	aga	gat	cgc	cac	atc	aaa	cgc	tat	gaa	aac	cct
															483

Gly	Ile	Lys	Glu	Glu	Arg	Asp	Arg	His	Ile	Lys	Arg	Tyr	Glu	Asn	Pro		
140						145					150						
gaa	aac	aaa	gtt	ttt	tat	aat	ctc	gcg	caa	atc	tgg	ctt	ttt	agc	gat	531	
Glu	Asn	Lys	Val	Phe	Tyr	Asn	Leu	Ala	Gln	Ile	Trp	Leu	Phe	Ser	Asp	170	
155					160					165							
aac	tta	ccc	tat	gat	gaa	aac	aaa	ccc	gat	caa	ggc	gcg	ttt	tat	agc	579	
Asn	Leu	Pro	Tyr	Asp	Glu	Asn	Lys	Pro	Asp	Gln	Gly	Ala	Phe	Tyr	Ser	185	
			175						180								
gct	tct	tat	tcg	ccc	att	ttc	caa	cgc	ttt	gtt	gaa	gct	cat	agg	cta	627	
Ala	Ser	Tyr	Ser	Pro	Ile	Phe	Gln	Arg	Phe	Val	Glu	Ala	His	Arg	Leu		
			190					195					200				
gat	att	wcc	ccc	ssn	ccc	csc	caa	aaa	aat	gat	caa	aat	cat	caa	aac	675	
Asp	Ile	Xaa	Pro	Xaa	Pro	Xaa	Gln	Lys	Asn	Asp	Gln	Asn	His	Gln	Asn		
		205					210					215					
gat	caa	aat	cat	cga	tcg	ctt	gaa	gaa	att	caa	aaa	agc	gtc	tta	aac	723	
Asp	Gln	Asn	His	Arg	Ser	Leu	Glu	Glu	Ile	Gln	Lys	Ser	Val	Leu	Asn		
220						225					230						
gaa	ttt	aac	ctt	aaa	gac	acc	gac	acc	cca	aaa	agc	cct	aaa	gac	acc	771	
Glu	Phe	Asn	Leu	Lys	Asp	Thr	Asp	Thr	Pro	Lys	Ser	Pro	Lys	Asp	Thr		
235					240					245					250		
ccc	aca	aac	tcc	ctt	tta	act	tcg	ttt	tgc	tct	cca	aaa	agg	ctt	tgc	819	
Pro	Thr	Asn	Ser	Leu	Leu	Thr	Ser	Phe	Cys	Ser	Pro	Lys	Arg	Leu	Cys		
			255						260					265			
ttt	atc	cta	aaa	tac	ggc	atc	act	ttc	tta	aaa	gaa	aaa	tca	gag	ttt	867	
Phe	Ile	Leu	Lys	Tyr	Gly	Ile	Ser	Phe	Leu	Lys	Glu	Lys	Ser	Glu	Phe		
		270					275						280				
aaa	aaa	cac	gtt	tgg	cgt	tat	gcg	cag	atc	ttt	gcg	agc	ttg	aac	gtt	915	
Lys	Lys	His	Val	Trp	Arg	Tyr	Ala	Gln	Met	Phe	Ala	Ser	Leu	Asn	Val		
		285					290					295					
tta	aaa	gaa	ttg	caa	aag	cat	tat	gca	aca	aac	caa	aac	cta	aaa	gat	963	
Leu	Lys	Glu	Leu	Gln	Lys	His	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	Lys	Asp		
300						305					310						
ccc	cta	aaa	ggc	atc	atc	tgg	cac	acg	caa	ggc	agc	ggt	aaa	acc	gcc	1011	
Pro	Leu	Lys	Gly	Ile	Ile	Trp	His	Thr	Gln	Gly	Ser	Gly	Lys	Thr	Ala		
315					320					325					330		
tta	acc	tac	cac	tta	acc	aaa	ctc	atc	aga	gac	ttt	ttt	agc	cga	tcc	1059	
Leu	Thr	Tyr	His	Leu	Thr	Lys	Leu	Ile	Arg	Asp	Phe	Phe	Ser	Arg	Ser		
				335					340					345			
aac	cta	aac	aaa	aag	act	aaa	ttt	tat	ttt	att	gtg	gac	agg	ttg	gat	1107	
Asn	Leu	Asn	Lys	Lys	Thr	Lys	Phe	Tyr	Phe	Ile	Val	Asp	Arg	Leu	Asp		
			350				355						360				
tta	ttg	gag	caa	gcc	aaa	aac	gag	ttt	tta	aaa	aga	ggc	ctt	tgt	gtc	1155	
Leu	Leu	Glu	Gln	Ala	Lys	Asn	Glu	Phe	Leu	Lys	Arg	Gly	Leu	Cys	Val		
		365					370					375					

cat gag gca gaa aat aaa gag gat ttg agc caa aaa tta aaa agc tct	1203
His Glu Ala Glu Asn Lys Glu Asp Leu Ser Gln Lys Leu Lys Ser Ser	
380 385 390	
agc gtt ttt gaa ggc tct caa ggg aat gat gaa atc atc gtt gtg aat	1251
Ser Val Phe Glu Gly Ser Gln Gly Asn Asp Glu Ile Ile Val Val Asn	
395 400 405 410	
atc caa aaa ttc aaa gcc ccc aat gaa gaa aaa tcc ccc aat gaa gac	1299
Ile Gln Lys Phe Lys Ala Pro Asn Glu Glu Lys Ser Pro Asn Glu Asp	
415 420 425	
ccc tct aat agc gct cct aaa gaa atc att tct aaa aca gaa tta caa	1347
Pro Ser Asn Ser Ala Pro Lys Glu Ile Ile Ser Lys Thr Glu Leu Gln	
430 435 440	
gaa tcc att caa aac agc cgc aat tta caa agg gtg ttt atc ata gat	1395
Glu Ser Ile Gln Asn Ser Arg Asn Leu Gln Arg Val Phe Ile Ile Asp	
445 450 455	
gaa gcc cac agg agc tac gat cct aaa ggt tgc ttt tac gct aat ttg	1443
Glu Ala His Arg Ser Tyr Asp Pro Lys Gly Cys Phe Tyr Ala Asn Leu	
460 465 470	
ata gaa tgc gac aag aca gca att aaa atc gcc ctc aca ggc acg ccc	1491
Ile Glu Cys Asp Lys Thr Ala Ile Lys Ile Ala Leu Thr Gly Thr Pro	
475 480 485 490	
cta tta gaa gac aac gcg caa gat aaa gcc act aaa aac act ttt ggc	1539
Leu Leu Glu Asp Asn Ala Gln Asp Lys Ala Thr Lys Asn Thr Phe Gly	
495 500 505	
aac tac ttg cac acc tat tct tat aca gaa tcc att aaa gac aga cac	1587
Asn Tyr Leu His Thr Tyr Ser Tyr Thr Glu Ser Ile Lys Asp Arg His	
510 515 520	
acc cta aaa ctc cag tta gaa agc att gaa acg agc tat aaa gaa aaa	1635
Thr Leu Lys Leu Gln Leu Glu Ser Ile Glu Thr Ser Tyr Lys Glu Lys	
525 530 535	
tta caa gaa atc tat cgc ctt tta caa gaa agc atc act att gaa gac	1683
Leu Gln Glu Ile Tyr Arg Leu Leu Gln Glu Ser Ile Thr Ile Glu Asp	
540 545 550	
aca gaa gtt aaa aaa gaa acg att ttt aac gat gaa aaa tac att aac	1731
Thr Glu Val Lys Lys Glu Thr Ile Phe Asn Asp Glu Lys Tyr Ile Asn	
555 560 565 570	
gcc atg ctc tat tat atc att aga gat tta ttg gat ttt agg cgt ttg	1779
Ala Met Leu Tyr Tyr Ile Ile Arg Asp Leu Leu Asp Phe Arg Arg Leu	
575 580 585	
aat gat aat gaa cgc tta aag gct atg gtg gtt tgt ttt tct agc aag	1827
Asn Asp Asn Glu Arg Leu Lys Ala Met Val Val Cys Phe Ser Ser Lys	
590 595 600	
caa gcc aga tta gct gat tgt ctt ttt aat gaa gtc caa gaa aaa gtc	1875
Gln Ala Arg Leu Ala Asp Cys Leu Phe Asn Glu Val Gln Glu Lys Val	
605 610 615	

tta caa gaa aac ccc aac cta agg att tta aac aaa ctc aaa tcc agc Leu Gln Glu Asn Pro Asn Leu Arg Ile Leu Asn Lys Leu Lys Ser Ser 620 625 630	1923
ctg att ttg cat gat gaa caa gaa gtc aaa gaa aag gtt cat tct ttc Leu Ile Leu His Asp Glu Gln Glu Val Lys Glu Lys Val His Ser Phe 635 640 645 650	1971
aaa cat gaa gat acc gat ata gtc ttt gtg ttt aac atg ctt tta acc Lys His Glu Asp Thr Asp Ile Val Phe Val Phe Asn Met Leu Leu Thr 655 660 665	2019
ggc ttt gat tta ccc agt ctc aaa cgc ctt tat atc cac aga gaa tta Gly Phe Asp Leu Pro Ser Leu Lys Arg Leu Tyr Ile His Arg Glu Leu 670 675 680	2067
aaa gat cac aat ttg ctc caa gcc cta gcc aga gtg aat cgc tcc tat Lys Asp His Asn Leu Leu Gln Ala Leu Ala Arg Val Asn Arg Ser Tyr 685 690 695	2115
aaa aac atg tct ttt ggc tac ctt ata gat ttt gta ggc att caa gaa Lys Asn Met Ser Phe Gly Tyr Leu Ile Asp Phe Val Gly Ile Gln Glu 700 705 710	2163
aat ttt gac aaa acg act gat gat tac ttg aaa gaa tta aac cga ttc Asn Phe Asp Lys Thr Thr Asp Asp Tyr Leu Lys Glu Leu Asn Arg Phe 715 720 725 730	2211
aat caa agc ggt gcc aat agc gat tct cat atc aaa gac atg ttt gcc Asn Gln Ser Gly Ala Asn Ser Asp Ser His Ile Lys Asp Met Phe Ala 735 740 745	2259
gat cgt aag act tta gaa gaa gac att aaa aac gcc tat gat gat ctt Asp Arg Lys Thr Leu Glu Glu Asp Ile Lys Asn Ala Tyr Asp Asp Leu 750 755 760	2307
ttt gat tac ccc att gac gat ata gag ggc atg act agc gcc att gtc Phe Asp Tyr Pro Ile Asp Asp Ile Glu Gly Met Thr Ser Ala Ile Val 765 770 775	2355
agc atg agc gca atg aac gag ctt gta aaa gtc tca cgc gcc att aac Ser Met Ser Ala Met Asn Glu Leu Val Lys Val Ser Arg Ala Ile Asn 780 785 790	2403
acg ctc aaa gag cgc tac aat tta atc cgc act tct aat gat aaa aaa Thr Leu Lys Glu Arg Tyr Asn Leu Ile Arg Thr Ser Asn Asp Lys Lys 795 800 805 810	2451
atc ctt tca cta aaa gaa aaa att gat att gaa aag atc cat aaa atc Ile Leu Ser Leu Lys Glu Lys Ile Asp Ile Glu Lys Ile His Lys Ile 815 820 825	2499
tct tca atg ctt cat caa aaa gcc aaa cac ctc cat gcg tta aag aat Ser Ser Met Leu His Gln Lys Ala Lys His Leu His Ala Leu Lys Asn 830 835 840	2547
atc aat gag cct aaa aac cca aac gat tta atg att tta gaa gac ctc Ile Asn Glu Pro Lys Asn Pro Asn Asp Leu Met Ile Leu Glu Asp Leu 850 855 860	2595

845	850	855	
atc gct ctt tta gac ttt aaa ata gag ttt aaa gaa cgc aaa gaa tta			2643
Ile Ala Leu Leu Asp Phe Lys Ile Glu Phe Lys Glu Arg Lys Glu Leu			
860	865	870	
cgc ttt aaa gaa caa gaa gag att acc acc aaa caa aag caa gct aaa			2691
Arg Phe Lys Glu Gln Glu Glu Ile Thr Thr Lys Gln Lys Gln Ala Lys			
875	880	885	890
gag att tta gaa aaa atc ccg gat caa caa gat aaa gaa atc caa aag			2739
Glu Ile Leu Glu Lys Ile Pro Asp Gln Gln Asp Lys Glu Ile Gln Lys			
	895	900	905
ttt tac aaa gac ttt tca aaa tta ctc caa acg ccc aca aca agc cag			2787
Phe Tyr Lys Asp Phe Ser Lys Leu Leu Gln Thr Pro Thr Thr Ser Gln			
	910	915	920
aat ttt gag gaa att tct cat tcc tat gat gcg atc att tca caa ctc			2835
Asn Phe Glu Glu Ile Ser His Ser Tyr Asp Ala Ile Ile Ser Gln Leu			
	925	930	935
aaa caa cac aaa gaa caa acc acc cac tta tta aac aaa tac gat aat			2883
Lys Gln His Lys Glu Gln Thr Thr His Leu Leu Asn Lys Tyr Asp Asn			
	940	945	950
gat ttg tct tat gcg atc acg aac aaa cgc ctt cat aag cac ctt atg			2931
Asp Leu Ser Tyr Ala Ile Thr Asn Lys Arg Leu His Lys His Leu Met			
	955	960	965
gaa caa aac att tct aac tca gcg gca att ttc acg ctt tta agc gcc			2979
Glu Gln Asn Ile Ser Asn Ser Ala Gly Ile Phe Thr Leu Leu Ser Ala			
	975	980	985
tta aaa aaa gct att gat gcg cgt att ttt aag cgt caa gaa atc tta			3027
Leu Lys Lys Ala Ile Asp Ala Arg Ile Phe Lys Arg Gln Glu Ile Leu			
	990	995	1000
aac gaa gag tat tac cta aaa aat gcc ata aaa gca gaa tta aat aac			3075
Asn Glu Glu Tyr Tyr Leu Lys Asn Ala Ile Lys Ala Glu Leu Asn Asn			
	1005	1010	1015
gct ttc aaa aaa gac ccc tcc tta aaa gat tta gaa aaa gaa aaa gaa			3123
Ala Phe Lys Lys Asp Pro Ser Leu Lys Asp Leu Glu Lys Glu Lys Glu			
	1020	1025	1030
ctt atc att caa acc ctt ttt aac gaa ctc aca caa aac cac cat caa			3171
Leu Ile Ile Gln Thr Leu Phe Asn Glu Leu Thr Gln Asn His His Gln			
	1035	1040	1045
gga aat ccg cat gcc taataacgct ttattgcaaa tcaaacaaga caccct			3222
Gly Asn Pro His Ala			
	1055		

<210> 596
 <211> 1055
 <212> PRT
 <213> Helicobacter pylori

<220>

<221> VARIANT

<222> 205, 207, 209

<223> Xaa = Any Amino Acid

<400> 596

Met	Pro	Tyr	Asn	Glu	Ile	Thr	Arg	Val	Gln	Ile	Pro	Ala	Leu	Met	His
1				5					10					15	
Leu	Ala	Lys	Leu	Gly	Tyr	Asp	Phe	Ile	Pro	Thr	Asn	Ser	Lys	Glu	Asn
			20					25					30		
Lys	Pro	Asn	Leu	Asp	Thr	Ala	Thr	Asn	Ile	Leu	Thr	Asn	Ser	Phe	Thr
		35					40					45			
Lys	Ser	Phe	Glu	Arg	Leu	Asn	Pro	Thr	Lys	Asn	Ala	Gln	Glu	Thr	Leu
	50					55					60				
Ala	Glu	Met	Lys	Lys	Arg	Leu	Asn	Cys	Asp	Asp	Leu	Gly	Lys	Ser	Phe
65					70					75					80
Tyr	Glu	Tyr	Leu	Leu	Lys	Ser	Glu	Asn	Gln	Ile	Ile	Asp	Phe	Asp	Asn
				85					90					95	
Pro	Asn	Asn	Asn	Leu	Tyr	Glu	Met	Met	Thr	Glu	Leu	Pro	Tyr	Lys	Ser
			100					105						110	
Phe	Arg	Pro	Asp	Thr	Thr	Leu	Phe	Ile	Asn	Gly	Leu	Pro	Leu	Val	Asn
		115					120					125			
Ile	Glu	Val	Lys	Gln	Pro	Tyr	Ala	Lys	Lys	Gly	Ile	Lys	Glu	Glu	Arg
	130					135					140				
Asp	Arg	His	Ile	Lys	Arg	Tyr	Glu	Asn	Pro	Glu	Asn	Lys	Val	Phe	Tyr
145					150					155					160
Asn	Leu	Ala	Gln	Ile	Trp	Leu	Phe	Ser	Asp	Asn	Leu	Pro	Tyr	Asp	Glu
			165						170					175	
Asn	Lys	Pro	Asp	Gln	Gly	Ala	Phe	Tyr	Ser	Ala	Ser	Tyr	Ser	Pro	Ile
			180					185					190		
Phe	Gln	Arg	Phe	Val	Glu	Ala	His	Arg	Leu	Asp	Ile	Xaa	Pro	Xaa	Pro
		195					200					205			
Xaa	Gln	Lys	Asn	Asp	Gln	Asn	His	Gln	Asn	Asp	Gln	Asn	His	Arg	Ser
	210					215					220				
Leu	Glu	Glu	Ile	Gln	Lys	Ser	Val	Leu	Asn	Glu	Phe	Asn	Leu	Lys	Asp
225					230					235					240
Thr	Asp	Thr	Pro	Lys	Ser	Pro	Lys	Asp	Thr	Pro	Thr	Asn	Ser	Leu	Leu
				245					250					255	
Thr	Ser	Phe	Cys	Ser	Pro	Lys	Arg	Leu	Cys	Phe	Ile	Leu	Lys	Tyr	Gly
		260						265					270		
Ile	Ser	Phe	Leu	Lys	Glu	Lys	Ser	Glu	Phe	Lys	Lys	His	Val	Trp	Arg
	275						280					285			
Tyr	Ala	Gln	Met	Phe	Ala	Ser	Leu	Asn	Val	Leu	Lys	Glu	Leu	Gln	Lys
	290					295					300				
His	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	Lys	Asp	Pro	Leu	Lys	Gly	Ile	Ile
305					310					315					320
Trp	His	Thr	Gln	Gly	Ser	Gly	Lys	Thr	Ala	Leu	Thr	Tyr	His	Leu	Thr
			325						330					335	
Lys	Leu	Ile	Arg	Asp	Phe	Phe	Ser	Arg	Ser	Asn	Leu	Asn	Lys	Lys	Thr
			340					345					350		
Lys	Phe	Tyr	Phe	Ile	Val	Asp	Arg	Leu	Asp	Leu	Leu	Glu	Gln	Ala	Lys
		355					360					365			
Asn	Glu	Phe	Leu	Lys	Arg	Gly	Leu	Cys	Val	His	Glu	Ala	Glu	Asn	Lys
	370					375					380				
Glu	Asp	Leu	Ser	Gln	Lys	Leu	Lys	Ser	Ser	Ser	Val	Phe	Glu	Gly	Ser
385					390					395					400
Gln	Gly	Asn	Asp	Glu	Ile	Ile	Val	Val	Asn	Ile	Gln	Lys	Phe	Lys	Ala
				405					410					415	
Pro	Asn	Glu	Glu	Lys	Ser	Pro	Asn	Glu	Asp	Pro	Ser	Asn	Ser	Ala	Pro

			420					425					430				
Lys	Glu	Ile	Ile	Ser	Lys	Thr	Glu	Leu	Gln	Glu	Ser	Ile	Gln	Asn	Ser		
		435					440					445					
Arg	Asn	Leu	Gln	Arg	Val	Phe	Ile	Ile	Asp	Glu	Ala	His	Arg	Ser	Tyr		
	450					455					460						
Asp	Pro	Lys	Gly	Cys	Phe	Tyr	Ala	Asn	Leu	Ile	Glu	Cys	Asp	Lys	Thr		
465					470					475					480		
Ala	Ile	Lys	Ile	Ala	Leu	Thr	Gly	Thr	Pro	Leu	Leu	Glu	Asp	Asn	Ala		
				485					490					495			
Gln	Asp	Lys	Ala	Thr	Lys	Asn	Thr	Phe	Gly	Asn	Tyr	Leu	His	Thr	Tyr		
			500					505					510				
Ser	Tyr	Thr	Glu	Ser	Ile	Lys	Asp	Arg	His	Thr	Leu	Lys	Leu	Gln	Leu		
	515						520					525					
Glu	Ser	Ile	Glu	Thr	Ser	Tyr	Lys	Glu	Lys	Leu	Gln	Glu	Ile	Tyr	Arg		
	530					535					540						
Leu	Leu	Gln	Glu	Ser	Ile	Thr	Ile	Glu	Asp	Thr	Glu	Val	Lys	Lys	Glu		
545					550				555						560		
Thr	Ile	Phe	Asn	Asp	Glu	Lys	Tyr	Ile	Asn	Ala	Met	Leu	Tyr	Tyr	Ile		
			565					570						575			
Ile	Arg	Asp	Leu	Leu	Asp	Phe	Arg	Arg	Leu	Asn	Asp	Asn	Glu	Arg	Leu		
			580					585					590				
Lys	Ala	Met	Val	Val	Cys	Phe	Ser	Ser	Lys	Gln	Ala	Arg	Leu	Ala	Asp		
	595						600					605					
Cys	Leu	Phe	Asn	Glu	Val	Gln	Glu	Lys	Val	Leu	Gln	Glu	Asn	Pro	Asn		
	610					615					620						
Leu	Arg	Ile	Leu	Asn	Lys	Leu	Lys	Ser	Ser	Leu	Ile	Leu	His	Asp	Glu		
625					630					635					640		
Gln	Glu	Val	Lys	Glu	Lys	Val	His	Ser	Phe	Lys	His	Glu	Asp	Thr	Asp		
			645						650					655			
Ile	Val	Phe	Val	Phe	Asn	Met	Leu	Leu	Thr	Gly	Phe	Asp	Leu	Pro	Ser		
			660					665					670				
Leu	Lys	Arg	Leu	Tyr	Ile	His	Arg	Glu	Leu	Lys	Asp	His	Asn	Leu	Leu		
	675						680					685					
Gln	Ala	Leu	Ala	Arg	Val	Asn	Arg	Ser	Tyr	Lys	Asn	Met	Ser	Phe	Gly		
	690					695					700						
Tyr	Leu	Ile	Asp	Phe	Val	Gly	Ile	Gln	Glu	Asn	Phe	Asp	Lys	Thr	Thr		
705					710				715						720		
Asp	Asp	Tyr	Leu	Lys	Glu	Leu	Asn	Arg	Phe	Asn	Gln	Ser	Gly	Ala	Asn		
			725					730						735			
Ser	Asp	Ser	His	Ile	Lys	Asp	Met	Phe	Ala	Asp	Arg	Lys	Thr	Leu	Glu		
	740						745						750				
Glu	Asp	Ile	Lys	Asn	Ala	Tyr	Asp	Asp	Leu	Phe	Asp	Tyr	Pro	Ile	Asp		
	755						760					765					
Asp	Ile	Glu	Gly	Met	Thr	Ser	Ala	Ile	Val	Ser	Met	Ser	Ala	Met	Asn		
	770					775					780						
Glu	Leu	Val	Lys	Val	Ser	Arg	Ala	Ile	Asn	Thr	Leu	Lys	Glu	Arg	Tyr		
785					790					795					800		
Asn	Leu	Ile	Arg	Thr	Ser	Asn	Asp	Lys	Lys	Ile	Leu	Ser	Leu	Lys	Glu		
			805						810					815			
Lys	Ile	Asp	Ile	Glu	Lys	Ile	His	Lys	Ile	Ser	Ser	Met	Leu	His	Gln		
			820					825					830				
Lys	Ala	Lys	His	Leu	His	Ala	Leu	Lys	Asn	Ile	Asn	Glu	Pro	Lys	Asn		
	835						840					845					
Pro	Asn	Asp	Leu	Met	Ile	Leu	Glu	Asp	Leu	Ile	Ala	Leu	Leu	Asp	Phe		
	850					855					860						
Lys	Ile	Glu	Phe	Lys	Glu	Arg	Lys	Glu	Leu	Arg	Phe	Lys	Glu	Gln	Glu		
865					870				875						880		
Glu	Ile	Thr	Thr	Lys	Gln	Lys	Gln	Ala	Lys	Glu	Ile	Leu	Glu	Lys	Ile		
			885						890					895			

Pro Asp Gln Gln Asp Lys Glu Ile Gln Lys Phe Tyr Lys Asp Phe Ser
 900 905 910
 Lys Leu Leu Gln Thr Pro Thr Thr Ser Gln Asn Phe Glu Glu Ile Ser
 915 920 925
 His Ser Tyr Asp Ala Ile Ile Ser Gln Leu Lys Gln His Lys Glu Gln
 930 935 940
 Thr Thr His Leu Leu Asn Lys Tyr Asp Asn Asp Leu Ser Tyr Ala Ile
 945 950 955 960
 Thr Asn Lys Arg Leu His Lys His Leu Met Glu Gln Asn Ile Ser Asn
 965 970 975
 Ser Ala Gly Ile Phe Thr Leu Leu Ser Ala Leu Lys Lys Ala Ile Asp
 980 985 990
 Ala Arg Ile Phe Lys Arg Gln Glu Ile Leu Asn Glu Glu Tyr Tyr Leu
 995 1000 1005
 Lys Asn Ala Ile Lys Ala Glu Leu Asn Asn Ala Phe Lys Lys Asp Pro
 1010 1015 1020
 Ser Leu Lys Asp Leu Glu Lys Glu Lys Glu Leu Ile Ile Gln Thr Leu
 1025 1030 1035 1040
 Phe Asn Glu Leu Thr Gln Asn His His Gln Gly Asn Pro His Ala
 1045 1050 1055

<210> 597
 <211> 574
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (26)...(511)

<400> 597
 tagaagaatt tgaaaggttg ctcgc atg caa aga gaa tta agg ctt tta aat 52
 Met Gln Arg Glu Leu Arg Leu Leu Asn
 1 5

 aac aag cat tgc atg gaa tac ttg caa ttt ctg tcc aaa aac cat ttg 100
 Asn Lys His Cys Met Glu Tyr Leu Gln Phe Leu Ser Lys Asn His Leu
 10 15 20 25

 agt ttt aac ctt ttg tgc gaa aga gat gcg att gat ttt tcc ccc aag 148
 Ser Phe Asn Leu Leu Cys Glu Arg Asp Ala Ile Asp Phe Ser Pro Lys
 30 35 40

 ctc cct aaa gaa att cat gaa aaa ttc gcc gcg tta gtg cta ttt gtt 196
 Leu Pro Lys Glu Ile His Glu Lys Phe Gly Ala Leu Val Leu Phe Val
 45 50 55

 tta gcc gga tac acc tta gaa agc ttg ata att gat aca aaa agc gtc 244
 Leu Ala Gly Tyr Thr Leu Glu Ser Leu Ile Ile Asp Thr Lys Ser Val
 60 65 70

 caa ttt gaa gcc ggg ttt gcc cct aat aac att gcc agt gtg gtt caa 292
 Gln Phe Glu Ala Gly Phe Gly Pro Asn Asn Ile Gly Ser Val Val Gln
 75 80 85

 gta aaa ctt cct gcc atc att caa atc ctt atc aaa gaa aaa aat gaa 340
 Val Lys Leu Pro Gly Ile Ile Gln Ile Leu Ile Lys Glu Lys Asn Glu
 90 95 100 105

aat gcc gtt tta ttc aat cgt tgc gat tcg ctt gaa ttg ttt caa aaa 386
 Asn Ala Val Leu Phe Asn Arg Cys Asp Ser Leu Glu Leu Phe Gln Lys
 110 115 120

gaa gat tca atc gcg caa gag cca aaa aaa gac gag cgg gag tct aaa 436
 Glu Asp Ser Ile Ala Gln Glu Pro Lys Lys Asp Glu Arg Glu Ser Lys
 125 130 135

gaa tgg ctg gat tct aaa gag gct ctt ttt tcc aat tcc aaa aac cgc 484
 Glu Trp Leu Asp Ser Lys Glu Ala Leu Phe Ser Asn Ser Lys Asn Arg
 140 145 150

gcg att tta gaa aat ctg cac aaa agc taaaggaatc attgatgagc 531
 Ala Ile Leu Glu Asn Leu His Lys Ser
 155 160

gttttgaaat tgcattgtaaa agtctttcgt tttgaaacca ata 574

<210> 598

<211> 162

<212> PRT

<213> Helicobacter pylori

<400> 598

Met Gln Arg Glu Leu Arg Leu Leu Asn Asn Lys His Cys Met Glu Tyr
 1 5 10 15
 Leu Gln Phe Leu Ser Lys Asn His Leu Ser Phe Asn Leu Leu Cys Glu
 20 25 30
 Arg Asp Ala Ile Asp Phe Ser Pro Lys Leu Pro Lys Glu Ile His Glu
 35 40 45
 Lys Phe Gly Ala Leu Val Leu Phe Val Leu Ala Gly Tyr Thr Leu Glu
 50 55 60
 Ser Leu Ile Ile Asp Thr Lys Ser Val Gln Phe Glu Ala Gly Phe Gly
 65 70 75 80
 Pro Asn Asn Ile Gly Ser Val Val Gln Val Lys Leu Pro Gly Ile Ile
 85 90 95
 Gln Ile Leu Ile Lys Glu Lys Asn Glu Asn Ala Val Leu Phe Asn Arg
 100 105 110
 Cys Asp Ser Leu Glu Leu Phe Gln Lys Glu Asp Ser Ile Ala Gln Glu
 115 120 125
 Pro Lys Lys Asp Glu Arg Glu Ser Lys Glu Trp Leu Asp Ser Lys Glu
 130 135 140
 Ala Leu Phe Ser Asn Ser Lys Asn Arg Ala Ile Leu Glu Asn Leu His
 145 150 155 160
 Lys Ser

<210> 599

<211> 1697

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (14)...(1648)

<400> 599

tttagggggg taa atg cct tca aac gct ctt ttg att gaa gaa atc act	49
Met Pro Ser Asn Ala Leu Leu Ile Glu Glu Ile Thr	
1 5 10	
cat tta atc aat gtt tct cat agt agc gtg cat aat tgg atc aaa acc	97
His Leu Ile Asn Val Ser His Ser Ser Val His Asn Trp Ile Lys Thr	
15 20 25	
aat ctt tta gag aaa cta gaa att gat cat aaa att tat gtg aaa acg	145
Asn Leu Leu Glu Lys Leu Glu Ile Asp His Lys Ile Tyr Val Lys Thr	
30 35 40	
agt tct ttt tta gat ttt tgc cgc aac cat tta ggg aaa aac aag ctt	193
Ser Ser Phe Leu Asp Phe Cys Arg Asn His Leu Gly Lys Asn Lys Leu	
45 50 55 60	
aac aaa tac gct aac aaa tcc tta aaa ggc gtg cat aac cat caa gaa	241
Asn Lys Tyr Ala Asn Lys Ser Leu Lys Gly Val His Asn His Gln Glu	
65 70 75	
ttg att tta aaa tac cta gaa ata tta gaa aat agc tct gat cta gaa	289
Leu Ile Leu Lys Tyr Leu Glu Ile Leu Glu Asn Ser Ser Asp Leu Glu	
80 85 90	
aag ttg ggt tct tat tat gaa gaa gag ctt tct aac gcc acc aga aat	337
Lys Leu Gly Ser Tyr Tyr Glu Glu Glu Leu Ser Asn Ala Thr Arg Asn	
95 100 105	
tta gaa ggc att tac tac act cct aac agg ata gta gaa caa ctt ttc	385
Leu Glu Gly Ile Tyr Tyr Thr Pro Asn Arg Ile Val Glu Gln Leu Phe	
110 115 120	
acc ctc cct aaa gat ttt gat gtc tct caa gcc att ttt tgc gat ccg	433
Thr Leu Pro Lys Asp Phe Asp Val Ser Gln Ala Ile Phe Cys Asp Pro	
125 130 135 140	
gct gtg ggg agt ggg aat ttt atc atg cat gct tta aaa ctg ggt ttt	481
Ala Val Gly Ser Gly Asn Phe Ile Met His Ala Leu Lys Leu Gly Phe	
145 150 155	
aag gtt gaa aac att tat ggc tat gat acg gac gct ttt gct gtc gct	529
Lys Val Glu Asn Ile Tyr Gly Tyr Asp Thr Asp Ala Phe Ala Val Ala	
160 165 170	
ttg act aaa aag cgt att aaa gag cgt tat cat tta gat tgc ctt aat	577
Leu Thr Lys Lys Arg Ile Lys Glu Arg Tyr His Leu Asp Cys Leu Asn	
175 180 185	
att gtg caa aaa gat ttt tta aat tta aaa cac acc ccg caa ttt gat	625
Ile Val Gln Lys Asp Phe Leu Asn Leu Lys His Thr Pro Gln Phe Asp	
190 195 200	
tgc att ttc act aac ccg cca tgg ggc aag aaa tac aat caa aac caa	673
Cys Ile Phe Thr Asn Pro Pro Trp Gly Lys Lys Tyr Asn Gln Asn Gln	
205 210 215 220	
aaa gaa aat ttt aaa cag caa ttc aac ctc tct caa agc cta gat agc	721
Lys Glu Asn Phe Lys Gln Gln Phe Asn Leu Ser Gln Ser Leu Asp Ser	
225 230 235	

gcg tcg ctc ttt ttt ata gcg agt ttg aat tgt tta aaa gaa aac gct	769
Ala Ser Leu Phe Phe Ile Ala Ser Leu Asn Cys Leu Lys Glu Asn Ala	
240 245 250	
cat ttg ggg tta tta tta ccc gaa agt tgt ttg aat att gat gcg ttt	817
His Leu Gly Leu Leu Leu Pro Glu Ser Cys Leu Asn Ile Asp Ala Phe	
255 260 265	
aaa aaa atg cga gaa atg gct tta aag ttt cac att aga agc ctg att	865
Lys Lys Met Arg Glu Met Ala Leu Lys Phe His Ile Arg Ser Leu Ile	
270 275 280	
gat ttt gac aaa cct ttt aaa aat cta atg act aag gct gtg ggt ttg	913
Asp Phe Asp Lys Pro Phe Lys Asn Leu Met Thr Lys Ala Val Gly Leu	
285 290 295 300	
gcg ctt aaa aaa acc cct aat aag gat caa aaa atc tca tgc ttt tat	961
Ala Leu Lys Lys Thr Pro Asn Lys Asp Gln Lys Ile Ser Cys Phe Tyr	
305 310 315	
caa aat agc aag ttc aaa cgc tcg ccc tct tct ttt ttt aac aac cct	1009
Gln Asn Ser Lys Phe Lys Arg Ser Pro Ser Ser Phe Phe Asn Asn Pro	
320 325 330	
aaa aag att ttt aat atc cat tgc tct agc aaa gaa aat aaa att tta	1057
Lys Lys Ile Phe Asn Ile His Cys Ser Ser Lys Glu Asn Lys Ile Leu	
335 340 345	
gac cac ctt ttt tcc ctc cct cat atg act tta aaa aat aac gct cat	1105
Asp His Leu Phe Ser Leu Pro His Met Thr Leu Lys Asn Asn Ala His	
350 355 360	
ttt gct tta ggg att gtt aca ggc aac aat aaa gaa aaa tta cac ccc	1153
Phe Ala Leu Gly Ile Val Thr Gly Asn Asn Lys Glu Lys Leu His Pro	
365 370 375 380	
aaa caa gaa aaa aat acc att ccc att ttt agg ggt tca gat att tta	1201
Lys Gln Glu Lys Asn Thr Ile Pro Ile Phe Arg Gly Ser Asp Ile Leu	
385 390 395	
aaa gac gga tta aaa gcc cct agc caa ttc att aac gct ggt tta aaa	1249
Lys Asp Gly Leu Lys Ala Pro Ser Gln Phe Ile Asn Ala Gly Leu Lys	
400 405 410	
gac tgc cag caa gtc gcc ccc tta agc ctt tat caa gct aga gaa aaa	1297
Asp Cys Gln Gln Val Ala Pro Leu Ser Leu Tyr Gln Ala Arg Glu Lys	
415 420 425	
atc gtg tat aaa ttc att tct tca aag ctt gtc ttt ttt tat gac aat	1345
Ile Val Tyr Lys Phe Ile Ser Ser Lys Leu Val Phe Phe Tyr Asp Asn	
430 435 440	
aag caa cgc ctt ttt tta aac agc gcg aac atg ttt gtt tta aaa gaa	1393
Lys Gln Arg Leu Phe Leu Asn Ser Ala Asn Met Phe Val Leu Lys Glu	
445 450 455 460	
aat ttc cct atc aac gct cat gca tta aaa gaa ttg tta aac agc gat	1441
Asn Phe Pro Ile Asn Ala His Ala Leu Lys Glu Leu Leu Asn Ser Asp	

465	470	475	
tta atg caa ttc att ttt gaa tcg ctt ttt aaa acg cat aaa atc tta			1489
Leu Met Gln Phe Ile Phe Glu Ser Leu Phe Lys Thr His Lys Ile Leu			
480	485	490	
aga aaa gat ttg gaa tgt ttg ccc cta ttt gtg caa ttt att aac gat			1537
Arg Lys Asp Leu Glu Cys Leu Pro Leu Phe Val Gln Phe Ile Asn Asp			
495	500	505	
aat ttt gat gaa aaa ttt tat tta aaa aat tta ggg ata gaa aaa aaa			1585
Asn Phe Asp Glu Lys Phe Tyr Leu Lys Asn Leu Gly Ile Glu Lys Lys			
510	515	520	
gac cct aaa cat ttc acc atc agg aaa aat cat gca tgt tgc ttg tct			1633
Asp Pro Lys His Phe Thr Ile Arg Lys Asn His Ala Cys Cys Leu Ser			
525	530	535	540
ttt ggc ttt agg gga taatctcatc acgcttagcc ttttaaaga aatcgctttc			1688
Phe Gly Phe Arg Gly			
545			
aaacagcaa			1697
<210> 600			
<211> 545			
<212> PRT			
<213> Helicobacter pylori			
<400> 600			
Met Pro Ser Asn Ala Leu Leu Ile Glu Glu Ile Thr His Leu Ile Asn			
1 5 10 15			
Val Ser His Ser Val His Asn Trp Ile Lys Thr Asn Leu Leu Glu			
20 25 30			
Lys Leu Glu Ile Asp His Lys Ile Tyr Val Lys Thr Ser Ser Phe Leu			
35 40 45			
Asp Phe Cys Arg Asn His Leu Gly Lys Asn Lys Leu Asn Lys Tyr Ala			
50 55 60			
Asn Lys Ser Leu Lys Gly Val His Asn His Gln Glu Leu Ile Leu Lys			
65 70 75 80			
Tyr Leu Glu Ile Leu Glu Asn Ser Ser Asp Leu Glu Lys Leu Gly Ser			
85 90 95			
Tyr Tyr Glu Glu Glu Leu Ser Asn Ala Thr Arg Asn Leu Glu Gly Ile			
100 105 110			
Tyr Tyr Thr Pro Asn Arg Ile Val Glu Gln Leu Phe Thr Leu Pro Lys			
115 120 125			
Asp Phe Asp Val Ser Gln Ala Ile Phe Cys Asp Pro Ala Val Gly Ser			
130 135 140			
Gly Asn Phe Ile Met His Ala Leu Lys Leu Gly Phe Lys Val Glu Asn			
145 150 155 160			
Ile Tyr Gly Tyr Asp Thr Asp Ala Phe Ala Val Ala Leu Thr Lys Lys			
165 170 175			
Arg Ile Lys Glu Arg Tyr His Leu Asp Cys Leu Asn Ile Val Gln Lys			
180 185 190			
Asp Phe Leu Asn Leu Lys His Thr Pro Gln Phe Asp Cys Ile Phe Thr			
195 200 205			
Asn Pro Pro Trp Gly Lys Lys Tyr Asn Gln Asn Gln Lys Glu Asn Phe			
210 215 220			
Lys Gln Gln Phe Asn Leu Ser Gln Ser Leu Asp Ser Ala Ser Leu Phe			

225					230					235					240
Phe	Ile	Ala	Ser	Leu	Asn	Cys	Leu	Lys	Glu	Asn	Ala	His	Leu	Gly	Leu
				245					250					255	
Leu	Leu	Pro	Glu	Ser	Cys	Leu	Asn	Ile	Asp	Ala	Phe	Lys	Lys	Met	Arg
			260					265						270	
Glu	Met	Ala	Leu	Lys	Phe	His	Ile	Arg	Ser	Leu	Ile	Asp	Phe	Asp	Lys
		275					280					285			
Pro	Phe	Lys	Asn	Leu	Met	Thr	Lys	Ala	Val	Gly	Leu	Ala	Leu	Lys	Lys
	290					295					300				
Thr	Pro	Asn	Lys	Asp	Gln	Lys	Ile	Ser	Cys	Phe	Tyr	Gln	Asn	Ser	Lys
305					310					315					320
Phe	Lys	Arg	Ser	Pro	Ser	Ser	Phe	Phe	Asn	Asn	Pro	Lys	Lys	Ile	Phe
				325					330					335	
Asn	Ile	His	Cys	Ser	Ser	Lys	Glu	Asn	Lys	Ile	Leu	Asp	His	Leu	Phe
			340					345					350		
Ser	Leu	Pro	His	Met	Thr	Leu	Lys	Asn	Asn	Ala	His	Phe	Ala	Leu	Gly
		355					360					365			
Ile	Val	Thr	Gly	Asn	Asn	Lys	Glu	Lys	Leu	His	Pro	Lys	Gln	Glu	Lys
	370					375					380				
Asn	Thr	Ile	Pro	Ile	Phe	Arg	Gly	Ser	Asp	Ile	Leu	Lys	Asp	Gly	Leu
385					390				395						400
Lys	Ala	Pro	Ser	Gln	Phe	Ile	Asn	Ala	Gly	Leu	Lys	Asp	Cys	Gln	Gln
				405					410					415	
Val	Ala	Pro	Leu	Ser	Leu	Tyr	Gln	Ala	Arg	Glu	Lys	Ile	Val	Tyr	Lys
		420						425					430		
Phe	Ile	Ser	Lys	Leu	Val	Phe	Phe	Tyr	Asp	Asn	Lys	Gln	Arg	Leu	
	435					440				445					
Phe	Leu	Asn	Ser	Ala	Asn	Met	Phe	Val	Leu	Lys	Glu	Asn	Phe	Pro	Ile
	450				455					460					
Asn	Ala	His	Ala	Leu	Lys	Glu	Leu	Leu	Asn	Ser	Asp	Leu	Met	Gln	Phe
465					470				475					480	
Ile	Phe	Glu	Ser	Leu	Phe	Lys	Thr	His	Lys	Ile	Leu	Arg	Lys	Asp	Leu
			485						490					495	
Glu	Cys	Leu	Pro	Leu	Phe	Val	Gln	Phe	Ile	Asn	Asp	Asn	Phe	Asp	Glu
			500					505					510		
Lys	Phe	Tyr	Leu	Lys	Asn	Leu	Gly	Ile	Glu	Lys	Lys	Asp	Pro	Lys	His
	515						520					525			
Phe	Thr	Ile	Arg	Lys	Asn	His	Ala	Cys	Cys	Leu	Ser	Phe	Gly	Phe	Arg
	530					535					540				
Gly															
545															

<210> 601
 <211> 1884
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (46)...(1842)

<400> 601
 tatttgtgta tacttctaatt ttcaattttg ctgttagga cattt atg aaa aat att 57
 Met Lys Asn Ile
 1

aga aat atc gct gta atc gcg cat gtt gat cat ggg aaa acc act cta 105
 Arg Asn Ile Ala Val Ile Ala His Val Asp His Gly Lys Thr Thr Leu

5	10	15	20	
gta gat ggc tta ctt tct caa tct ggc aca ttt agt gag agg gaa aaa	153			
Val Asp Gly Leu Leu Ser Gln Ser Gly Thr Phe Ser Glu Arg Glu Lys				
25 30 35				
gtg gat gaa agg gtg atg gat agc aat gat ttg gaa aga gaa aga ggg	201			
Val Asp Glu Arg Val Met Asp Ser Asn Asp Leu Glu Arg Glu Arg Gly				
40 45 50				
att act atc ctg tct aaa aac acc gct att tat tac aaa gac act aaa	249			
Ile Thr Ile Leu Ser Lys Asn Thr Ala Ile Tyr Tyr Lys Asp Thr Lys				
55 60 65				
atc aat atc att gac act ccc ggg cat gct gat ttt ggg ggc gaa gtg	297			
Ile Asn Ile Ile Asp Thr Pro Gly His Ala Asp Phe Gly Gly Glu Val				
70 75 80				
gag cgc gtt tta aaa atg gtg gat ggg gtg ttg ctt tta gtg gac gct	345			
Glu Arg Val Leu Lys Met Val Asp Gly Val Leu Leu Leu Val Asp Ala				
85 90 95 100				
caa gaa ggg gtc atg cct caa act aaa ttc gtg gtt aaa aag gct ttg	393			
Gln Glu Gly Val Met Pro Gln Thr Lys Phe Val Val Lys Lys Ala Leu				
105 110 115				
agt ttt ggg att tgc cct att gtg gtg gtg aat aaa att gat aag cct	441			
Ser Phe Gly Ile Cys Pro Ile Val Val Val Asn Lys Ile Asp Lys Pro				
120 125 130				
gcc gct gaa ccg gac aga gtg gtg gat gaa gtt ttt gac ttg ttc gta	489			
Ala Ala Glu Pro Asp Arg Val Val Asp Glu Val Phe Asp Leu Phe Val				
135 140 145				
gcc atg ggg cct agc gat aag caa ttg gat ttc cct gtg gtg tat gcc	537			
Ala Met Gly Ala Ser Asp Lys Gln Leu Asp Phe Pro Val Val Tyr Ala				
150 155 160				
gcc gca cga gat ggc tat gcg atg aaa agt tta gac gat gaa aag aaa	585			
Ala Ala Arg Asp Gly Tyr Ala Met Lys Ser Leu Asp Asp Glu Lys Lys				
165 170 175 180				
aat tta gag cct ttg ttt gaa acg att tta gag cat gtg cca agc cct	633			
Asn Leu Glu Pro Leu Phe Glu Thr Ile Leu Glu His Val Pro Ser Pro				
185 190 195				
agc ggg agc gtt gat gag cct ttg caa atg caa att ttc acg ctt gat	681			
Ser Gly Ser Val Asp Glu Pro Leu Gln Met Gln Ile Phe Thr Leu Asp				
200 205 210				
tat gac aat tat gtg ggc aaa atc ggt atc gct agg gtg ttt aat ggc	729			
Tyr Asp Asn Tyr Val Gly Lys Ile Gly Ile Ala Arg Val Phe Asn Gly				
215 220 225				
tcg gtt aaa aag aat gaa agc gtg ctg ttg atg aaa agc gat ggg agt	777			
Ser Val Lys Lys Asn Glu Ser Val Leu Leu Met Lys Ser Asp Gly Ser				
230 235 240				
aaa gaa aat ggc cgt atc act aag ctt ata ggt ttt tta ggg ctg gct	825			

Lys 245	Glu	Asn	Gly	Arg	Ile 250	Thr	Lys	Leu	Ile	Gly 255	Phe	Leu	Gly	Leu	Ala 260	
agg	act	gag	att	gaa	aac	gct	tat	gcg	ggc	gat	att	gta	gcg	att	gcc	873
Arg	Thr	Glu	Ile	Glu 265	Asn	Ala	Tyr	Ala	Gly 270	Asp	Ile	Val	Ala	Ile	Ala 275	
ggg	ttt	aat	gca	atg	gat	gtg	ggc	gat	agc	gtc	ggt	gat	cct	gct	aac	921
Gly	Phe	Asn	Ala 280	Met	Asp	Val	Gly	Asp 285	Ser	Val	Val	Asp	Pro 290	Ala	Asn	
ccc	atg	cct	tta	gat	ccc	atg	cat	tta	gaa	gag	cct	acg	atg	agc	gtg	969
Pro	Met	Pro 295	Leu	Asp	Pro	Met	His 300	Leu	Glu	Glu	Pro	Thr 305	Met	Ser	Val	
tat	ttt	gct	gtc	aat	gat	tca	ccc	tta	gcc	ggg	tta	gaa	gga	aag	cat	1017
Tyr	Phe	Ala	Val	Asn	Asp	Ser 315	Pro	Leu	Ala	Gly 320	Leu	Glu	Gly	Lys	His	
310																
ggt	act	gct	aat	aaa	ttg	aaa	gac	agg	ctc	tta	aaa	gaa	atg	caa	acc	1065
Val	Thr	Ala	Asn	Lys	Leu 330	Lys	Asp	Arg	Leu	Leu 335	Lys	Glu	Met	Gln	Thr 340	
325																
aat	atc	gct	atg	aaa	tgc	gaa	gaa	atg	ggc	gag	ggc	aag	ttt	aaa	gtg	1113
Asn	Ile	Ala	Met	Lys 345	Cys	Glu	Glu	Met	Gly 350	Glu	Gly	Lys	Phe	Lys	Val 355	
345																
agt	ggg	cgt	ggg	gaa	ttg	caa	atc	act	att	tta	gct	gaa	aac	ttg	cgc	1161
Ser	Gly	Arg	Gly 360	Glu	Leu	Gln	Ile	Thr 365	Ile	Leu	Ala	Glu	Asn	Leu	Arg 370	
360																
cgt	gaa	ggg	ttt	gaa	ttt	agc	att	tca	cgc	cct	gaa	gtc	atc	att	aaa	1209
Arg	Glu	Gly 375	Phe	Glu	Phe	Ser	Ile 380	Ser	Arg	Pro	Glu	Val	Ile	Ile	Lys 385	
375																
gaa	gaa	aat	ggc	ggt	aaa	tgc	gag	cct	ttt	gag	cat	tta	gtg	att	gac	1257
Glu	Glu	Asn	Gly	Val	Lys	Cys 395	Glu	Pro	Phe	Glu	His 400	Leu	Val	Ile	Asp	
390																
acg	ccc	caa	gat	ttt	agt	ggg	gct	atc	att	gag	aga	ttg	ggc	aaa	aga	1305
Thr	Pro	Gln	Asp	Phe	Ser 410	Gly	Ala	Ile	Ile	Glu 415	Arg	Leu	Gly	Lys	Arg 420	
405																
aaa	gct	gag	atg	aaa	gcg	atg	aat	ccc	atg	agt	gat	ggc	tat	aca	aga	1353
Lys	Ala	Glu	Met	Lys 425	Ala	Met	Asn	Pro	Met 430	Ser	Asp	Gly	Tyr	Thr	Arg 435	
425																
tta	gaa	ttt	gaa	att	cct	gca	aga	ggg	ctt	atc	ggt	tat	agg	agc	gag	1401
Leu	Glu	Phe	Glu 440	Ile	Pro	Ala	Arg	Gly 445	Leu	Ile	Gly	Tyr	Arg	Ser	Glu 450	
440																
ttt	tta	acc	gac	acc	aag	ggc	gaa	ggc	gtg	atg	aat	cat	agc	ttt	tta	1449
Phe	Leu	Thr 455	Asp	Thr	Lys	Gly	Glu 460	Gly	Val	Met	Asn	His 465	Ser	Phe	Leu 470	
455																
gaa	ttc	cgc	cct	ttc	agc	ggg	agc	gtg	gaa	tcg	cgc	aaa	aat	ggg	ggc	1497
Glu	Phe	Arg	Pro	Phe	Ser 475	Gly	Ser	Val	Glu	Ser	Arg 480	Lys	Asn	Gly	Ala 485	
470																

cta atc aqc atg gaa aat ggc gaa gcg acc gct ttt tcc ctt ttc aat 1545
 Leu Ile Ser Met Glu Asn Gly Glu Ala Thr Ala Phe Ser Leu Phe Asn
 485 490 495 500

atc caa gaa aga ggc acg ctt ttt atc aac ccc caa acg aag gtt tat 1593
 Ile Gln Glu Arg Gly Thr Leu Phe Ile Asn Pro Gln Thr Lys Val Tyr
 505 510 515

gtg ggc atg gtc att ggc gag cac agc cgg gat aat gat tta gat gtc 1641
 Val Gly Met Val Ile Gly Glu His Ser Arg Asp Asn Asp Leu Asp Val
 520 525 530

aat cct att aaa tcc aag cat tta acc aac atg aga gcg agc ggg agc 1689
 Asn Pro Ile Lys Ser Lys His Leu Thr Asn Met Arg Ala Ser Gly Ser
 535 540 545

gat gat gcg atc aaa ctc acc ccg cct agg act atg gtg tta gaa aga 1737
 Asp Asp Ala Ile Lys Leu Thr Pro Pro Arg Thr Met Val Leu Glu Arg
 550 555 560

gcg tta gaa tgg att gaa gaa gat gag att ttg gaa gtt acc ccc ttg 1785
 Ala Leu Glu Trp Ile Glu Glu Asp Glu Ile Leu Glu Val Thr Pro Leu
 565 570 575 580

aat tta agg atc agg aaa aag att tta gac cct aac atg agg aaa agg 1833
 Asn Leu Arg Ile Arg Lys Lys Ile Leu Asp Pro Asn Met Arg Lys Arg
 585 590 595

gcg aaa aaa taaatagaat tttttggaat gcatgccaat ttattcaacc 1862
 Ala Lys Lys

aa 1884

<210> 602

<211> 599

<212> PRT

<213> Helicobacter pylori

<400> 602

Met Lys Asn Ile Arg Asn Ile Ala Val Ile Ala His Val Asp His Gly
 1 5 10 15
 Lys Thr Thr Leu Val Asp Gly Leu Leu Ser Gln Ser Gly Thr Phe Ser
 20 25 30
 Glu Arg Glu Lys Val Asp Glu Arg Val Met Asp Ser Asn Asp Leu Glu
 35 40 45
 Arg Glu Arg Gly Ile Thr Ile Leu Ser Lys Asn Thr Ala Ile Tyr Tyr
 50 55 60
 Lys Asp Thr Lys Ile Asn Ile Ile Asp Thr Pro Gly His Ala Asp Phe
 65 70 75 80
 Gly Gly Glu Val Glu Arg Val Leu Lys Met Val Asp Gly Val Leu Leu
 85 90 95
 Leu Val Asp Ala Gln Glu Gly Val Met Pro Gln Thr Lys Phe Val Val
 100 105 110
 Lys Lys Ala Leu Ser Phe Gly Ile Cys Pro Ile Val Val Val Asn Lys
 115 120 125
 Ile Asp Lys Pro Ala Ala Glu Pro Asp Arg Val Val Asp Glu Val Phe
 130 135 140
 Asp Leu Phe Val Ala Met Gly Ala Ser Asp Lys Gln Leu Asp Phe Pro

145					150					155					160
Val	Val	Tyr	Ala	Ala	Ala	Arg	Asp	Gly	Tyr	Ala	Met	Lys	Ser	Leu	Asp
				165					170						175
Asp	Glu	Lys	Lys	Asn	Leu	Glu	Pro	Leu	Phe	Glu	Thr	Ile	Leu	Glu	His
			180					185					190		
Val	Pro	Ser	Pro	Ser	Gly	Ser	Val	Asp	Glu	Pro	Leu	Gln	Met	Gln	Ile
		195					200					205			
Phe	Thr	Leu	Asp	Tyr	Asp	Asn	Tyr	Val	Gly	Lys	Ile	Gly	Ile	Ala	Arg
	210					215					220				
Val	Phe	Asn	Gly	Ser	Val	Lys	Lys	Asn	Glu	Ser	Val	Leu	Leu	Met	Lys
225					230					235					240
Ser	Asp	Gly	Ser	Lys	Glu	Asn	Gly	Arg	Ile	Thr	Lys	Leu	Ile	Gly	Phe
				245					250					255	
Leu	Gly	Leu	Ala	Arg	Thr	Glu	Ile	Glu	Asn	Ala	Tyr	Ala	Gly	Asp	Ile
			260					265					270		
Val	Ala	Ile	Ala	Gly	Phe	Asn	Ala	Met	Asp	Val	Gly	Asp	Ser	Val	Val
		275					280					285			
Asp	Pro	Ala	Asn	Pro	Met	Pro	Leu	Asp	Pro	Met	His	Leu	Glu	Glu	Pro
	290					295					300				
Thr	Met	Ser	Val	Tyr	Phe	Ala	Val	Asn	Asp	Ser	Pro	Leu	Ala	Gly	Leu
305					310					315					320
Glu	Gly	Lys	His	Val	Thr	Ala	Asn	Lys	Leu	Lys	Asp	Arg	Leu	Leu	Lys
			325						330					335	
Glu	Met	Gln	Thr	Asn	Ile	Ala	Met	Lys	Cys	Glu	Glu	Met	Gly	Glu	Gly
			340					345					350		
Lys	Phe	Lys	Val	Ser	Gly	Arg	Gly	Glu	Leu	Gln	Ile	Thr	Ile	Leu	Ala
	355						360					365			
Glu	Asn	Leu	Arg	Arg	Glu	Gly	Phe	Glu	Phe	Ser	Ile	Ser	Arg	Pro	Glu
	370					375					380				
Val	Ile	Ile	Lys	Glu	Glu	Asn	Gly	Val	Lys	Cys	Glu	Pro	Phe	Glu	His
385					390					395					400
Leu	Val	Ile	Asp	Thr	Pro	Gln	Asp	Phe	Ser	Gly	Ala	Ile	Ile	Glu	Arg
			405						410					415	
Leu	Gly	Lys	Arg	Lys	Ala	Glu	Met	Lys	Ala	Met	Asn	Pro	Met	Ser	Asp
			420					425					430		
Gly	Tyr	Thr	Arg	Leu	Glu	Phe	Glu	Ile	Pro	Ala	Arg	Gly	Leu	Ile	Gly
		435					440					445			
Tyr	Arg	Ser	Glu	Phe	Leu	Thr	Asp	Thr	Lys	Gly	Glu	Gly	Val	Met	Asn
	450					455					460				
His	Ser	Phe	Leu	Glu	Phe	Arg	Pro	Phe	Ser	Gly	Ser	Val	Glu	Ser	Arg
465					470					475					480
Lys	Asn	Gly	Ala	Leu	Ile	Ser	Met	Glu	Asn	Gly	Glu	Ala	Thr	Ala	Phe
			485						490					495	
Ser	Leu	Phe	Asn	Ile	Gln	Glu	Arg	Gly	Thr	Leu	Phe	Ile	Asn	Pro	Gln
			500					505					510		
Thr	Lys	Val	Tyr	Val	Gly	Met	Val	Ile	Gly	Glu	His	Ser	Arg	Asp	Asn
		515					520						525		
Asp	Leu	Asp	Val	Asn	Pro	Ile	Lys	Ser	Lys	His	Leu	Thr	Asn	Met	Arg
	530					535					540				
Ala	Ser	Gly	Ser	Asp	Asp	Ala	Ile	Lys	Leu	Thr	Pro	Pro	Arg	Thr	Met
545					550					555					560
Val	Leu	Glu	Arg	Ala	Leu	Glu	Trp	Ile	Glu	Glu	Asp	Glu	Ile	Leu	Glu
			565						570					575	
Val	Thr	Pro	Leu	Asn	Leu	Arg	Ile	Arg	Lys	Lys	Ile	Leu	Asp	Pro	Asn
			580					585					590		
Met	Arg	Lys	Arg	Ala	Lys	Lys									
		595													

<210> 603
 <211> 880
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (54)...(839)

```

<400> 603
ttctactagg cggaccacca tgccagagct attctaccct tggcaaaaga aaa atg      56
                                         Met
                                         1

gat gaa aaa gcg aat ctg ttt aaa gaa tat ttg cgg ctt tta gat tta      104
Asp Glu Lys Ala Asn Leu Phe Lys Glu Tyr Leu Arg Leu Leu Asp Leu
                    5                      10                      15

gta aaa cca aaa ata ttt gtt ttt gaa aat gtg gtg ggt tta atg tct      152
Val Lys Pro Lys Ile Phe Val Phe Glu Asn Val Val Gly Leu Met Ser
                    20                      25                      30

atg caa aaa ggg caa tta ttc aaa caa att tgt aac gct ttt aaa gag      200
Met Gln Lys Gly Gln Leu Phe Lys Gln Ile Cys Asn Ala Phe Lys Glu
                    35                      40                      45

aga gat tat att tta gag cat gcc att ttg aac gcc cta gat tat ggt      248
Arg Asp Tyr Ile Leu Glu His Ala Ile Leu Asn Ala Leu Asp Tyr Gly
                    50                      55                      60                      65

gtg cct caa atg aga gaa cga gtg att tta gtg ggc gtg ctt aaa agc      296
Val Pro Gln Met Arg Glu Arg Val Ile Leu Val Gly Val Leu Lys Ser
                    70                      75                      80

ttt aaa caa aaa ttt tac ttc cct aaa ccc ata aaa acg cat ttt tct      344
Phe Lys Gln Lys Phe Tyr Phe Pro Lys Pro Ile Lys Thr His Phe Ser
                    85                      90                      95

ctg aaa gac gct tta ggg gat tta cca ccc att caa agc ggt gaa aat      392
Leu Lys Asp Ala Leu Gly Asp Leu Pro Pro Ile Gln Ser Gly Glu Asn
                    100                      105                      110

ggg gat gct tta ggt tat ctt aaa aat gcg gat aat gtt ttt ttg gaa      440
Gly Asp Ala Leu Gly Tyr Leu Lys Asn Ala Asp Asn Val Phe Leu Glu
                    115                      120                      125

ttt gtg cga aat tct aaa gaa tta agc gaa cat agc agt cct aaa aac      488
Phe Val Arg Asn Ser Lys Glu Leu Ser Glu His Ser Ser Pro Lys Asn
                    130                      135                      140                      145

aat gaa aaa ctg ata aaa atc atg caa acg cta aaa gac gga cag agt      536
Asn Glu Lys Leu Ile Lys Ile Met Gln Thr Leu Lys Asp Gly Gln Ser
                    150                      155                      160

aaa gat gat ttg cca gaa agt ctg cgt ccc aaa agt ggt tat att aat      584
Lys Asp Asp Leu Pro Glu Ser Leu Arg Pro Lys Ser Gly Tyr Ile Asn
                    165                      170                      175

acc tat gcc aaa atg tgg tgg gaa aaa cca gcc ccc acc att aca aga      632

```

Thr	Tyr	Ala	Lys	Met	Trp	Trp	Glu	Lys	Pro	Ala	Pro	Thr	Ile	Thr	Arg		
		180					185					190					
aat	ttt	tct	acc	cca	agc	agt	tct	agg	tgt	atc	cat	cca	aga	gac	tct	680	
Asn	Phe	Ser	Thr	Pro	Ser	Ser	Ser	Arg	Cys	Ile	His	Pro	Arg	Asp	Ser		
	195					200					205						
aga	gcg	tta	agc	att	aga	gag	ggg	gca	aga	ttg	caa	agc	ttt	cct	gat	728	
Arg	Ala	Leu	Ser	Ile	Arg	Glu	Gly	Ala	Arg	Leu	Gln	Ser	Phe	Pro	Asp		
	210				215					220					225		
aat	tat	aaa	ttc	tgt	ggg	agt	ggg	agc	gct	aaa	aga	ttg	caa	att	ggc	776	
Asn	Tyr	Lys	Phe	Cys	Gly	Ser	Gly	Ser	Ala	Lys	Arg	Leu	Gln	Ile	Gly		
				230					235					240			
aat	gcc	gtg	ccg	cct	tta	ttg	agt	gta	gcg	ctc	gcg	cag	gcg	gtc	ttt	824	
Asn	Ala	Val		Pro	Leu	Leu	Ser	Val	Ala	Leu	Ala	Gln	Ala	Val	Phe		
			245					250					255				
gac	ttt	tta	aag	ggg	taagatg	ttt	aacaataatg	actttaagga	ttacagaaaa							879	
Asp	Phe	Leu	Lys	Gly													
		260															
t																	880

<210> 604
 <211> 262
 <212> PRT
 <213> Helicobacter pylori

<400> 604

Met	Asp	Glu	Lys	Ala	Asn	Leu	Phe	Lys	Glu	Tyr	Leu	Arg	Leu	Leu	Asp		
1				5					10					15			
Leu	Val	Lys	Pro	Lys	Ile	Phe	Val	Phe	Glu	Asn	Val	Val	Gly	Leu	Met		
			20					25					30				
Ser	Met	Gln	Lys	Gly	Gln	Leu	Phe	Lys	Gln	Ile	Cys	Asn	Ala	Phe	Lys		
		35					40					45					
Glu	Arg	Asp	Tyr	Ile	Leu	Glu	His	Ala	Ile	Leu	Asn	Ala	Leu	Asp	Tyr		
	50				55						60						
Gly	Val	Pro	Gln	Met	Arg	Glu	Arg	Val	Ile	Leu	Val	Gly	Val	Leu	Lys		
	65			70					75					80			
Ser	Phe	Lys	Gln	Lys	Phe	Tyr	Phe	Pro	Lys	Pro	Ile	Lys	Thr	His	Phe		
			85					90						95			
Ser	Leu	Lys	Asp	Ala	Leu	Gly	Asp	Leu	Pro	Pro	Ile	Gln	Ser	Gly	Glu		
			100					105					110				
Asn	Gly	Asp	Ala	Leu	Gly	Tyr	Leu	Lys	Asn	Ala	Asp	Asn	Val	Phe	Leu		
		115					120					125					
Glu	Phe	Val	Arg	Asn	Ser	Lys	Glu	Leu	Ser	Glu	His	Ser	Ser	Pro	Lys		
	130				135						140						
Asn	Asn	Glu	Lys	Leu	Ile	Lys	Ile	Met	Gln	Thr	Leu	Lys	Asp	Gly	Gln		
	145			150					155						160		
Ser	Lys	Asp	Asp	Leu	Pro	Glu	Ser	Leu	Arg	Pro	Lys	Ser	Gly	Tyr	Ile		
			165					170						175			
Asn	Thr	Tyr	Ala	Lys	Met	Trp	Trp	Glu	Lys	Pro	Ala	Pro	Thr	Ile	Thr		
			180					185					190				
Arg	Asn	Phe	Ser	Thr	Pro	Ser	Ser	Ser	Arg	Cys	Ile	His	Pro	Arg	Asp		
		195				200						205					
Ser	Arg	Ala	Leu	Ser	Ile	Arg	Glu	Gly	Ala	Arg	Leu	Gln	Ser	Phe	Pro		
	210					215					220						

Asp Asn Tyr Lys Phe Cys Gly Ser Gly Ser Ala Lys Arg Leu Gln Ile
 225 230 235 240
 Gly Asn Ala Val Pro Pro Leu Leu Ser Val Ala Leu Ala Gln Ala Val
 245 250 255
 Phe Asp Phe Leu Lys Gly
 260

<210> 605
 <211> 1376
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (13)...(1338)

<400> 605
 tggtagttaa ga atg ggt aat cat ttt tct aaa tta gga ttt gtt tta gcc 51
 Met Gly Asn His Phe Ser Lys Leu Gly Phe Val Leu Ala
 1 5 10

 gca tta gga agc gcg ata ggt tta ggg cat atc tgg cgt ttc ccc tac 99
 Ala Leu Gly Ser Ala Ile Gly Leu Gly His Ile Trp Arg Phe Pro Tyr
 15 20 25

 atg act ggg gtg act ggt ggg ggt gct ttt gtt tta ttg ttt tta ttt 147
 Met Thr Gly Val Ser Gly Gly Gly Ala Phe Val Leu Leu Phe Leu Phe
 30 35 40 45

 tta tct tta aoc gtt ggc gcg gcg atg ttt atc gct gaa atg cta tta 195
 Leu Ser Leu Ser Val Gly Ala Ala Met Phe Ile Ala Glu Met Leu Leu
 50 55 60

 gga caa agc act caa aaa aat gta aca gaa gct ttt aaa gag ctt gac 243
 Gly Gln Ser Thr Gln Lys Asn Val Thr Glu Ala Phe Lys Glu Leu Asp
 65 70 75

 att aac ccc aaa aaa cgc tgg aaa tac gca ggg ctt ttg ctt gtt tct 291
 Ile Asn Pro Lys Lys Arg Trp Lys Tyr Ala Gly Leu Leu Leu Val Ser
 80 85 90

 ggg cca tta ata ctg act ttt tac ggc acg att tta ggt tgg gtg ctt 339
 Gly Pro Leu Ile Leu Thr Phe Tyr Gly Thr Ile Leu Gly Trp Val Leu
 95 100 105

 tat tat ttg gtg agt gtt agt ttt aat ttg cct aac aat atc caa gaa 387
 Tyr Tyr Leu Val Ser Val Ser Phe Asn Leu Pro Asn Asn Ile Gln Glu
 110 115 120 125

 tct gaa caa att ttt act caa act ttg cag tct ata ggg cta caa tcc 435
 Ser Glu Gln Ile Phe Thr Gln Thr Leu Gln Ser Ile Gly Leu Gln Ser
 130 135 140

 ata ggg ctt ttt agc gtt tta ttg ata acc gga tgg att gtt tct agc 483
 Ile Gly Leu Phe Ser Val Leu Leu Ile Thr Gly Trp Ile Val Ser Arg
 145 150 155

 ggg att aaa gaa ggc att gaa aag ctc aat ttg gtt tta atg ccc tta 531

Gly	Ile	Lys	Glu	Gly	Ile	Glu	Lys	Leu	Asn	Leu	Val	Leu	Met	Pro	Leu	
		160					165					170				
ctc	ttt	gct	act	ttt	ttt	ggt	ttg	ctt	ttc	tat	gcg	atg	agc	atg	gat	579
Leu	Phe	Ala	Thr	Phe	Phe	Gly	Leu	Leu	Phe	Tyr	Ala	Met	Ser	Met	Asp	
		175				180					185					
tct	ttt	tct	aaa	gct	ttt	cat	ttc	atg	ttt	gat	ttc	aaa	cca	aaa	gat	627
Ser	Phe	Ser	Lys	Ala	Phe	His	Phe	Met	Phe	Asp	Phe	Lys	Pro	Lys	Asp	
		190			195					200					205	
ttg	acc	tct	caa	gtg	ttc	act	tat	tcc	ttg	ggg	cag	gtt	ttc	ttt	tcc	675
Leu	Thr	Ser	Gln	Val	Phe	Thr	Tyr	Ser	Leu	Gly	Gln	Val	Phe	Phe	Ser	
				210					215					220		
tta	agc	atc	ggt	tta	ggg	atc	aat	atc	act	tac	gct	gcg	gtt	acg	gat	723
Leu	Ser	Ile	Gly	Leu	Gly	Ile	Asn	Ile	Thr	Tyr	Ala	Ala	Val	Thr	Asp	
			225					230					235			
aaa	acg	cag	aat	ttg	ctt	aaa	agc	act	att	tgg	gtg	gtt	tta	tca	gga	771
Lys	Thr	Gln	Asn	Leu	Leu	Lys	Ser	Thr	Ile	Trp	Val	Val	Leu	Ser	Gly	
		240					245					250				
att	cta	att	tct	ctt	gtg	gca	gga	ctt	atg	att	ttc	act	ttt	gtg	ttt	819
Ile	Leu	Ile	Ser	Leu	Val	Ala	Gly	Leu	Met	Ile	Phe	Thr	Phe	Val	Phe	
		255				260					265					
gaa	tat	ggg	gcg	aat	gtc	tca	caa	ggc	aca	ggg	tta	atc	ttc	act	tct	867
Glu	Tyr	Gly	Ala	Asn	Val	Ser	Gln	Gly	Thr	Gly	Leu	Ile	Phe	Thr	Ser	
		270			275					280					285	
tta	ccg	gtg	gtt	ttt	ggc	caa	atg	gga	gcg	ata	ggc	att	ctt	gtt	tcc	915
Leu	Pro	Val	Val	Phe	Gly	Gln	Met	Gly	Ala	Ile	Gly	Ile	Leu	Val	Ser	
				290					295					300		
att	ctt	ttc	ttg	ctc	ggc	ctc	gct	ttt	gct	ggc	atc	act	tct	acg	gtg	963
Ile	Leu	Phe	Leu	Leu	Ala	Leu	Ala	Phe	Ala	Gly	Ile	Thr	Ser	Thr	Val	
			305					310					315			
gct	tta	ttg	gag	cca	agc	gtg	atg	tat	ctt	acc	gaa	agg	tat	caa	tac	1011
Ala	Leu	Leu	Glu	Pro	Ser	Val	Met	Tyr	Leu	Thr	Glu	Arg	Tyr	Gln	Tyr	
			320				325					330				
tct	cgt	ttt	aag	gtt	act	tgg	ggt	ctt	gta	gca	cta	att	ttt	gtg	gta	1059
Ser	Arg	Phe	Lys	Val	Thr	Trp	Gly	Leu	Val	Ala	Leu	Ile	Phe	Val	Val	
		335				340					345					
ggc	gtg	gtg	ttg	att	ttc	tcg	ctc	cat	aag	gat	tat	aaa	gat	tat	ctc	1107
Gly	Val	Val	Leu	Ile	Phe	Ser	Leu	His	Lys	Asp	Tyr	Lys	Asp	Tyr	Leu	
					355					360					365	
act	ttc	ttt	gaa	aaa	agt	ctt	ttt	gat	tgg	ttg	gat	ttt	gca	tca	agc	1155
Thr	Phe	Phe	Glu	Lys	Ser	Leu	Phe	Asp	Trp	Leu	Asp	Phe	Ala	Ser	Ser	
				370					375					380		
acc	att	atc	atg	cct	tta	ggc	ggg	atg	gca	acc	ttt	att	ttt	atg	ggt	1203
Thr	Ile	Ile	Met	Pro	Leu	Gly	Gly	Met	Ala	Thr	Phe	Ile	Phe	Met	Gly	
			385					390					395			

tgg gtt ttg aaa aaa gaa aaa ttg cgt ctt ttg agc gtg cac ttt tta	1251
Trp Val Leu Lys Lys Glu Lys Leu Arg Leu Leu Ser Val His Phe Leu	
400 405 410	

ggc cct aaa ttg ttt gca act ttg tat ttc ttg ctt aaa tat atc acc	1299
Gly Pro Lys Leu Phe Ala Thr Trp Tyr Phe Leu Leu Lys Tyr Ile Thr	
415 420 425	

cct tta att gtg ttt tcc att ttg ttg agc aag att tat taaaatattt	1346
Pro Leu Ile Val Phe Ser Ile Trp Leu Ser Lys Ile Tyr	
430 435 440	

ggcatgggaa aattttctaa attaggct	1376
--------------------------------	------

<210> 606

<211> 442

<212> PRT

<213> Helicobacter pylori

<400> 606

Met Gly Asn His Phe Ser Lys Leu Gly Phe Val Leu Ala Ala Leu Gly	
1 5 10 15	
Ser Ala Ile Gly Leu Gly His Ile Trp Arg Phe Pro Tyr Met Thr Gly	
20 25 30	
Val Ser Gly Gly Gly Ala Phe Val Leu Leu Phe Leu Phe Leu Ser Leu	
35 40 45	
Ser Val Gly Ala Ala Met Phe Ile Ala Glu Met Leu Leu Gly Gln Ser	
50 55 60	
Thr Gln Lys Asn Val Thr Glu Ala Phe Lys Glu Leu Asp Ile Asn Pro	
65 70 75 80	
Lys Lys Arg Trp Lys Tyr Ala Gly Leu Leu Leu Val Ser Gly Pro Leu	
85 90 95	
Ile Leu Thr Phe Tyr Gly Thr Ile Leu Gly Trp Val Leu Tyr Tyr Leu	
100 105 110	
Val Ser Val Ser Phe Asn Leu Pro Asn Asn Ile Gln Glu Ser Glu Gln	
115 120 125	
Ile Phe Thr Gln Thr Leu Gln Ser Ile Gly Leu Gln Ser Ile Gly Leu	
130 135 140	
Phe Ser Val Leu Leu Ile Thr Gly Trp Ile Val Ser Arg Gly Ile Lys	
145 150 155 160	
Glu Gly Ile Glu Lys Leu Asn Leu Val Leu Met Pro Leu Leu Phe Ala	
165 170 175	
Thr Phe Phe Gly Leu Leu Phe Tyr Ala Met Ser Met Asp Ser Phe Ser	
180 185 190	
Lys Ala Phe His Phe Met Phe Asp Phe Lys Pro Lys Asp Leu Thr Ser	
195 200 205	
Gln Val Phe Thr Tyr Ser Leu Gly Gln Val Phe Phe Ser Leu Ser Ile	
210 215 220	
Gly Leu Gly Ile Asn Ile Thr Tyr Ala Ala Val Thr Asp Lys Thr Gln	
225 230 235 240	
Asn Leu Leu Lys Ser Thr Ile Trp Val Val Leu Ser Gly Ile Leu Ile	
245 250 255	
Ser Leu Val Ala Gly Leu Met Ile Phe Thr Phe Val Phe Glu Tyr Gly	
260 265 270	
Ala Asn Val Ser Gln Gly Thr Gly Leu Ile Phe Thr Ser Leu Pro Val	
275 280 285	
Val Phe Gly Gln Met Gly Ala Ile Gly Ile Leu Val Ser Ile Leu Phe	
290 295 300	
Leu Leu Ala Leu Ala Phe Ala Gly Ile Thr Ser Thr Val Ala Leu Leu	

305					310					315					320
Glu	Pro	Ser	Val	Met	Tyr	Leu	Thr	Glu	Arg	Tyr	Gln	Tyr	Ser	Arg	Phe
				325					330					335	
Lys	Val	Thr	Trp	Gly	Leu	Val	Ala	Leu	Ile	Phe	Val	Val	Gly	Val	Val
			340					345					350		
Leu	Ile	Phe	Ser	Leu	His	Lys	Asp	Tyr	Lys	Asp	Tyr	Leu	Thr	Phe	Phe
		355					360					365			
Glu	Lys	Ser	Leu	Phe	Asp	Trp	Leu	Asp	Phe	Ala	Ser	Ser	Thr	Ile	Ile
	370					375					380				
Met	Pro	Leu	Gly	Gly	Met	Ala	Thr	Phe	Ile	Phe	Met	Gly	Trp	Val	Leu
385					390					395					400
Lys	Lys	Glu	Lys	Leu	Arg	Leu	Leu	Ser	Val	His	Phe	Leu	Gly	Pro	Lys
				405					410					415	
Leu	Phe	Ala	Thr	Trp	Tyr	Phe	Leu	Leu	Lys	Tyr	Ile	Thr	Pro	Leu	Ile
			420				425						430		
Val	Phe	Ser	Ile	Trp	Leu	Ser	Lys	Ile	Tyr						
		435					440								

<210> 607
 <211> 1120
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (17)...(1081)

<400> 607
 gaaataagga tgcttg atg aaa agc att ttg ctc ttt atg att ttt gta gtt 52
 Met Lys Ser Ile Leu Leu Phe Met Ile Phe Val Val
 1 5 10

tgt cag tta gaa ggc aaa aaa ttt tca caa gat aat ttt aag gtg gat 100
 Cys Gln Leu Glu Gly Lys Lys Phe Ser Gln Asp Asn Phe Lys Val Asp
 15 20 25

tat aac tac tat ttg cgc aaa cag gat ttg cac atc att aaa acg caa 148
 Tyr Asn Tyr Tyr Leu Arg Lys Gln Asp Leu His Ile Ile Lys Thr Gln
 30 35 40

aac gat ttg tcc aat tct tgg tat ctc cct cca caa aaa gcc ccc aaa 196
 Asn Asp Leu Ser Asn Ser Trp Tyr Leu Pro Pro Gln Lys Ala Pro Lys
 45 50 55 60

gaa cat tct tgg gtg gat ttt gct aaa aaa tat tta aac atg atg gat 244
 Glu His Ser Trp Val Asp Phe Ala Lys Lys Tyr Leu Asn Met Met Asp
 65 70 75

tat cta ggc act tat ttt ctg cct ttt tat cat agt ttc acc ccc att 292
 Tyr Leu Gly Thr Tyr Phe Leu Pro Phe Tyr His Ser Phe Thr Pro Ile
 80 85 90

ttt caa tgg tac cac ccc aat atc aac ccg tat caa cgc aat gag ttt 340
 Phe Gln Trp Tyr His Pro Asn Ile Asn Pro Tyr Gln Arg Asn Glu Phe
 95 100 105

aag ttc caa att agt ttt aga gtg cct gta ttt agg cat att ctt tgc 388
 Lys Phe Gln Ile Ser Phe Arg Val Pro Val Phe Arg His Ile Leu Trp

110	115	120	
act aaa ggc acg ctg tat tta gct tat acc caa act gac tgg ttt caa			436
Thr Lys Gly Thr Leu Tyr Leu Ala Tyr Thr Gln Thr Asp Trp Phe Gln			
125	130	135	140
att tac aat gac ccc caa tcc gct ccc atg cga atg atg aat ttc atg			484
Ile Tyr Asn Asp Pro Gln Ser Ala Pro Met Arg Met Met Asn Phe Met			
	145	150	155
cct gaa ctc att tat gtt tat cct atc aat ttt aaa cct ttt ggg ggt			532
Pro Glu Leu Ile Tyr Val Tyr Pro Ile Asn Phe Lys Pro Phe Gly Gly			
	160	165	170
aaa ata ggg aat ttt tct gaa att tgg ata ggt tgg cag cac att tct			580
Lys Ile Gly Asn Phe Ser Glu Ile Trp Ile Gly Trp Gln His Ile Ser			
	175	180	185
aat ggc gtg ggg ggc gcg caa tgt tac caa cct ttt aat aaa gaa ggc			628
Asn Gly Val Gly Gly Ala Gln Cys Tyr Gln Pro Phe Asn Lys Glu Gly			
	190	195	200
aat cct gaa aac cag ttt cca gga caa cct gta atc gtt aaa gat tat			676
Asn Pro Glu Asn Gln Phe Pro Gly Gln Pro Val Ile Val Lys Asp Tyr			
205	210	215	220
aat ggg caa aaa gat gtg cgc tgg ggg ggg tgt cgt tcg gtg agc gcg			724
Asn Gly Gln Lys Asp Val Arg Trp Gly Gly Cys Arg Ser Val Ser Ala			
	225	230	235
ggc caa cgc cct gtg ttt cgt ttg gtg tgg gaa aag gga ggc cta aaa			772
Gly Gln Arg Pro Val Phe Arg Leu Val Trp Glu Lys Gly Gly Leu Lys			
	240	245	250
atc atg gtc gct tat tgg ccc tat gtc cct tat gat caa tcc aat cct			820
Ile Met Val Ala Tyr Trp Pro Tyr Val Pro Tyr Asp Gln Ser Asn Pro			
	255	260	265
aat ttg att gat tac atg ggg tat ggt aac gct aaa att gat tac agc			868
Asn Leu Ile Asp Tyr Met Gly Tyr Gly Asn Ala Lys Ile Asp Tyr Arg			
	270	275	280
aga ggg cgc cac cat ttt gaa ttg cag ctt tat gat att ttc acg caa			916
Arg Gly Arg His His Phe Glu Leu Gln Leu Tyr Asp Ile Phe Thr Gln			
285	290	295	300
tac tgg cgt tat gat cgc tgg cat gga gct ttc cgc tta ggc tat acc			964
Tyr Trp Arg Tyr Asp Arg Trp His Gly Ala Phe Arg Leu Gly Tyr Thr			
	305	310	315
tat cgc att aac cct ttt gtg ggg att tat gcg cag tgg ttt aac ggc			1012
Tyr Arg Ile Asn Pro Phe Val Gly Ile Tyr Ala Gln Trp Phe Asn Gly			
	320	325	330
tat ggc gat ggc ttg tat gaa tac gat gtt ttt tcc aat cgt ata ggc			1060
Tyr Gly Asp Gly Leu Tyr Glu Tyr Asp Val Phe Ser Asn Arg Ile Gly			
	335	340	345
gta gga ata cgc tta aac cct taaaaaagcg ttcttttayg ctataattaa			1111

Val Gly Ile Arg Leu Asn Pro
 350 355

gaccaaaaa

1120

<210> 608
 <211> 355
 <212> PRT
 <213> Helicobacter pylori

<400> 608
 Met Lys Ser Ile Leu Leu Phe Met Ile Phe Val Val Cys Gln Leu Glu
 1 5 10 15
 Gly Lys Lys Phe Ser Gln Asp Asn Phe Lys Val Asp Tyr Asn Tyr Tyr
 20 25 30
 Leu Arg Lys Gln Asp Leu His Ile Ile Lys Thr Gln Asn Asp Leu Ser
 35 40 45
 Asn Ser Trp Tyr Leu Pro Pro Gln Lys Ala Pro Lys Glu His Ser Trp
 50 55 60
 Val Asp Phe Ala Lys Lys Tyr Leu Asn Met Met Asp Tyr Leu Gly Thr
 65 70 75 80
 Tyr Phe Leu Pro Phe Tyr His Ser Phe Thr Pro Ile Phe Gln Trp Tyr
 85 90 95
 His Pro Asn Ile Asn Pro Tyr Gln Arg Asn Glu Phe Lys Phe Gln Ile
 100 105 110
 Ser Phe Arg Val Pro Val Phe Arg His Ile Leu Trp Thr Lys Gly Thr
 115 120 125
 Leu Tyr Leu Ala Tyr Thr Gln Thr Asp Trp Phe Gln Ile Tyr Asn Asp
 130 135 140
 Pro Gln Ser Ala Pro Met Arg Met Met Asn Phe Met Pro Glu Leu Ile
 145 150 155 160
 Tyr Val Tyr Pro Ile Asn Phe Lys Pro Phe Gly Gly Lys Ile Gly Asn
 165 170 175
 Phe Ser Glu Ile Trp Ile Gly Trp Gln His Ile Ser Asn Gly Val Gly
 180 185 190
 Gly Ala Gln Cys Tyr Gln Pro Phe Asn Lys Glu Gly Asn Pro Glu Asn
 195 200 205
 Gln Phe Pro Gly Gln Pro Val Ile Val Lys Asp Tyr Asn Gly Gln Lys
 210 215 220
 Asp Val Arg Trp Gly Gly Cys Arg Ser Val Ser Ala Gly Gln Arg Pro
 225 230 235 240
 Val Phe Arg Leu Val Trp Glu Lys Gly Gly Leu Lys Ile Met Val Ala
 245 250 255
 Tyr Trp Pro Tyr Val Pro Tyr Asp Gln Ser Asn Pro Asn Leu Ile Asp
 260 265 270
 Tyr Met Gly Tyr Gly Asn Ala Lys Ile Asp Tyr Arg Arg Gly Arg His
 275 280 285
 His Phe Glu Leu Gln Leu Tyr Asp Ile Phe Thr Gln Tyr Trp Arg Tyr
 290 295 300
 Asp Arg Trp His Gly Ala Phe Arg Leu Gly Tyr Thr Tyr Arg Ile Asn
 305 310 315 320
 Pro Phe Val Gly Ile Tyr Ala Gln Trp Phe Asn Gly Tyr Gly Asp Gly
 325 330 335
 Leu Tyr Glu Tyr Asp Val Phe Ser Asn Arg Ile Gly Val Gly Ile Arg
 340 345 350
 Leu Asn Pro
 355

<210> 609
 <211> 697
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (34)...(669)

<400> 609

```

aaaaaattca ttttatcttt tagagggttt tta atg tct tat ttt aag aat gct 54
                                Met Ser Tyr Phe Lys Asn Ala
                                1                               5

ttc aat caa aaa tct tta ata gat gat tct agt gtg tat tta gag cct 102
Phe Asn Gln Lys Ser Leu Ile Asp Asp Ser Ser Val Tyr Leu Glu Pro
                        10                               15                               20

tgt tct agc tct aat ttc ata gaa tta aaa cgc atg cat tat aat gaa 150
Cys Ser Ser Ser Asn Phe Ile Glu Leu Lys Arg Met His Tyr Asn Glu
                        25                               30                               35

gag aat act aag aaa aca tgg gat att att aag tct tta gac agc gtg 198
Glu Asn Thr Lys Lys Thr Trp Asp Ile Ile Lys Ser Leu Asp Ser Val
                        40                               45                               50                               55

gcg gtt tta ctc tat gaa aaa gaa tcc gat tgc ttt gtg att gtg aaa 246
Ala Val Leu Leu Tyr Glu Lys Glu Ser Asp Cys Phe Val Ile Val Lys
                        60                               65                               70

caa ttc cgc cca gcc att tat gcc cgc cgt ttt cat ttt aag tgc gat 294
Gln Phe Arg Pro Ala Ile Tyr Ala Arg Arg Phe His Phe Lys Cys Asp
                        75                               80                               85

caa gat caa act att gac gga tac act tat gaa ttg tgc gca ggg ctt 342
Gln Asp Gln Thr Ile Asp Gly Tyr Thr Tyr Glu Leu Cys Ala Gly Leu
                        90                               95                               100

gtg gat aaa gct aat aag agt tta gaa gaa atc gct tgc gaa gaa gcc 390
Val Asp Lys Ala Asn Lys Ser Leu Glu Glu Ile Ala Cys Glu Glu Ala
                        105                               110                               115

cta gaa gaa tgc ggt tat caa att agc cct aaa aat tta gaa acc ata 438
Leu Glu Glu Cys Gly Tyr Gln Ile Ser Pro Lys Asn Leu Glu Thr Ile
                        120                               125                               130                               135

ggc caa ttt tat agc gcg act ggg ttg agt ggg agt ttg caa acg ctc 486
Gly Gln Phe Tyr Ser Ala Thr Gly Leu Ser Gly Ser Leu Gln Thr Leu
                        140                               145                               150

tat tac gct gaa gtg cat aag aat ttg aaa gtt tca aag ggt ggg ggc 534
Tyr Tyr Ala Glu Val His Lys Asn Leu Lys Val Ser Lys Gly Gly Gly
                        155                               160                               165

att gat acc gaa agg att gaa gtg ctg ttt tta gag cga tca aaa gct 582
Ile Asp Thr Glu Arg Ile Glu Val Leu Phe Leu Glu Arg Ser Lys Ala
                        170                               175                               180

ctt gat ttt ata atg gat ttt caa tac gct aaa acc acc gga ttg tct 630

```

Leu Asp Phe Ile Met Asp Phe Gln Tyr Ala Lys Thr Thr Gly Leu Ser
 185 190 195

tta gcc att tta tgg cat tta aaa aag ttt aaa aat gtt taaaaggaat 679
 Leu Ala Ile Leu Trp His Leu Lys Lys Phe Lys Asn Val
 200 205 210

tttatgttaa ggcttttc 697

<210> 610

<211> 212

<212> PRT

<213> Helicobacter pylori

<400> 610

Met Ser Tyr Phe Lys Asn Ala Phe Asn Gln Lys Ser Leu Ile Asp Asp
 1 5 10 15
 Ser Ser Val Tyr Leu Glu Pro Cys Ser Ser Asn Phe Ile Glu Leu
 20 25 30
 Lys Arg Met His Tyr Asn Glu Glu Asn Thr Lys Lys Thr Trp Asp Ile
 35 40 45
 Ile Lys Ser Leu Asp Ser Val Ala Val Leu Leu Tyr Glu Lys Glu Ser
 50 55 60
 Asp Cys Phe Val Ile Val Lys Gln Phe Arg Pro Ala Ile Tyr Ala Arg
 65 70 75 80
 Arg Phe His Phe Lys Cys Asp Gln Asp Gln Thr Ile Asp Gly Tyr Thr
 85 90 95
 Tyr Glu Leu Cys Ala Gly Leu Val Asp Lys Ala Asn Lys Ser Leu Glu
 100 105 110
 Glu Ile Ala Cys Glu Glu Ala Leu Glu Glu Cys Gly Tyr Gln Ile Ser
 115 120 125
 Pro Lys Asn Leu Glu Thr Ile Gly Gln Phe Tyr Ser Ala Thr Gly Leu
 130 135 140
 Ser Gly Ser Leu Gln Thr Leu Tyr Tyr Ala Glu Val His Lys Asn Leu
 145 150 155 160
 Lys Val Ser Lys Gly Gly Gly Ile Asp Thr Glu Arg Ile Glu Val Leu
 165 170 175
 Phe Leu Glu Arg Ser Lys Ala Leu Asp Phe Ile Met Asp Phe Gln Tyr
 180 185 190
 Ala Lys Thr Thr Gly Leu Ser Leu Ala Ile Leu Trp His Leu Lys Lys
 195 200 205
 Phe Lys Asn Val
 210

<210> 611

<211> 2071

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (49)...(2022)

<400> 611

tgcgaacaat tatgggatga tattataaaa attgggtggga atgataag atg aac gga 57
 Met Asn Gly
 1

cat ttt atc ggt tct att ttg tat gtg cta gat agt aat acg cac tct	105
His Phe Ile Gly Ser Ile Leu Tyr Val Leu Asp Ser Asn Thr His Ser	
5 10 15	
aac aat aca tta ctc atc att gac ggc caa caa agg ctc acc act atc	153
Asn Asn Thr Leu Leu Ile Ile Asp Gly Gln Gln Arg Leu Thr Thr Ile	
20 25 30 35	
acg ctt tta ctc atc gct tta agg aat cat cta aqc gaa gaa gtt gaa	201
Thr Leu Leu Leu Ile Ala Leu Arg Asn His Leu Ser Glu Glu Val Glu	
40 45 50	
att ttg gag aaa ttt tcg cgt aaa gaa ata gag aqc tat ctt atc aac	249
Ile Leu Glu Lys Phe Ser Arg Lys Glu Ile Glu Ser Tyr Leu Ile Asn	
55 60 65	
agc aat aag gac ggc gat aag aaa ttc agg ctc att ctt tca gag tcc	297
Ser Asn Lys Asp Gly Asp Lys Lys Phe Arg Leu Ile Leu Ser Glu Ser	
70 75 80	
gat aaa gac acc ttg ctg tct ttg att gat aaa aac aaa aga aag ccg	345
Asp Lys Asp Thr Leu Leu Ser Leu Ile Asp Lys Asn Lys Arg Lys Pro	
85 90 95	
agc gag cct tcg gta aaa ata gtg gaa aat ttt gaa ttg ttt gaa aaa	393
Ser Glu Pro Ser Val Lys Ile Val Glu Asn Phe Glu Leu Phe Glu Lys	
100 105 110 115	
tgg atc agt gaa aac acc gac aaa cta gaa aqc att ttt aaa gga tta	441
Trp Ile Ser Glu Asn Thr Asp Lys Leu Glu Thr Ile Phe Lys Gly Leu	
120 125 130	
aaa aaa ctc atg ata gtt tgg att tct tta gat aaa gga aaa gat gat	489
Lys Lys Leu Met Ile Val Trp Ile Ser Leu Asp Lys Gly Lys Asp Asp	
135 140 145	
cct caa ctt att ttt gag aqc atg aac tca aaa gat atc gaa ctc aqc	537
Pro Gln Leu Ile Phe Glu Ser Met Asn Ser Lys Asp Ile Glu Leu Thr	
150 155 160	
caa acg gat ttg atc aga aat tat atc gta atg gaa acg gag gtt gaa	585
Gln Thr Asp Leu Ile Arg Asn Tyr Ile Val Met Glu Thr Glu Val Glu	
165 170 175	
aaa cag gaa gac ttt tat aat caa tat tgg agg gct atg gag gag aga	633
Lys Gln Glu Asp Phe Tyr Asn Gln Tyr Trp Arg Ala Met Glu Glu Arg	
180 185 190 195	
ttt gaa caa aat gaa aca ttg ttt aat cgg ttt gtc cgg cat tat ctc	681
Phe Glu Gln Asn Glu Thr Leu Phe Asn Arg Phe Val Arg His Tyr Leu	
200 205 210	
acg atc aaa ata gga aag att ccc aat gag aaa aga gtt tat gaa gct	729
Thr Ile Lys Ile Gly Lys Ile Pro Asn Glu Lys Arg Val Tyr Glu Ala	
215 220 225	
ttc aag gat tac cgg caa aaa aag ggg ata gaa ata gag gat tta tta	777
Phe Lys Asp Tyr Arg Gln Lys Lys Gly Ile Glu Ile Glu Asp Leu Leu	
230 235 240	

aaa gat tta caa aaa tac tgc ggg tat ttt tgc cag att gca ttc aaa	825
Lys Asp Leu Gln Lys Tyr Cys Gly Tyr Phe Cys Gln Ile Ala Phe Lys	
245 250 255	
aaa gaa gac gat aaa gat tta aac aag gct tta agt ttt ttg gtg aat	873
Lys Glu Asp Asp Lys Asp Leu Asn Lys Ala Leu Ser Phe Leu Val Asn	
260 265 270 275	
tta gag atg gat gtg atc tat ccg cta cta cta gag ctt tat agc gat	921
Leu Glu Met Asp Val Ile Tyr Pro Leu Leu Leu Glu Leu Tyr Ser Asp	
280 285 290	
tat aag gat ggc gtt tta tcc aag cag gat ttt atc cct att atc tat	969
Tyr Lys Asp Gly Val Leu Ser Lys Gln Asp Phe Ile Pro Ile Ile Tyr	
295 300 305	
tta ata gag agc tat att tgc aga agg gcg gtg tgt ggg ctt ggc aca	1017
Leu Ile Glu Ser Tyr Ile Cys Arg Arg Ala Val Cys Gly Leu Gly Thr	
310 315 320	
aat agt ctc aat aaa gtt ttt ccc tct ttt aca aag cac atc caa aaa	1065
Asn Ser Leu Asn Lys Val Phe Pro Ser Phe Thr Lys His Ile Gln Lys	
325 330 335	
gat gaa tat ttt aaa agc cta aag gcg cat ttt gtc tgt ctg aca gaa	1113
Asp Glu Tyr Phe Lys Ser Leu Lys Ala His Phe Val Cys Leu Thr Glu	
340 345 350 355	
aaa caa aga ttt cca aac aat gac gag ttt aaa aag ctt ttt att acc	1161
Lys Gln Arg Phe Pro Asn Asn Asp Glu Phe Lys Lys Leu Phe Ile Thr	
360 365 370	
ata gat ttt tat aag ttt aaa aaa aat aaa tac ttt ctt gaa agg tta	1209
Ile Asp Phe Tyr Lys Phe Lys Lys Asn Lys Tyr Phe Leu Glu Arg Leu	
375 380 385	
gaa aat ttt gac aca aaa gaa ccg gtc gat act caa aaa tgc aat ata	1257
Glu Asn Phe Asp Thr Lys Glu Pro Val Asp Thr Gln Lys Cys Asn Ile	
390 395 400	
gaa cat ata atg cct caa acc ctt act cca gaa tgg caa agg gat ttg	1305
Glu His Ile Met Pro Gln Thr Leu Thr Pro Glu Trp Gln Arg Asp Leu	
405 410 415	
ggt gaa aat ttt caa gca ata cac gag aaa tac ctc cac aca ata ggc	1353
Gly Glu Asn Phe Gln Ala Ile His Glu Lys Tyr Leu His Thr Ile Gly	
420 425 430 435	
aat ctc act cta acc ggt tat aac tct aag tat agc aac aat tct ttc	1401
Asn Leu Thr Leu Thr Gly Tyr Asn Ser Lys Tyr Ser Asn Asn Ser Phe	
440 445 450	
caa gaa aaa aga gat atg gag aag ggc ttt aaa caa agc tca tta aaa	1449
Gln Glu Lys Arg Asp Met Glu Lys Gly Phe Lys Gln Ser Ser Leu Lys	
455 460 465	
ctc aat caa agt ttg aaa gat ttg gaa tct ttt ggc gaa aaa gag att	1497
Leu Asn Gln Ser Leu Lys Asp Leu Glu Ser Phe Gly Glu Lys Glu Ile	

470	475	480	
gaa aaa agg gct agt gat tta gcg gat tgg gct tta aag att tgg act			1545
Glu Lys Arg Ala Ser Asp Leu Ala Asp Trp Ala Leu Lys Ile Trp Thr			
485	490	495	
tac cca att cta gag gca gaa aca tta gag gaa tat aaa ccc aaa aaa			1593
Tyr Pro Ile Leu Glu Ala Glu Thr Leu Glu Glu Tyr Lys Pro Lys Lys			
500	505	510	515
gaa aag aaa gaa aag aaa gaa aaa gag gag tat aaa ctc aag aaa gaa			1641
Glu Lys Lys Glu Lys Lys Glu Lys Glu Glu Tyr Lys Leu Lys Lys Glu			
	520	525	530
aaa aag gtt tat gat tta agc tct tat aag ttt agc tct gat tca agg			1689
Lys Lys Val Tyr Asp Leu Ser Ser Tyr Lys Phe Ser Ser Asp Ser Arg			
	535	540	545
gaa ttg ttt gat att tta aga gaa aag att aaa gct ctt gat gaa agg			1737
Glu Leu Phe Asp Ile Leu Arg Glu Lys Ile Lys Ala Leu Asp Glu Arg			
	550	555	560
ata act gaa aaa ttt aat caa aaa tat ata gct tat aag ttt tgt aaa			1785
Ile Thr Glu Lys Phe Asn Gln Lys Tyr Ile Ala Tyr Lys Phe Cys Lys			
	565	570	575
ata agt ttt gtg gat att gtt gtg caa gaa aaa ggc tta aaa ttg tat			1833
Ile Ser Phe Val Asp Ile Val Val Gln Glu Lys Gly Leu Lys Leu Tyr			
	580	585	590
595			
tta aaa atg aac ttg aat gaa ttg caa gat gaa ata aag gaa aaa cta			1881
Leu Lys Met Asn Leu Asn Glu Leu Gln Asp Glu Ile Lys Glu Lys Leu			
	600	605	610
aaa att aga gac gtt tct aat atc ggt cgt cca tgc gtt gga aac atg			1929
Lys Ile Arg Asp Val Ser Asn Ile Gly Arg Pro Cys Val Gly Asn Met			
	615	620	625
gaa gta gag cta gaa aca aaa gaa aat atc cct tat tgt ttg gga ttg			1977
Glu Val Glu Leu Glu Thr Lys Glu Asn Ile Pro Tyr Cys Leu Gly Leu			
	630	635	640
645			
atc aag cag gct tta gaa aaa cag atg ggt ggt agg aat agg caa			2022
Ile Lys Gln Ala Leu Glu Lys Gln Met Gly Gly Arg Asn Arg Gln			
	650	655	
taaaaaccca acttattcaa aataaagagt ataattacaa attacttac			2071

<210> 612

<211> 658

<212> PRT

<213> Helicobacter pylori

<400> 612

Met	Asn	Gly	His	Phe	Ile	Gly	Ser	Ile	Leu	Tyr	Val	Leu	Asp	Ser	Asn
1				5					10					15	
Thr	His	Ser	Asn	Asn	Thr	Leu	Leu	Ile	Ile	Asp	Gly	Gln	Gln	Arg	Leu
			20					25				30			
Thr	Thr	Ile	Thr	Leu	Leu	Leu	Ile	Ala	Leu	Arg	Asn	His	Leu	Ser	Glu

35					40					45					
Glu	Val	Glu	Ile	Leu	Glu	Lys	Phe	Ser	Arg	Lys	Glu	Ile	Glu	Ser	Tyr
50					55					60					
Leu	Ile	Asn	Ser	Asn	Lys	Asp	Gly	Asp	Lys	Lys	Phe	Arg	Leu	Ile	Leu
65					70					75					80
Ser	Glu	Ser	Asp	Lys	Asp	Thr	Leu	Leu	Ser	Leu	Ile	Asp	Lys	Asn	Lys
				85					90					95	
Arg	Lys	Pro	Ser	Glu	Pro	Ser	Val	Lys	Ile	Val	Glu	Asn	Phe	Glu	Leu
				100					105					110	
Phe	Glu	Lys	Trp	Ile	Ser	Glu	Asn	Thr	Asp	Lys	Leu	Glu	Thr	Ile	Phe
				115					120					125	
Lys	Gly	Leu	Lys	Lys	Leu	Met	Ile	Val	Trp	Ile	Ser	Leu	Asp	Lys	Gly
				130					135					140	
Lys	Asp	Asp	Pro	Gln	Leu	Ile	Phe	Glu	Ser	Met	Asn	Ser	Lys	Asp	Ile
145				150					155					160	
Glu	Leu	Thr	Gln	Thr	Asp	Leu	Ile	Arg	Asn	Tyr	Ile	Val	Met	Glu	Thr
				165					170					175	
Glu	Val	Glu	Lys	Gln	Glu	Asp	Phe	Tyr	Asn	Gln	Tyr	Trp	Arg	Ala	Met
				180					185					190	
Glu	Glu	Arg	Phe	Glu	Gln	Asn	Glu	Thr	Leu	Phe	Asn	Arg	Phe	Val	Arg
				195					200					205	
His	Tyr	Leu	Thr	Ile	Lys	Ile	Gly	Lys	Ile	Pro	Asn	Glu	Lys	Arg	Val
				210					215					220	
Tyr	Glu	Ala	Phe	Lys	Asp	Tyr	Arg	Gln	Lys	Lys	Gly	Ile	Glu	Ile	Glu
225				230					235					240	
Asp	Leu	Leu	Lys	Asp	Leu	Gln	Lys	Tyr	Cys	Gly	Tyr	Phe	Cys	Gln	Ile
				245					250					255	
Ala	Phe	Lys	Lys	Glu	Asp	Asp	Lys	Asp	Leu	Asn	Lys	Ala	Leu	Ser	Phe
				260					265					270	
Leu	Val	Asn	Leu	Glu	Met	Asp	Val	Ile	Tyr	Pro	Leu	Leu	Leu	Glu	Leu
				275					280					285	
Tyr	Ser	Asp	Tyr	Lys	Asp	Gly	Val	Leu	Ser	Lys	Gln	Asp	Phe	Ile	Pro
				290					295					300	
Ile	Ile	Tyr	Leu	Ile	Glu	Ser	Tyr	Ile	Cys	Arg	Arg	Ala	Val	Cys	Gly
305				310					315					320	
Leu	Gly	Thr	Asn	Ser	Leu	Asn	Lys	Val	Phe	Pro	Ser	Phe	Thr	Lys	His
				325					330					335	
Ile	Gln	Lys	Asp	Glu	Tyr	Phe	Lys	Ser	Leu	Lys	Ala	His	Phe	Val	Cys
				340					345					350	
Leu	Thr	Glu	Lys	Gln	Arg	Phe	Pro	Asn	Asn	Asp	Glu	Phe	Lys	Lys	Leu
				355					360					365	
Phe	Ile	Thr	Ile	Asp	Phe	Tyr	Lys	Phe	Lys	Lys	Asn	Lys	Tyr	Phe	Leu
				370					375					380	
Glu	Arg	Leu	Glu	Asn	Phe	Asp	Thr	Lys	Glu	Pro	Val	Asp	Thr	Gln	Lys
385				390					395					400	
Cys	Asn	Ile	Glu	His	Ile	Met	Pro	Gln	Thr	Leu	Thr	Pro	Glu	Trp	Gln
				405					410					415	
Arg	Asp	Leu	Gly	Glu	Asn	Phe	Gln	Ala	Ile	His	Glu	Lys	Tyr	Leu	His
				420					425					430	
Thr	Ile	Gly	Asn	Leu	Thr	Leu	Thr	Gly	Tyr	Asn	Ser	Lys	Tyr	Ser	Asn
				435					440					445	
Asn	Ser	Phe	Gln	Glu	Lys	Arg	Asp	Met	Glu	Lys	Gly	Phe	Lys	Gln	Ser
				450					455					460	
Ser	Leu	Lys	Leu	Asn	Gln	Ser	Leu	Lys	Asp	Leu	Glu	Ser	Phe	Gly	Glu
465				470					475					480	
Lys	Glu	Ile	Glu	Lys	Arg	Ala	Ser	Asp	Leu	Ala	Asp	Trp	Ala	Leu	Lys
				485					490					495	
Ile	Trp	Thr	Tyr	Pro	Ile	Leu	Glu	Ala	Glu	Thr	Leu	Glu	Glu	Tyr	Lys
				500					505					510	

Pro Lys Lys Glu Lys Lys Glu Lys Lys Glu Lys Glu Glu Tyr Lys Leu
 515 520 525
 Lys Lys Glu Lys Lys Val Tyr Asp Leu Ser Ser Tyr Lys Phe Ser Ser
 530 535 540
 Asp Ser Arg Glu Leu Phe Asp Ile Leu Arg Glu Lys Ile Lys Ala Leu
 545 550 555 560
 Asp Glu Arg Ile Thr Glu Lys Phe Asn Gln Lys Tyr Ile Ala Tyr Lys
 565 570 575
 Phe Cys Lys Ile Ser Phe Val Asp Ile Val Val Gln Glu Lys Gly Leu
 580 585 590
 Lys Leu Tyr Leu Lys Met Asn Leu Asn Glu Leu Gln Asp Glu Ile Lys
 595 600 605
 Glu Lys Leu Lys Ile Arg Asp Val Ser Asn Ile Gly Arg Pro Cys Val
 610 615 620
 Gly Asn Met Glu Val Glu Leu Glu Thr Lys Glu Asn Ile Pro Tyr Cys
 625 630 635 640
 Leu Gly Leu Ile Lys Gln Ala Leu Glu Lys Gln Met Gly Gly Arg Asn
 645 650 655
 Arg Gln

<210> 613
 <211> 598
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (19)...(558)

<400> 613
 gtggtggctg agtagaaa atg ttt gaa gcg acg acg att tta ggc tat aga 51
 Met Phe Glu Ala Thr Thr Ile Leu Gly Tyr Arg
 1 5 10

 ggg gaa ttg aat cat aaa aag ttc gcg ctc att gga ggc gat ggg cag 99
 Gly Glu Leu Asn His Lys Lys Phe Ala Leu Ile Gly Gly Asp Gly Gln
 15 20 25

 gta act ttg ggt aat tgc gtg gtc aaa gcc aat gcg aca aaa atc aga 147
 Val Thr Leu Gly Asn Cys Val Val Lys Ala Asn Ala Thr Lys Ile Arg
 30 35 40

 agc ttg tat cac aac cag gtt tta agc ggg ttt gcc gga agc acc gcg 195
 Ser Leu Tyr His Asn Gln Val Leu Ser Gly Phe Ala Gly Ser Thr Ala
 45 50 55

 gac gct ttt agt ttg ttt gat atg ttt gaa cgc att tta gag agc aaa 243
 Asp Ala Phe Ser Leu Phe Asp Met Phe Glu Arg Ile Leu Glu Ser Lys
 60 65 70 75

 aag ggg gat ttg ttt aaa agc gtg gtg gat ttc agt aaa gaa tgg cgc 291
 Lys Gly Asp Leu Phe Lys Ser Val Val Asp Phe Ser Lys Glu Trp Arg
 80 85 90

 aaa gat aag tat tta cgc cga ctg gaa gcg atg atg atc gtt tta aac 339
 Lys Asp Lys Tyr Leu Arg Arg Leu Glu Ala Met Met Ile Val Leu Asn
 95 100 105

ttc gat cac att ttc att ttg agc ggc atg ggc gat gtt tta gaa gct 387
Phe Asp His Ile Phe Ile Leu Ser Gly Met Gly Asp Val Leu Glu Ala
110 115 120

gaa gac aat aag atc gct gct att ggg agt ggg ggg aat tac gct tta 435
Glu Asp Asn Lys Ile Ala Ala Ile Gly Ser Gly Gly Asn Tyr Ala Leu
125 130 135

agc gcg gct agg gct tta gat cat ttc gct cat tta gag cct aga aaa 483
Ser Ala Ala Arg Ala Leu Asp His Phe Ala His Leu Glu Pro Arg Lys
140 145 150 155

ctt gta gaa gag tcc tta aaa atc gca ggg gat ctt tgc att tac acc 531
Leu Val Glu Glu Ser Leu Lys Ile Ala Gly Asp Leu Cys Ile Tyr Thr
160 165 170

aac acg aat att aaa att ttg gag ctt taatgtctaa attgaatatc 578
Asn Thr Asn Ile Lys Ile Leu Glu Leu
175 180

acccacgag aaattgtcgc 598

<210> 614

<211> 180

<212> PRT

<213> Helicobacter pylori

<400> 614

Met Phe Glu Ala Thr Thr Ile Leu Gly Tyr Arg Gly Glu Leu Asn His
1 5 10 15
Lys Lys Phe Ala Leu Ile Gly Gly Asp Gly Gln Val Thr Leu Gly Asn
20 25 30
Cys Val Val Lys Ala Asn Ala Thr Lys Ile Arg Ser Leu Tyr His Asn
35 40 45
Gln Val Leu Ser Gly Phe Ala Gly Ser Thr Ala Asp Ala Phe Ser Leu
50 55 60
Phe Asp Met Phe Glu Arg Ile Leu Glu Ser Lys Lys Gly Asp Leu Phe
65 70 75 80
Lys Ser Val Val Asp Phe Ser Lys Glu Trp Arg Lys Asp Lys Tyr Leu
85 90 95
Arg Arg Leu Glu Ala Met Met Ile Val Leu Asn Phe Asp His Ile Phe
100 105 110
Ile Leu Ser Gly Met Gly Asp Val Leu Glu Ala Glu Asp Asn Lys Ile
115 120 125
Ala Ala Ile Gly Ser Gly Gly Asn Tyr Ala Leu Ser Ala Ala Arg Ala
130 135 140
Leu Asp His Phe Ala His Leu Glu Pro Arg Lys Leu Val Glu Glu Ser
145 150 155 160
Leu Lys Ile Ala Gly Asp Leu Cys Ile Tyr Thr Asn Thr Asn Ile Lys
165 170 175
Ile Leu Glu Leu
180

<210> 615

<211> 450

<212> DNA

<213> Helicobacter pylori

<222> (34) ... (396)

tgtttcataag taacaaattg aaaatatacc att atg tat gga ggt aat gct atc 54
Met Tyr Gly Gly Asn Ala Met
1 5

gct gac aca atc aat aca act gaa gca act cat gaa aca aaa aaa cca 102
Ala Asp Thr Ile Asn Thr Thr Glu Ala Thr His Glu Thr Lys Lys Pro
10 15 20

aac gct ttt gta aat ttt ttc aaa aac aat ttg act gat aag cgt tat 150
Asn Ala Phe Val Asn Phe Phe Lys Asn Asn Leu Thr Asp Lys Arg Tyr
25 30 35

gat tca tta ggt ctc att gga gca ggg gtt tta tgt tgt gtc ttg agc 198
Asp Ser Leu Gly Leu Ile Gly Ala Gly Val Leu Cys Cys Val Leu Ser
40 45 50 55

ggt gct atg ggg att gtt ggg afa atc ttt gtc gca ata gga atc ttt 246
Gly Ala Met Gly Ile Val Gly Ile Ile Phe Val Ala Ile Gly Ile Phe
60 65 70

ttg tct ttt tct aat atc aac tta gtg aaa tta gtt gaa aaa ttg tcc 294
Leu Ser Phe Ser Asn Ile Asn Leu Val Lys Leu Val Glu Lys Leu Ser
7^e 8^e

aaa aaa caa tct aaa gtg cca aca act gtc aat aac gaa act caa aaa 342
Lys Lys Gln Ser Lys Val Pro Thr Thr Val Asn Asn Glu Thr Gln Lys
90 95 100

tct caa gca aca aac gtt acc aac gaa cca act gaa gcc aaa gag act 390
Ser Gln Ala Thr Ser Val Thr Asn Glu Pro Thr Glu Ala Lys Glu Thr
105 110 115

aaa gat tgaggcaaaa caacgatttt gactgaagaa agaatgagag aaaatttcaa 446
Lys Asp
120

aaat 450

<213> Helicobacter pylori

Met 1	Tyr	Gly	Gly	Asn 5	Ala	Met	Ala	Asp	Thr 10	Ile	Asn	Thr	Thr	Glu 15	Ala
Thr	His	Glu	Thr	Lys	Lys	Pro	Asn	Ala	Phe	Val	Asn	Phe	Phe	Lys	Asn
			20					25					30		
Asn	Leu	Thr	Asp	Lys	Arg	Tyr	Asp	Ser	Leu	Gly	Leu	Ile	Gly	Ala	Gly
		35					40					45			
Val	Leu	Cys	Cys	Val	Leu	Ser	Gly	Ala	Met	Gly	Ile	Val	Gly	Ile	Ile
	50					55					60				
Phe	Val	Ala	Ile	Gly	Ile	Phe	Leu	Ser	Phe	Ser	Asn	Ile	Asn	Leu	Val
65					70					75					80

Met	Cys	Arg	Thr	Leu	Ile	Ser	Ile	Ala	Leu	Leu	Glu	Ser	Ser	Leu	Gly
1				5					10					15	
Leu	Asn	Asn	Arg	Arg	Glu	Lys	Ser	Leu	Lys	Asp	Thr	Ser	Tyr	Ser	Met
			20					25					30		
Phe	His	Ile	Thr	Leu	Asn	Thr	Ala	Lys	Lys	Phe	Tyr	Pro	Thr	Tyr	Ser
		35					40					45			
Lys	Thr	Leu	Leu	Lys	Phe	Lys	Leu	Leu	Asn	Asp	Val	Gly	Phe	Ala	Ile
	50				55					60					
Gln	Leu	Ala	Lys	Gln	Ile	Leu	Lys	Glu	Asn	Phe	Asp	Tyr	Tyr	Lys	Gln
65					70					75					80
Lys	His	Pro	Asn	Lys	Ser	Val	Tyr	Gln	Leu	Val	Glu	Met	Ala	Ile	Gly
			85						90				95		
Ala	Tyr	Asn	Gly	Gly	Met	Lys	His	Asn	Pro	Asn	Gly	Ala	Tyr	Val	Lys
			100					105					110		
Lys	Phe	Arg	Cys	Ile	Tyr	Ser	Gln	Val	Arg	Tyr	Asn	Glu			
		115					120					125			

<213> Helicobacter pylori.

<222> (31) ... (2274)

atatttatatc aaacacaggt agtaggcaca atg gaa gac ttt ttg tat aac acc																54	
									Met	Glu	Asp	Phe	Leu	Tyr	Asn	Thr	
									1				5				
tta tat ttc ata gag gat tat aag ttg gtt gtt att ttt agt ttc ata	102																
Leu Tyr Phe Ile Glu Asp Tyr Lys Leu Val Val Ile Phe Ser Phe Ile																	
10 15 20																	
ggg tta ata gcg tta ttt ttt ctt tac aaa ttc ata aaa gct caa aaa	150																
Gly Leu Ile Ala Leu Phe Phe Leu Tyr Lys Phe Ile Lys Ala Gln Lys																	
25 30 35 40																	
aag gct ttt aaa gat aaa gct aac cag cct caa aag aaa aaa agc ttt	198																
Lys Ala Phe Lys Asp Lys Ala Asn Gln Pro Gln Lys Lys Lys Ser Phe																	
45 50 55																	
aaa gaa atc att ata gat ggg ctg aaa gaa agg gtt aaa acc ttt ggc	246																
Lys Glu Ile Ile Ile Asp Gly Leu Lys Glu Arg Val Lys Thr Phe Gly																	
60 65 70																	
ttt tgg ttg caa gct ata cta tta cta tcc tat tct ttt atc aca tca	294																
Phe Trp Leu Gln Ala Ile Leu Leu Leu Ser Tyr Ser Phe Ile Thr Ser																	
75 80 85																	
gga tta ttt ttc ttg att ctg tta ggt aat ttt tat gat gat aat cga	342																
Gly Leu Phe Phe Leu Ile Leu Leu Gly Asn Phe Tyr Asp Asp Asn Arg																	
90 95 100																	
tcg cct gag agc gat gat gat ctt ttt gat ata tgg atc tat gcg ata	390																
Ser Pro Glu Ser Asp Asp Asp Leu Phe Asp Ile Trp Ile Tyr Ala Ile																	

105	110	115	120	
caa gat ttt cct aat tac tat ttt aaa gcg ctt ggt ttt agt tca ctc				438
Gln Asp Phe Pro Asn Tyr Tyr Phe Lys Ala Leu Gly Phe Ser Ser Leu	125	130	135	
aag att tat ggg ttc aat ata tcc tta gtc gta tat ggt tct att tta				486
Lys Ile Tyr Gly Phe Asn Ile Ser Leu Val Val Tyr Gly Ser Ile Leu	140	145	150	
tgc tct tat atc ttc att acc ttt ttt gtg tgg ttc tta aaa tac tta				534
Cys Ser Tyr Ile Phe Ile Thr Phe Phe Val Trp Phe Leu Lys Tyr Leu	155	160	165	
act cgg act aga gat ata gga gcg aat aaa aaa gtt gat gat ctc ttt				582
Thr Arg Thr Arg Asp Ile Gly Ala Asn Lys Lys Val Asp Asp Leu Phe	170	175	180	
ggg agc gcg agt tgg gaa act gaa gag aaa atg atc aaa gcc aaa ctc				630
Gly Ser Ala Ser Trp Glu Thr Glu Glu Lys Met Ile Lys Ala Lys Leu	185	190	195	200
atc acg ccc aac aat aaa aaa cgc gcc ttt gac aaa cga gag gtg att				678
Ile Thr Pro Asn Asn Lys Lys Arg Ala Phe Asp Lys Arg Glu Val Ile	205	210	215	
gta ggc agg cgt ggc ttg ggg gat ttt atc gct tac gca ggg cag gcg				726
Val Gly Arg Arg Gly Leu Gly Asp Phe Ile Ala Tyr Ala Gly Gln Ala	220	225	230	
ttc att ggc ttg att gct cct act aga agc ggt aag ggg gtg ggt ttc				774
Phe Ile Gly Leu Ile Ala Pro Thr Arg Ser Gly Lys Gly Val Gly Phe	235	240	245	
atc atg ccc aat atc atc aat tat cct caa aat atc gtt gtg ttt gac				822
Ile Met Pro Asn Met Ile Asn Tyr Pro Gln Asn Ile Val Val Phe Asp	250	255	260	
cct aaa gct gac act atg gag act tgc gga aaa atc aga gaa aaa cgc				870
Pro Lys Ala Asp Thr Met Glu Thr Cys Gly Lys Ile Arg Glu Lys Arg	265	270	275	280
ttc aac caa aaa gtg ttc atc tat gaa cct ttc tcc tta aaa aca cac				918
Phe Asn Gln Lys Val Phe Ile Tyr Glu Pro Phe Ser Leu Lys Thr His	285	290	295	
cga ttt aat cct ttc gct tat gtg gat ttt ggt aat gat gtg gtt ttg				966
Arg Phe Asn Pro Phe Ala Tyr Val Asp Phe Gly Asn Asp Val Val Leu	300	305	310	
acc gaa gac ata ctc tct caa att gac aca cgc cta aaa ggg cat ggc				1014
Thr Glu Asp Ile Leu Ser Gln Ile Asp Thr Arg Leu Lys Gly His Gly	315	320	325	
atg gtg gct agt gga ggg gat ttt tcc act caa atc ttt gga tta gca				1062
Met Val Ala Ser Gly Gly Asp Phe Ser Thr Gln Ile Phe Gly Leu Ala	330	335	340	
aag ctc gtg ttc cct gaa aga cct aat gaa aaa gat cct ttc ttt agc				1110

Lys 345	Leu	Val	Phe	Pro	Glu 350	Arg	Pro	Asn	Glu	Lys 355	Asp	Pro	Phe	Phe	Ser 360	
aat Asn	caa Gln	gcg Ala	cga Arg	aat Asn 365	ctt Leu	ttt Phe	gtc Val	atc Ile	aat Asn 370	tgc Cys	aat Asn	att Ile	tac Tyr	agg Arg 375	gat Asp	1158
ctc Leu	atg Met	tgg Trp	act Thr 380	aaa Lys	aag Lys	ggg Gly	ctt Leu	gag Glu 385	ttt Phe	gtc Val	aaa Lys	aga Arg	aaa Lys 390	aaa Lys	atc Ile	1206
atc Ile	atg Met	cct Pro 395	gaa Glu	aca Thr	ccc Pro	acg Thr	atg Met 400	ttt Phe	ttc Phe	ata Ile	ggg Gly	tct Ser 405	atg Met	gca Ala	agc Ser	1254
ggg Gly 410	atc Ile	aac Asn	ttg Leu	att Ile	gat Asp	gaa Glu 415	gac Asp	aca Thr	aac Asn	atg Met	gaa Glu 420	aaa Lys	gtc Val	gtg Val	tct Ser	1302
tta Leu 425	atg Met	gaa Glu	ttt Phe	ttt Phe	gga Gly 430	ggg Gly	gaa Glu	gaa Glu	gat Asp	aag Lys 435	agt Ser	ggc Gly	gat Asp	aat Asn	cta Leu 440	1350
aga Arg	gtg Val	ctt Leu	agt Ser 445	cct Pro	gcc Ala	act Thr	aga Arg	aac Asn	atg Met 450	tgg Trp	aat Asn	agc Ser	ttc Phe	aag Lys 455	aca Thr	1398
atg Met	ggc Gly	ggc Gly	gct Ala 460	aga Arg	gaa Glu	act Thr	tat Tyr	agc Ser 465	tgc Ser	gtt Val	caa Gln	ggg Gly	gta Val 470	tac Tyr	act Thr	1446
tca Ser	gcc Ala	ttt Phe 475	gcg Ala	cct Pro	tat Tyr	aat Asn	aac Asn 480	aca Ala	atg Met	att Ile	aga Arg	aat Asn 485	ttc Phe	acg Thr	agc Ser	1494
gcc Ala 490	aat Asn	gat Asp	ttt Phe	gat Asp	ttc Phe	agg Arg 495	cct Arg	tta Leu	agg Arg	atc Ile	gat Asp 500	gaa Glu	gtg Val	agt Ser	att Ile	1542
ggg Gly 505	gtg Val	atc Ile	gct Ala	aat Asn	cct Pro 510	aaa Lys	gaa Glu	agc Ser	act Thr	att Ile 515	gtt Val	gga Gly	ccg Pro	ata Ile	tta Leu 520	1590
gag Glu	ctg Leu	ttt Phe	ttc Phe	aat Asn 525	gtg Val	atg Met	att Ile	tat Tyr	agc Ser 530	aat Asn	ttg Leu	att Ile	ctg Leu	cca Pro 535	atc Ile	1638
cat His	gat Asp	cca Pro	cag Gln 540	tgc Cys	aaa Lys	aga Arg	agt Ser	tgc Cys 545	ttg Leu	atg Met	ctc Leu	atg Met	gac Asp 550	gaa Glu	ttc Phe	1686
act Thr	tta Leu	tgt Cys 555	ggc Gly	tat Tyr	tta Leu	gag Glu	acc Thr 560	ttt Phe	gtt Val	aaa Lys	gcg Ala	gta Val 565	ggg Gly	att Ile	atc Met	1734
gca Ala 570	gaa Glu	tac Tyr	aac Asn	atg Met	cgc Arg	ccc Pro 575	gct Ala	ttt Phe	gtg Val	ttt Phe	caa Gln 580	agt Ser	aag Lys	gcg Ala	caa Gln	1782

cta gag aat gac ccc cca ctt ggt tat ggt agg aat ggc gct aag act	1830
Leu Glu Asn Asp Pro Pro Leu Gly Tyr Gly Arg Asn Gly Ala Lys Thr	
585 590 595 600	
att tta gac aac ctt tct ttg aat atg tat tat ggg att aac aac gat	1878
Ile Leu Asp Asn Leu Ser Leu Asn Met Tyr Tyr Gly Ile Asn Asn Asp	
605 610 615	
aac tac tat gaa cat ttt gaa aaa ctt tct aag gta tta ggg aaa tac	1926
Asn Tyr Tyr Glu His Phe Glu Lys Leu Ser Lys Val Leu Gly Lys Tyr	
620 625 630	
aca agg caa gac gtg agc cga agc att gat gat aat aca ggt aag acc	1974
Thr Arg Gln Asp Val Ser Arg Ser Ile Asp Asp Asn Thr Gly Lys Thr	
635 640 645	
aac act tct atc agc aac aaa gag cgg ttt ttg atg acc cct gat gaa	2022
Asn Thr Ser Ile Ser Asn Lys Glu Arg Phe Leu Met Thr Pro Asp Glu	
650 655 660	
ttg atg act atg ggc gat gag ctt atc att cta gag aat acg ctc aaa	2070
Leu Met Thr Met Gly Asp Glu Leu Ile Ile Leu Glu Asn Thr Leu Lys	
665 670 675 680	
cct atc aag tgc cac aag gcg ctt tac tat gat gat cca ttc ttc acc	2118
Pro Ile Lys Cys His Lys Ala Leu Tyr Tyr Asp Asp Pro Phe Phe Thr	
685 690 695	
gat gaa ctc att aag gta agt cca agc ttg agc aag aaa tac aaa ttg	2166
Asp Glu Leu Ile Lys Val Ser Pro Ser Leu Ser Lys Lys Tyr Lys Leu	
700 705 710	
ggg aaa gtg cct aat caa gca act ttc tat gat gat ttg caa gcc gct	2214
Gly Lys Val Pro Asn Gln Ala Thr Phe Tyr Asp Asp Leu Gln Ala Ala	
715 720 725	
aaa act aga ggt gaa ttg agt tat gat aaa tct tta gtg cct gtg ggt	2262
Lys Thr Arg Gly Glu Leu Ser Tyr Asp Lys Ser Leu Val Pro Val Gly	
730 735 740	
tca agt gaa ctg tgattaagac aaaatatctt aacaaaaaga aaattaaaag	2314
Ser Ser Glu Leu	
745	
ataatgatataaata	2329
<210> 620	
<211> 748	
<212> PRT	
<213> Helicobacter pylori	
<400> 620	
Met Glu Asp Phe Leu Tyr Asn Thr Leu Tyr Phe Ile Glu Asp Tyr Lys	
1 5 10 15	
Leu Val Val Ile Phe Ser Phe Ile Gly Leu Ile Ala Leu Phe Phe Leu	
20 25 30	
Tyr Lys Phe Ile Lys Ala Gln Lys Lys Ala Phe Lys Asp Lys Ala Asn	
35 40 45	
Gln Pro Gln Lys Lys Lys Ser Phe Lys Glu Ile Ile Ile Asp Gly Leu	

50		55		60
Lys Glu Arg Val Lys Thr Phe Gly Phe Trp Leu Gln Ala Ile Leu Leu				
65		70		80
Leu Ser Tyr Ser Phe Ile Thr Ser Gly Leu Phe Phe Leu Ile Leu Leu				
	85		90	95
Gly Asn Phe Tyr Asp Asp Asn Arg Ser Pro Glu Ser Asp Asp Asp Leu				
	100		105	110
Phe Asp Ile Trp Ile Tyr Ala Ile Gln Asp Phe Pro Asn Tyr Tyr Phe				
	115		120	125
Lys Ala Leu Gly Phe Ser Ser Leu Lys Ile Tyr Gly Phe Asn Ile Ser				
	130		135	140
Leu Val Val Tyr Gly Ser Ile Leu Cys Ser Tyr Ile Phe Ile Thr Phe				
	145		150	155
Phe Val Trp Phe Leu Lys Tyr Leu Thr Arg Thr Arg Asp Ile Gly Ala				
	165		170	175
Asn Lys Lys Val Asp Asp Leu Phe Gly Ser Ala Ser Trp Glu Thr Glu				
	180		185	190
Glu Lys Met Ile Lys Ala Lys Leu Ile Thr Pro Asn Asn Lys Lys Arg				
	195		200	205
Ala Phe Asp Lys Arg Glu Val Ile Val Gly Arg Arg Gly Leu Gly Asp				
	210		215	220
Phe Ile Ala Tyr Ala Gly Gln Ala Phe Ile Gly Leu Ile Ala Pro Thr				
	225		230	235
Arg Ser Gly Lys Gly Val Gly Phe Ile Met Pro Asn Met Ile Asn Tyr				
	245		250	255
Pro Gln Asn Ile Val Val Phe Asp Pro Lys Ala Asp Thr Met Glu Thr				
	260		265	270
Cys Gly Lys Ile Arg Glu Lys Arg Phe Asn Gln Lys Val Phe Ile Tyr				
	275		280	285
Glu Pro Phe Ser Leu Lys Thr His Arg Phe Asn Pro Phe Ala Tyr Val				
	290		295	300
Asp Phe Gly Asn Asp Val Val Leu Thr Glu Asp Ile Leu Ser Gln Ile				
	305		310	315
Asp Thr Arg Leu Lys Gly His Gly Met Val Ala Ser Gly Gly Asp Phe				
	325		330	335
Ser Thr Gln Ile Phe Gly Leu Ala Lys Leu Val Phe Pro Glu Arg Pro				
	340		345	350
Asn Glu Lys Asp Pro Phe Phe Ser Asn Gln Ala Arg Asn Leu Phe Val				
	355		360	365
Ile Asn Cys Asn Ile Tyr Arg Asp Leu Met Trp Thr Lys Lys Gly Leu				
	370		375	380
Glu Phe Val Lys Arg Lys Lys Ile Ile Met Pro Glu Thr Pro Thr Met				
	385		390	395
Phe Phe Ile Gly Ser Met Ala Ser Gly Ile Asn Leu Ile Asp Glu Asp				
	405		410	415
Thr Asn Met Glu Lys Val Val Ser Leu Met Glu Phe Phe Gly Gly Glu				
	420		425	430
Glu Asp Lys Ser Gly Asp Asn Leu Arg Val Leu Ser Pro Ala Thr Arg				
	435		440	445
Asn Met Trp Asn Ser Phe Lys Thr Met Gly Gly Ala Arg Glu Thr Tyr				
	450		455	460
Ser Ser Val Gln Gly Val Tyr Thr Ser Ala Phe Ala Pro Tyr Asn Asn				
	465		470	475
Ala Met Ile Arg Asn Phe Thr Ser Ala Asn Asp Phe Asp Phe Arg Arg				
	485		490	495
Leu Arg Ile Asp Glu Val Ser Ile Gly Val Ile Ala Asn Pro Lys Glu				
	500		505	510
Ser Thr Ile Val Gly Pro Ile Leu Glu Leu Phe Phe Asn Val Met Ile				
	515		520	525

Tyr	Ser	Asn	Leu	Ile	Leu	Pro	Ile	His	Asp	Pro	Gln	Cys	Lys	Arg	Ser
530						535					540				
Cys	Leu	Met	Leu	Met	Asp	Glu	Phe	Thr	Leu	Cys	Gly	Tyr	Leu	Glu	Thr
545					550					555					560
Phe	Val	Lys	Ala	Val	Gly	Ile	Met	Ala	Glu	Tyr	Asn	Met	Arg	Pro	Ala
				565					570						575
Phe	Val	Phe	Gln	Ser	Lys	Ala	Gln	Leu	Glu	Asn	Asp	Pro	Pro	Leu	Gly
			580					585						590	
Tyr	Gly	Arg	Asn	Gly	Ala	Lys	Thr	Ile	Leu	Asp	Asn	Leu	Ser	Leu	Asn
		595					600					605			
Met	Tyr	Tyr	Gly	Ile	Asn	Asn	Asp	Asn	Tyr	Tyr	Glu	His	Phe	Glu	Lys
	610					615					620				
Leu	Ser	Lys	Val	Leu	Gly	Lys	Tyr	Thr	Arg	Gln	Asp	Val	Ser	Arg	Ser
625					630					635					640
Ile	Asp	Asp	Asn	Thr	Gly	Lys	Thr	Asn	Thr	Ser	Ile	Ser	Asn	Lys	Glu
				645					650					655	
Arg	Phe	Leu	Met	Thr	Pro	Asp	Glu	Leu	Met	Thr	Met	Gly	Asp	Glu	Leu
			660					665					670		
Ile	Ile	Leu	Glu	Asn	Thr	Leu	Lys	Pro	Ile	Lys	Cys	His	Lys	Ala	Leu
		675					680					685			
Tyr	Tyr	Asp	Asp	Pro	Phe	Phe	Thr	Asp	Glu	Leu	Ile	Lys	Val	Ser	Pro
	690					695					700				
Ser	Leu	Ser	Lys	Lys	Tyr	Lys	Leu	Gly	Lys	Val	Pro	Asn	Gln	Ala	Thr
705					710				715						720
Phe	Tyr	Asp	Asp	Leu	Gln	Ala	Ala	Lys	Thr	Arg	Gly	Glu	Leu	Ser	Tyr
				725					730					735	
Asp	Lys	Ser	Leu	Val	Pro	Val	Gly	Ser	Ser	Glu	Leu				
			740					745							

<210> 621
 <211> 1037
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (19)...(1008)

<400> 621																
taaatttgga	ataagaac	atg	act	gaa	gac	aga	ttg	agt	gca	gaa	gat	aaa			51	
		Met	Thr	Glu	Asp	Arg	Leu	Ser	Ala	Glu	Asp	Lys				
		1				5					10					
aag	ttt	cta	gaa	gta	gaa	aga	gct	tta	aaa	gaa	gcg	gca	tta	aat	cct	99
Lys	Phe	Leu	Glu	Val	Glu	Arg	Ala	Leu	Lys	Glu	Ala	Ala	Leu	Asn	Pro	
			15				20						25			
cta	agg	cat	gct	act	gaa	gaa	ctt	ttt	ggt	gat	ttt	tta	aaa	atg	gaa	147
Leu	Arg	His	Ala	Thr	Glu	Glu	Leu	Phe	Gly	Asp	Phe	Leu	Lys	Met	Glu	
		30					35					40				
aat	atc	act	gag	att	tgt	tac	aat	ggg	aac	aag	gtt	gta	tgg	gtt	tta	195
Asn	Ile	Thr	Glu	Ile	Cys	Tyr	Asn	Gly	Asn	Lys	Val	Val	Trp	Val	Leu	
		45				50					55					
aaa	aat	aat	ggc	gaa	tgg	caa	cca	ttt	gat	gtg	aga	gac	agg	aaa	gcc	243
Lys	Asn	Asn	Gly	Glu	Trp	Gln	Pro	Phe	Asp	Val	Arg	Asp	Arg	Lys	Ala	
					65					70					75	
60																

ttt agc ctg tct cgt tta atg cat ttt gct cgg tgt tgt gca agt ttt	291
Phe Ser Leu Ser Arg Leu Met His Phe Ala Arg Cys Cys Ala Ser Phe	
80 85 90	
aag aaa aaa aca ata gac aac tat gaa aat cct att ttg agc agc aat	339
Lys Lys Lys Thr Ile Asp Asn Tyr Glu Asn Pro Ile Leu Ser Ser Asn	
95 100 105	
tta gcg aat ggt gaa agg gtg cag att gtc ctt tcc cct gtt aca gtt	387
Leu Ala Asn Gly Glu Arg Val Gln Ile Val Leu Ser Pro Val Thr Val	
110 115 120	
aat gat gaa acc att tcc ata tcc ata agg ata cct agc aaa aca acc	435
Asn Asp Glu Thr Ile Ser Ile Ser Ile Arg Ile Pro Ser Lys Thr Thr	
125 130 135	
tat cct cat agc ttc ttt gaa gag caa ggt ttt tat aat cta cta gac	483
Tyr Pro His Ser Phe Phe Glu Glu Gln Gly Phe Tyr Asn Leu Leu Asp	
140 145 150 155	
aac aaa gaa caa gcg atc agc gcg att aaa gat ggt att gct att ggt	531
Asn Lys Glu Gln Ala Ile Ser Ala Ile Lys Asp Gly Ile Ala Ile Gly	
160 165 170	
aaa aat gtg att gtt tgt ggt ggc aca gga agc ggt aaa acg act tat	579
Lys Asn Val Ile Val Cys Gly Gly Thr Gly Ser Gly Lys Thr Thr Tyr	
175 180 185	
atc aaa agc atc atg gag ttt atc cct aaa gaa gaa agg atc ata tcc	627
Ile Lys Ser Ile Met Glu Phe Ile Pro Lys Glu Glu Arg Ile Ile Ser	
190 195 200	
att gaa gac acc gaa gag att gta ttc aaa cac cac aaa aac tac aca	675
Ile Glu Asp Thr Glu Glu Ile Val Phe Lys His His Lys Asn Tyr Thr	
205 210 215	
cag ctt ttt ttt ggt ggg aat atc acc tct gct gat tgc tta aag tca	723
Gln Leu Phe Phe Gly Gly Asn Ile Thr Ser Ala Asp Cys Leu Lys Ser	
220 225 230 235	
tgt ctg aga atg cgg cct gat aga atc att tta ggg gaa ctg aga agc	771
Cys Leu Arg Met Arg Pro Asp Arg Ile Ile Leu Gly Glu Leu Arg Ser	
240 245 250	
agt gag gca tac gat ttt tat aat gtg ctt tgt agc ggt cat aaa ggc	819
Ser Glu Ala Tyr Asp Phe Tyr Asn Val Leu Cys Ser Gly His Lys Gly	
255 260 265	
aca cta acc act ctg cat gca ggg agc agt gaa gaa gcg ttt atc cgt	867
Thr Leu Thr Thr Leu His Ala Gly Ser Ser Glu Glu Ala Phe Ile Arg	
270 275 280	
ttg gcc aac atg agt tca tct aat agc gca gca agg aat atc aag ttt	915
Leu Ala Asn Met Ser Ser Ser Asn Ser Ala Ala Arg Asn Ile Lys Phe	
285 290 295	
gaa agt ctt att gag ggc ttt aaa gat ttg att gat atg att gtc cat	963
Glu Ser Leu Ile Glu Gly Phe Lys Asp Leu Ile Asp Met Ile Val His	

300		305		310		315	
atc aac cac cac aaa cag tgt gat gaa ttt tat atc aaa cac agg							1008
Ile Asn His His Lys Gln Cys Asp Glu Phe Tyr Ile Lys His Arg							
	320			325		330	

tagtaggcac aatggaagac tttttgtat 1037

<210> 622
 <211> 330
 <212> PRT
 <213> Helicobacter pylori

<400> 622

Met	Thr	Glu	Asp	Arg	Leu	Ser	Ala	Glu	Asp	Lys	Lys	Phe	Leu	Glu	Val
1				5					10					15	
Glu	Arg	Ala	Leu	Lys	Glu	Ala	Ala	Leu	Asn	Pro	Leu	Arg	His	Ala	Thr
		20						25					30		
Glu	Glu	Leu	Phe	Gly	Asp	Phe	Leu	Lys	Met	Glu	Asn	Ile	Thr	Glu	Ile
		35					40					45			
Cys	Tyr	Asn	Gly	Asn	Lys	Val	Val	Trp	Val	Leu	Lys	Asn	Asn	Gly	Glu
	50					55					60				
Trp	Gln	Pro	Phe	Asp	Val	Arg	Asp	Arg	Lys	Ala	Phe	Ser	Leu	Ser	Arg
65					70				75					80	
Leu	Met	His	Phe	Ala	Arg	Cys	Cys	Ala	Ser	Phe	Lys	Lys	Lys	Thr	Ile
				85					90					95	
Asp	Asn	Tyr	Glu	Asn	Pro	Ile	Leu	Ser	Ser	Asn	Leu	Ala	Asn	Gly	Glu
			100					105					110		
Arg	Val	Gln	Ile	Val	Leu	Ser	Pro	Val	Thr	Val	Asn	Asp	Glu	Thr	Ile
		115					120					125			
Ser	Ile	Ser	Ile	Arg	Ile	Pro	Ser	Lys	Thr	Thr	Tyr	Pro	His	Ser	Phe
	130					135					140				
Phe	Glu	Glu	Gln	Gly	Phe	Tyr	Asn	Leu	Leu	Asp	Asn	Lys	Glu	Gln	Ala
145					150					155				160	
Ile	Ser	Ala	Ile	Lys	Asp	Gly	Ile	Ala	Ile	Gly	Lys	Asn	Val	Ile	Val
				165					170					175	
Cys	Gly	Gly	Thr	Gly	Ser	Gly	Lys	Thr	Thr	Tyr	Ile	Lys	Ser	Ile	Met
			180					185					190		
Glu	Phe	Ile	Pro	Lys	Glu	Glu	Arg	Ile	Ile	Ser	Ile	Glu	Asp	Thr	Glu
		195					200						205		
Glu	Ile	Val	Phe	Lys	His	His	Lys	Asn	Tyr	Thr	Gln	Leu	Phe	Phe	Gly
	210					215					220				
Gly	Asn	Ile	Thr	Ser	Ala	Asp	Cys	Leu	Lys	Ser	Cys	Leu	Arg	Met	Arg
225					230					235				240	
Pro	Asp	Arg	Ile	Ile	Leu	Gly	Glu	Leu	Arg	Ser	Ser	Glu	Ala	Tyr	Asp
				245					250					255	
Phe	Tyr	Asn	Val	Leu	Cys	Ser	Gly	His	Lys	Gly	Thr	Leu	Thr	Thr	Leu
			260					265						270	
His	Ala	Gly	Ser	Ser	Glu	Glu	Ala	Phe	Ile	Arg	Leu	Ala	Asn	Met	Ser
		275					280					285			
Ser	Ser	Asn	Ser	Ala	Ala	Arg	Asn	Ile	Lys	Phe	Glu	Ser	Leu	Ile	Glu
	290					295					300				
Gly	Phe	Lys	Asp	Leu	Ile	Asp	Met	Ile	Val	His	Ile	Asn	His	His	Lys
305					310					315					320
Gln	Cys	Asp	Glu	Phe	Tyr	Ile	Lys	His	Arg						
				325					330						

<210> 623

<211> 5334
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (22)...(5250)

```

<400> 623
taaataaaaaa ggcgttaaga c atg aat gaa gaa aac gat aaa ctt gaa act 51
                        Met Asn Glu Glu Asn Asp Lys Leu Glu Thr 10

tct aaa aaa gcc caa caa gat tca ccc caa gat tta tcc aat gaa gaa 99
Ser Lys Lys Ala Gln Gln Asp Ser Pro Gln Asp Leu Ser Asn Glu Glu 25

gca aca gaa gcc aat cat ttt gaa aat ctt tta aaa gaa tcc aaa gaa 147
Ala Thr Glu Ala Asn His Phe Glu Asn Leu Leu Lys Glu Ser Lys Glu 40

agc tca gat cat cat ctt gac aac ccc aca gaa act caa acc cat ttt 195
Ser Ser Asp His His Leu Asp Asn Pro Thr Glu Thr Gln Thr His Phe 55

gat gga gac aag tca gaa gaa acc caa act caa atg gat tct gaa ggt 243
Asp Gly Asp Lys Ser Glu Glu Thr Gln Thr Gln Met Asp Ser Glu Gly 70

aat gaa act tca gaa tct agc aat ggc agt cta gca gac aag tta ttc 291
Asn Glu Thr Ser Glu Ser Ser Asn Gly Ser Leu Ala Asp Lys Leu Phe 90

aaa aaa gcc aga aaa tta gtt gat aat aaa aaa cct ttc act cag caa 339
Lys Lys Ala Arg Lys Leu Val Asp Asn Lys Lys Pro Phe Thr Gln Gln 105

aag aat tta gat gaa gaa acc caa gaa ctg aac gaa gaa gac gat caa 387
Lys Asn Leu Asp Glu Glu Thr Gln Glu Leu Asn Glu Glu Asp Asp Gln 120

gaa aat aat gag tat caa gaa gaa act caa acg gac tta att gat gat 435
Glu Asn Asn Glu Tyr Gln Glu Glu Thr Gln Thr Asp Leu Ile Asp Asp 135

gaa act tct aaa aaa acc caa caa cat tca ccc caa gat tta tcc aat 483
Glu Thr Ser Lys Lys Thr Gln Gln His Ser Pro Gln Asp Leu Ser Asn 150

gaa gaa gca aca gaa gcc aat cat ttt gaa aat ctt tta aaa gaa tcc 531
Glu Glu Ala Thr Glu Ala Asn His Phe Glu Asn Leu Leu Lys Glu Ser 170

aaa gaa agc tca gat cat cat ctt gac aac ccc aca gaa act caa acc 579
Lys Glu Ser Ser Asp His His Leu Asp Asn Pro Thr Glu Thr Gln Thr 185

aat ttt gat gga gac aag tca gaa gaa acc caa act caa atg gat tct 627
Asn Phe Asp Gly Asp Lys Ser Glu Glu Thr Gln Thr Gln Met Asp Ser

```

190						195						200						
gaa ggt aat gaa act tca	gaa tct agc aat ggc agt cta	gca gac aag	675															
Glu Gly Asn Glu Thr Ser	Glu Ser Ser Asn Gly Ser	Leu Ala Asp Lys																
205	210	215																
tta ttc aaa aaa gcc aga	aaa tta gtt gat aat aaa	aaa cct ttc act	723															
Leu Phe Lys Lys Ala Arg	Lys Leu Val Asp Asn Lys	Lys Pro Phe Thr																
220	225	230																
cag caa aag aat tta gat	gaa gaa acc caa gaa ctg	aac gaa gaa gac	771															
Gln Gln Lys Asn Leu Asp	Glu Glu Thr Gln Glu Leu	Asn Glu Glu Asp																
235	240	245	250															
gat caa gaa aat aat gag	tat caa gaa gaa act caa	acg gac tta att	819															
Asp Gln Glu Asn Asn Glu	Tyr Gln Glu Glu Thr Gln	Thr Asp Leu Ile																
255	260	265																
gat gat gaa act tct aaa	aaa acc caa caa cat tca	ccc caa gat tta	867															
Asp Asp Glu Thr Ser Lys	Lys Thr Gln Gln His Ser	Pro Gln Asp Leu																
270	275	280																
tcc aat gaa gaa gca aca	gaa gcc aat cat ttt gaa	aat ctt tta aaa	915															
Ser Asn Glu Glu Ala Thr	Glu Ala Asn His Phe Glu	Asn Leu Leu Lys																
285	290	295																
gaa tcc aaa gaa aoc tca	gat cat cat ctt gac aac	ccc aca gaa act	963															
Glu Ser Lys Glu Ser Ser	Asp His His Leu Asp Asn	Pro Thr Glu Thr																
300	305	310																
caa acc aat ttt gat gca	gac aag tca gaa gaa ata	act gac gac tct	1011															
Gln Thr Asn Phe Asp Gly	Asp Lys Ser Glu Glu Ile	Thr Asp Asp Ser																
315	320	325	330															
aac gat caa gag att atc	aaa gga aoc aaa aag	aaa tat att att ggt	1059															
Asn Asp Gln Glu Ile Ile	Lys Gly Ser Lys Lys Lys	Tyr Ile Ile Gly																
335	340	345																
goc att gta gtc gct gtt	ctt atc gtg att att tta	ttt tct aga aoc	1107															
Gly Ile Val Val Ala Val	Leu Ile Val Ile Ile Leu	Phe Ser Arg Ser																
350	355	360																
att ttt cac tac ttc atg	cct ttg gaa gat aaa aoc	tct cgt ttt agc	1155															
Ile Phe His Tyr Phe Met	Pro Leu Glu Asp Lys Ser	Ser Arg Phe Ser																
365	370	375																
aaa gac agg aat ctt tat	gtc aat gat gaa atc caa	ata agg caa gac	1203															
Lys Asp Arg Asn Leu Tyr	Val Asn Asp Glu Ile Gln	Ile Arg Gln Glu																
380	385	390																
tat aac cga ttg ctg aaa	gaa cgg aat gaa aaa ggc	aat atg atc gat	1251															
Tyr Asn Arg Leu Leu Lys	Glu Arg Asn Glu Lys Gly	Asn Met Ile Asp																
395	400	405	410															
aag aat ctt ttc ttc aat	gac gat ccc aat aga acc	tta tac aac tat	1299															
Lys Asn Leu Phe Phe Asn	Asp Asp Pro Asn Arg Thr	Leu Tyr Asn Tyr																
415	420	425																
ttg aat att gca gaa att	gag gac aaa aac ccg ttg	aga gcc ttt tat	1347															

Leu Asn Ile Ala Glu Ile Glu Asp Lys Asn Pro Leu Arg Ala Phe Tyr	
430 435 440	
gaa tgt att agt aat ggt ggc aac tat gaa gaa tgt ttg aag ctt atc	1395
Glu Cys Ile Ser Asn Gly Gly Asn Tyr Glu Glu Cys Leu Lys Leu Ile	
445 450 455	
aaa gac aaa aaa ctt caa gat cag atg aaa aag act cta gag gct tat	1443
Lys Asp Lys Lys Leu Gln Asp Gln Met Lys Lys Thr Leu Glu Ala Tyr	
460 465 470	
aac gac tgc atc aaa aat gcc aaa act gaa gaa gaa agg atc aag tgt	1491
Asn Asp Cys Ile Lys Asn Ala Lys Thr Glu Glu Glu Arg Ile Lys Cys	
475 480 485 490	
tta gat tta atc aaa gat gaa aac cta aaa aaa agc tta ctg aac caa	1539
Leu Asp Leu Ile Lys Asp Glu Asn Leu Lys Lys Ser Leu Leu Asn Gln	
495 500 505	
caa aaa gtt caa gtg gcg cta gat tgt ttg aaa aac gct aaa acc gat	1587
Gln Lys Val Gln Val Ala Leu Asp Cys Leu Lys Asn Ala Lys Thr Asp	
510 515 520	
gaa gaa cga aac gag tgc cta aaa ctc ata aat gac cct gag att aga	1635
Glu Glu Arg Asn Glu Cys Leu Lys Leu Ile Asn Asp Pro Glu Ile Arg	
525 530 535	
gag aaa ttc cgt aag gaa tta gag ctt caa aaa gag ctt caa gag tat	1683
Glu Lys Phe Arg Lys Glu Leu Glu Leu Gln Lys Glu Leu Gln Glu Tyr	
540 545 550	
aag gat tgt atc aaa aac gcc aaa aca gaa gct gag aaa aac aaa tgc	1731
Lys Asp Cys Ile Lys Asn Ala Lys Thr Glu Ala Glu Lys Asn Lys Cys	
555 560 565 570	
ttg aaa ggc ttg tct aaa gaa gct ata gag aga ttg aaa cag caa gcg	1779
Leu Lys Gly Leu Ser Lys Glu Ala Ile Glu Arg Leu Lys Gln Gln Ala	
575 580 585	
cta gat tgt ttg aaa aac gct aaa acc gat gaa gaa cga aac gag tgc	1827
Leu Asp Cys Leu Lys Asn Ala Lys Thr Asp Glu Glu Arg Asn Glu Cys	
590 595 600	
ttg aaa aat att ccc caa gac ttg caa aaa gaa cta tta gct gat atg	1875
Leu Lys Asn Ile Pro Gln Asp Leu Gln Lys Glu Leu Leu Ala Asp Met	
605 610 615	
agc gtc aag gct tac aag gat tgc gta tca aaa gct aga aat gaa aaa	1923
Ser Val Lys Ala Tyr Lys Asp Cys Val Ser Lys Ala Arg Asn Glu Lys	
620 625 630	
gag aaa caa gaa tgc gag aaa ttg ctc acg cct gaa gcg agg aaa aac	1971
Glu Lys Gln Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala Arg Lys Lys	
635 640 645 650	
tta gaa caa cag gtt cta gat tgt ttg aaa aac gct aaa acc gat gaa	2019
Leu Glu Gln Gln Val Leu Asp Cys Leu Lys Asn Ala Lys Thr Asp Glu	
655 660 665	

gaa cga aaa aag tgt ttg aaa gat ctc cct aaa gac tta caa agc gat	2067
Glu Arg Lys Lys Cys Leu Lys Asp Leu Pro Lys Asp Leu Gln Ser Asp	
670 675 680	
att cta gcc aaa gag agc ctg aaa gct tat aaa gac tgc gta tct caa	2115
Ile Leu Ala Lys Glu Ser Leu Lys Ala Tyr Lys Asp Cys Val Ser Gln	
685 690 695	
gcc aaa acc gaa gct gag aaa aaa gaa tgc gag aaa tta ctc acc cct	2163
Ala Lys Thr Glu Ala Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro	
700 705 710	
gaa gcg aaa aaa ctt tta gaa gaa gaa gcc aaa gag agc gtt aag gct	2211
Glu Ala Lys Lys Leu Leu Glu Glu Glu Ala Lys Glu Ser Val Lys Ala	
715 720 725 730	
tat ttg gat tgc gta tct caa gcc aaa acc gaa gct gag aaa aaa gaa	2259
Tyr Leu Asp Cys Val Ser Gln Ala Lys Thr Glu Ala Glu Lys Lys Glu	
735 740 745	
tgc gag aaa ttg ctc acc cct gaa gcg aaa aaa aag tta gaa gaa gct	2307
Cys Glu Lys Leu Leu Thr Pro Glu Ala Lys Lys Lys Leu Glu Glu Ala	
750 755 760	
aaa aaa agc gtt aaa gct tac ttg gat tgc gta tca aga gct agg aat	2355
Lys Lys Ser Val Lys Ala Tyr Leu Asp Cys Val Ser Arg Ala Arg Asn	
765 770 775	
gaa aaa gag aaa aaa gaa tgc gag aaa ttg ctc acc cct gaa gcg aaa	2403
Glu Lys Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala Lys	
780 785 790	
aaa ctt tta gag caa caa gca cta gat tgt ttg aaa aac gct aaa acc	2451
Lys Leu Leu Glu Gln Gln Ala Leu Asp Cys Leu Lys Asn Ala Lys Thr	
795 800 805 810	
gat aaa gaa cga aaa aag tgt ttg aaa gat ctc cct aaa gac ttg cac	2499
Asp Lys Glu Arg Lys Lys Cys Leu Lys Asp Leu Pro Lys Asp Leu Gln	
815 820 825	
aaa aag gtt tta gct aaa gaa agc gtt aaa gct tac ttg gat tgc gta	2547
Lys Lys Val Leu Ala Lys Glu Ser Val Lys Ala Tyr Leu Asp Cys Val	
830 835 840	
tct caa gcc aaa act gaa gct gag aaa aaa gaa tgc gag aaa tta ctc	2595
Ser Gln Ala Lys Thr Glu Ala Glu Lys Lys Glu Cys Glu Lys Leu Leu	
845 850 855	
acc cct gaa gcg aga aaa ctt tta gaa gaa gct aaa aaa agc gtt aag	2643
Thr Pro Glu Ala Arg Lys Leu Leu Glu Glu Ala Lys Lys Ser Val Lys	
860 865 870	
gct tay ttg gat tgc gta tct caa gcc aaa act gaa gct gag aaa aaa	2691
Ala Tyr Leu Asp Cys Val Ser Gln Ala Lys Thr Glu Ala Glu Lys Lys	
875 880 885 890	
gaa tgc gag aaa tta ctc acc cct gaa gcg aga aaa ctc tta gaa gaa	2739
Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala Arg Lys Leu Leu Glu Glu	
895 900 905	

gct aaa gag agc gtt aaa gct tat aaa gac tgc gta tca aaa gct agc	2787
Ala Lys Glu Ser Val Lys Ala Tyr Lys Asp Cys Val Ser Lys Ala Arg	
910 915 920	
aat gaa aaa gag aaa aaa gaa tgc gag aaa tta ctc acg cct gaa gcg	2835
Asn Glu Lys Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala	
925 930 935	
aaa aaa ctt tta gag caa caa gtg cta gat tgt ttg aaa aac gct aaa	2883
Lys Lys Leu Leu Glu Gln Gln Val Leu Asp Cys Leu Lys Asn Ala Lys	
940 945 950	
acc gaa gct gat aaa aaa agg tgt gtc aaa gat ctc cct aaa gac ttg	2931
Thr Glu Ala Asp Lys Lys Arg Cys Val Lys Asp Leu Pro Lys Asp Leu	
955 960 965 970	
cag aaa aag gtt tta gct aaa gag agc gtt aag gct tat ttg gac tgc	2979
Gln Lys Lys Val Leu Ala Lys Glu Ser Val Lys Ala Tyr Leu Asp Cys	
975 980 985	
gta tca aga gct agg aat gaa aaa gag aaa aaa gaa tgc gag aaa ttg	3027
Val Ser Arg Ala Arg Asn Glu Lys Glu Lys Lys Glu Cys Glu Lys Leu	
990 995 1000	
ctc acc cct gaa gcg aaa aaa ctt tta gaa gaa gcc aaa gag agt ctt	3075
Leu Thr Pro Glu Ala Lys Lys Leu Leu Glu Glu Ala Lys Glu Ser Leu	
1005 1010 1015	
aaa gct tat aaa gac tgc ctc tct caa gct aga aat gaa gaa gaa agc	3123
Lys Ala Tyr Lys Asp Cys Leu Ser Gln Ala Arg Asn Glu Glu Glu Arg	
1020 1025 1030	
aga gct tgc gag aaa cta ctc acg cct gaa gcg aga aaa ctc tta gac	3171
Arg Ala Cys Glu Lys Leu Leu Thr Pro Glu Ala Arg Lys Leu Leu Glu	
1035 1040 1045 1050	
caa gaa gtt aag aaa agc att aag gct tat ttg gac tgc gta tca aga	3219
Gln Glu Val Lys Lys Ser Ile Lys Ala Tyr Leu Asp Cys Val Ser Arg	
1055 1060 1065	
gct agg aat gaa aaa gag aaa aaa gaa tgc gag aaa tta ctc acg cct	3267
Ala Arg Asn Glu Lys Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro	
1070 1075 1080	
gaa gcg aga aaa ttt tta gcg aag caa gtg cta aat tgt ttg gaa aaa	3315
Glu Ala Arg Lys Phe Leu Ala Lys Gln Val Leu Asn Cys Leu Glu Lys	
1085 1090 1095	
gct gga aat gaa gaa gaa aga aaa gca tgt ctt aaa aat ctc cct aaa	3363
Ala Gly Asn Glu Glu Glu Arg Lys Ala Cys Leu Lys Asn Leu Pro Lys	
1100 1105 1110	
gac tta cag gaa aat att tta gct aaa gag agt ctt aaa gct tat aaa	3411
Asp Leu Gln Glu Asn Ile Leu Ala Lys Glu Ser Leu Lys Ala Tyr Lys	
1115 1120 1125 1130	
gac tgc ctc tct caa gct aga aat gaa gaa gaa agg aga gct tgc gac	3459
Asp Cys Leu Ser Gln Ala Arg Asn Glu Glu Glu Arg Arg Ala Cys Glu	

1135	1140	1145	
aaa cta ctc acg cct gaa gcg aga	aaa ctc tta gag caa gaa gtt aag		3507
Lys Leu Leu Thr Pro Glu Ala Arg	Lys Leu Leu Glu Gln Glu Val Lys		
1150	1155	1160	
aaa agc gtt aag gct tat ttg gac tgc gta tca aga gct agg aat gaa			3555
Lys Ser Val Lys Ala Tyr Leu Asp Cys Val Ser Arg Ala Arg Asn Glu			
1165	1170	1175	
aaa gag aaa aaa gaa tgc gag aaa tta ctc acg cct gaa gcg aga aaa			3603
Lys Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala Arg Lys			
1180	1185	1190	
ttt tta gcg aaa gaa ctc caa caa aaa gat aaa gcg atc aaa gat tgc			3651
Phe Leu Ala Lys Glu Leu Gln Gln Lys Asp Lys Ala Ile Lys Asp Cys			
1195	1200	1205	1210
ttg aaa aac gcc gat cct aac gac aga gcg gct atc atg aag tgt ttg			3699
Leu Lys Asn Ala Asp Pro Asn Asp Arg Ala Ala Ile Met Lys Cys Leu			
1215	1220	1225	
gat ggt ttg agc gat gaa gag aag ctc aaa tac ctg caa gaa gct aga			3747
Asp Gly Leu Ser Asp Glu Glu Lys Leu Lys Tyr Leu Gln Glu Ala Arg			
1230	1235	1240	
gaa aag gct gtt gcg gat tgt ttg gct atg gct aaa acc gat gaa gaa			3795
Glu Lys Ala Val Ala Asp Cys Leu Ala Met Ala Lys Thr Asp Glu Glu			
1245	1250	1255	
aaa agg aaa tgc caa aac ctt tat agc gat ttg atc caa gaa atc caa			3843
Lys Arg Lys Cys Gln Asn Leu Tyr Ser Asp Leu Ile Gln Glu Ile Gln			
1260	1265	1270	
aat aaa agg aca caa aac aaa caa aat caa ttg agt aaa aca gaa agc			3891
Asn Lys Arg Thr Gln Asn Lys Gln Asn Gln Leu Ser Lys Thr Glu Arg			
1275	1280	1285	1290
ttg cat caa gca agc gag tgc ttg gat aac tta gat gac cct act gat			3939
Leu His Gln Ala Ser Glu Cys Leu Asp Asn Leu Asp Asp Pro Thr Asp			
1295	1300	1305	
caa gag gcc ata gag caa tct tta gag gcc ttg agc gat agt gaa agc			3987
Gln Glu Ala Ile Glu Gln Cys Leu Glu Gly Leu Ser Asp Ser Glu Arg			
1310	1315	1320	
gcg cta att cta gga att aaa cga caa gct gat gaa gtg gat ctg att			4035
Ala Leu Ile Leu Gly Ile Lys Arg Gln Ala Asp Glu Val Asp Leu Ile			
1325	1330	1335	
tat agc gat cta aga aac cgt aaa acc ttt gat aac atg gcg gct aaa			4083
Tyr Ser Asp Leu Arg Asn Arg Lys Thr Phe Asp Asn Met Ala Ala Lys			
1340	1345	1350	
ggt tat cca ttg tta cca atg gat ttc aaa aat gcc gcc gat att gcc			4131
Gly Tyr Pro Leu Leu Pro Met Asp Phe Lys Asn Gly Gly Asp Ile Ala			
1355	1360	1365	1370
act att aac gcc act aat gtt gat gcg gac aaa ata gct agc gat aat			4179

Thr Ile Asn Ala	Thr Asn Val Asp Ala	Asp Lys Ile Ala Ser Asp Asn	
1375	1380	1385	
cct att tat gct tcc ata gag cct gat att gcc aag caa tac gaa aca	4227		
Pro Ile Tyr Ala Ser Ile Glu Pro Asp Ile Ala Lys Gln Tyr Glu Thr			
1390	1395	1400	
gaa aaa acc att aag gat aag aat tta gaa gct aaa tta gct aag gct	4275		
Glu Lys Thr Ile Lys Asp Lys Asn Leu Glu Ala Lys Leu Ala Lys Ala			
1405	1410	1415	
tta ggt ggc aat aaa aaa gat gac gat aaa gaa aaa agt aaa aaa tcc	4323		
Leu Gly Gly Asn Lys Lys Asp Asp Asp Lys Glu Lys Ser Lys Lys Ser			
1420	1425	1430	
aca gca gaa gct aaa gca gaa aac aat aag ata gac aaa gat gtc gca	4371		
Thr Ala Glu Ala Lys Ala Glu Asn Asn Lys Ile Asp Lys Asp Val Ala			
1435	1440	1445	1450
gaa act gcc aag aat atc agt gaa atc gct ctt aag aac aaa aaa gaa	4419		
Glu Thr Ala Lys Asn Ile Ser Glu Ile Ala Leu Lys Asn Lys Lys Glu			
1455	1460	1465	
aag agt ggg gaa ttt gta gat gaa aat ggt aat ccc att gat gac aaa	4467		
Lys Ser Gly Glu Phe Val Asp Glu Asn Gly Asn Pro Ile Asp Asp Lys			
1470	1475	1480	
aag aaa gca gaa aaa caa gat gaa aca agc cct gtc aaa cag gcc ttt	4515		
Lys Lys Ala Glu Lys Gln Asp Glu Thr Ser Pro Val Lys Gln Ala Phe			
1485	1490	1495	
ata ggc aag agt gat ccc aca ttt gtt tta gcg caa tac acc ccc att	4563		
Ile Gly Lys Ser Asp Pro Thr Phe Val Leu Ala Gln Tyr Thr Pro Ile			
1500	1505	1510	
gaa atc act ctg act tct aaa gta gat gcc act ctc aca ggt ata gtc	4611		
Glu Ile Thr Leu Thr Ser Lys Val Asp Ala Thr Leu Thr Gly Ile Val			
1515	1520	1525	1530
agt ggg gtt gta gcc aaa gat gta tgg aac atg aac ggc act atg atc	4659		
Ser Gly Val Val Ala Lys Asp Val Trp Asn Met Asn Gly Thr Met Ile			
1535	1540	1545	
tta tta gac aaa ggc act aag gtg tat ggg aat tat caa agc gtg aaa	4707		
Leu Leu Asp Lys Gly Thr Lys Val Tyr Gly Asn Tyr Gln Ser Val Lys			
1550	1555	1560	
ggt ggc aca ccc att atg aca cgc tta atg ata gtc ttt act aaa gcc	4755		
Gly Gly Thr Pro Ile Met Thr Arg Leu Met Ile Val Phe Thr Lys Ala			
1565	1570	1575	
att acg cct gat ggt gtg ata ata cct cta gca aac gct caa gca gca	4803		
Ile Thr Pro Asp Gly Val Ile Ile Pro Leu Ala Asn Ala Gln Ala Ala			
1580	1585	1590	
ggc atg ttg ggt gaa gca ggg gta gat ggc tat gtg aat aat cac ttt	4851		
Gly Met Leu Gly Glu Ala Gly Val Asp Gly Tyr Val Asn Asn His Phe			
1595	1600	1605	1610

atg aag cgc ata ggc ttt gct gtg ata gca agc gtg gtt aat agc ttc	4899
Met Lys Arg Ile Gly Phe Ala Val Ile Ala Ser Val Val Asn Ser Phe	
1615 1620 1625	
ttg caa act gcg cct atc ata gct cta gat aaa ctc ata ggc ctt ggc	4947
Leu Gln Thr Ala Pro Ile Ile Ala Leu Asp Lys Leu Ile Gly Leu Gly	
1630 1635 1640	
aaa ggt aga agt gaa agg aca cct gaa ttt aat tac gct ttg ggt caa	4995
Lys Gly Arg Ser Glu Arg Thr Pro Glu Phe Asn Tyr Ala Leu Gly Gln	
1645 1650 1655	
gct atc aat ggt agc atg caa agt tca gct cag atg tct aat caa att	5043
Ala Ile Asn Gly Ser Met Gln Ser Ser Ala Gln Met Ser Asn Gln Ile	
1660 1665 1670	
cta ggg caa ctg atg aat atc ccc cca agt ttt tac aaa aac gag ggc	5091
Leu Gly Gln Leu Met Asn Ile Pro Pro Ser Phe Tyr Lys Asn Glu Gly	
1675 1680 1685 1690	
gat agt att aag att ctc aca atg gac gat att gat ttt agc ggt gtg	5139
Asp Ser Ile Lys Ile Leu Thr Met Asp Asp Ile Asp Phe Ser Gly Val	
1695 1700 1705	
tat gat gtt aaa att act aac aaa tct gtg gta gat gaa att atc aaa	5187
Tyr Asp Val Lys Ile Thr Asn Lys Ser Val Val Asp Glu Ile Ile Lys	
1710 1715 1720	
caa agc acc aaa act ttg tct aga gaa cat gaa gaa atc acc aca agc	5235
Gln Ser Thr Lys Thr Leu Ser Arg Glu His Glu Glu Ile Thr Thr Ser	
1725 1730 1735	
ccc aaa ggt ggc aat taattcaaga gaaaggataa aatatattca tgttactaaa	5290
Pro Lys Gly Gly Asn	
1740	
ctcggttctt tacaaaataa aagacaaaac caacaacagg ctct	5334

<210> 624

<211> 1743

<212> PRT

<213> Helicobacter pylori

<220>

<221> VARIANT

<222> 876

<223> Xaa = Any Amino Acid

<400> 624

Met Asn Glu Glu Asn Asp Lys Leu Glu Thr Ser Lys Lys Ala Gln Gln	
1 5 10 15	
Asp Ser Pro Gln Asp Leu Ser Asn Glu Ala Thr Glu Ala Asn His	
20 25 30	
Phe Glu Asn Leu Leu Lys Glu Ser Lys Glu Ser Ser Asp His His Leu	
35 40 45	
Asp Asn Pro Thr Glu Thr Gln Thr His Phe Asp Gly Asp Lys Ser Glu	
50 55 60	
Glu Thr Gln Thr Gln Met Asp Ser Glu Gly Asn Glu Thr Ser Glu Ser	
65 70 75 80	

Ser	Asn	Gly	Ser	Leu	Ala	Asp	Lys	Leu	Phe	Lys	Lys	Ala	Arg	Lys	Leu
				85					90					95	
Val	Asp	Asn	Lys	Lys	Pro	Phe	Thr	Gln	Gln	Lys	Asn	Leu	Asp	Glu	Glu
			100					105					110		
Thr	Gln	Glu	Leu	Asn	Glu	Glu	Asp	Asp	Gln	Glu	Asn	Asn	Glu	Tyr	Gln
		115					120					125			
Glu	Glu	Thr	Gln	Thr	Asp	Leu	Ile	Asp	Asp	Glu	Thr	Ser	Lys	Lys	Thr
	130					135					140				
Gln	Gln	His	Ser	Pro	Gln	Asp	Leu	Ser	Asn	Glu	Glu	Ala	Thr	Glu	Ala
145					150					155					160
Asn	His	Phe	Glu	Asn	Leu	Leu	Lys	Glu	Ser	Lys	Glu	Ser	Ser	Asp	His
				165					170					175	
His	Leu	Asp	Asn	Pro	Thr	Glu	Thr	Gln	Thr	Asn	Phe	Asp	Gly	Asp	Lys
			180					185					190		
Ser	Glu	Glu	Thr	Gln	Thr	Gln	Met	Asp	Ser	Glu	Gly	Asn	Glu	Thr	Ser
	195						200					205			
Glu	Ser	Ser	Asn	Gly	Ser	Leu	Ala	Asp	Lys	Leu	Phe	Lys	Lys	Ala	Arg
	210					215					220				
Lys	Leu	Val	Asp	Asn	Lys	Lys	Pro	Phe	Thr	Gln	Gln	Lys	Asn	Leu	Asp
225					230					235					240
Glu	Glu	Thr	Gln	Glu	Leu	Asn	Glu	Glu	Asp	Asp	Gln	Glu	Asn	Asn	Glu
				245					250					255	
Tyr	Gln	Glu	Glu	Thr	Gln	Thr	Asp	Leu	Ile	Asp	Asp	Glu	Thr	Ser	Lys
		260						265					270		
Lys	Thr	Gln	Gln	His	Ser	Pro	Gln	Asp	Leu	Ser	Asn	Glu	Glu	Ala	Thr
		275					280					285			
Glu	Ala	Asn	His	Phe	Glu	Asn	Leu	Leu	Lys	Glu	Ser	Lys	Glu	Ser	Ser
	290					295				300					
Asp	His	His	Leu	Asp	Asn	Pro	Thr	Glu	Thr	Gln	Thr	Asn	Phe	Asp	Gly
305					310					315					320
Asp	Lys	Ser	Glu	Glu	Ile	Thr	Asp	Asp	Ser	Asn	Asp	Gln	Glu	Ile	Ile
				325					330					335	
Lys	Gly	Ser	Lys	Lys	Lys	Tyr	Ile	Ile	Gly	Gly	Ile	Val	Val	Ala	Val
		340						345					350		
Leu	Ile	Val	Ile	Ile	Leu	Phe	Ser	Arg	Ser	Ile	Phe	His	Tyr	Phe	Met
		355					360					365			
Pro	Leu	Glu	Asp	Lys	Ser	Ser	Arg	Phe	Ser	Lys	Asp	Arg	Asn	Leu	Tyr
	370					375					380				
Val	Asn	Asp	Glu	Ile	Gln	Ile	Arg	Gln	Glu	Tyr	Asn	Arg	Leu	Leu	Lys
385					390					395					400
Glu	Arg	Asn	Glu	Lys	Gly	Asn	Met	Ile	Asp	Lys	Asn	Leu	Phe	Phe	Asn
				405					410					415	
Asp	Asp	Pro	Asn	Arg	Thr	Leu	Tyr	Asn	Tyr	Leu	Asn	Ile	Ala	Glu	Ile
			420					425					430		
Glu	Asp	Lys	Asn	Pro	Leu	Arg	Ala	Phe	Tyr	Glu	Cys	Ile	Ser	Asn	Gly
		435					440					445			
Gly	Asn	Tyr	Glu	Glu	Cys	Leu	Lys	Leu	Ile	Lys	Asp	Lys	Lys	Leu	Gln
	450					455					460				
Asp	Gln	Met	Lys	Lys	Thr	Leu	Glu	Ala	Tyr	Asn	Asp	Cys	Ile	Lys	Asn
465					470					475					480
Ala	Lys	Thr	Glu	Glu	Arg	Ile	Lys	Cys	Leu	Asp	Leu	Ile	Lys	Lys	Asp
				485				490						495	
Glu	Asn	Leu	Lys	Lys	Ser	Leu	Leu	Asn	Gln	Gln	Lys	Val	Gln	Val	Ala
		500						505					510		
Leu	Asp	Cys	Leu	Lys	Asn	Ala	Lys	Thr	Asp	Glu	Glu	Arg	Asn	Glu	Cys
		515					520					525			
Leu	Lys	Leu	Ile	Asn	Asp	Pro	Glu	Ile	Arg	Glu	Lys	Phe	Arg	Lys	Glu
	530					535					540				
Leu	Glu	Leu	Gln	Lys	Glu	Leu	Gln	Glu	Tyr	Lys	Asp	Cys	Ile	Lys	Asn

545	Ala	Lys	Thr	Glu	Ala	Glu	Lys	Asn	Lys	Cys	Leu	Lys	Gly	Leu	Ser	Lys	560
					565					570							575
	Glu	Ala	Ile	Glu	Arg	Leu	Lys	Gln	Gln	Ala	Leu	Asp	Cys	Leu	Lys	Asn	
					580					585							590
	Ala	Lys	Thr	Asp	Glu	Glu	Arg	Asn	Glu	Cys	Leu	Lys	Asn	Ile	Pro	Gln	
					595					600							
	Asp	Leu	Gln	Lys	Glu	Leu	Leu	Ala	Asp	Met	Ser	Val	Lys	Ala	Tyr	Lys	
					610					615							
	Asp	Cys	Val	Ser	Lys	Ala	Arg	Asn	Glu	Lys	Glu	Lys	Gln	Glu	Cys	Glu	
					625												640
	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Arg	Lys	Lys	Leu	Glu	Gln	Gln	Val	Leu	
					645												655
	Asp	Cys	Leu	Lys	Asn	Ala	Lys	Thr	Asp	Glu	Glu	Arg	Lys	Lys	Cys	Leu	
					660												670
	Lys	Asp	Leu	Pro	Lys	Asp	Leu	Gln	Ser	Asp	Ile	Leu	Ala	Lys	Glu	Ser	
					675												685
	Leu	Lys	Ala	Tyr	Lys	Asp	Cys	Val	Ser	Gln	Ala	Lys	Thr	Glu	Ala	Glu	
					690												700
	Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Lys	Lys	Leu	Leu	
					705												720
	Glu	Glu	Glu	Ala	Lys	Glu	Ser	Val	Lys	Ala	Tyr	Leu	Asp	Cys	Val	Ser	
					725												735
	Gln	Ala	Lys	Thr	Glu	Ala	Glu	Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	Thr	
					740												750
	Pro	Glu	Ala	Lys	Lys	Lys	Leu	Glu	Glu	Ala	Lys	Lys	Ser	Val	Lys	Ala	
					755												765
	Tyr	Leu	Asp	Cys	Val	Ser	Arg	Ala	Arg	Asn	Glu	Lys	Glu	Lys	Lys	Glu	
					770												780
	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Lys	Lys	Leu	Leu	Glu	Gln	Gln	
					785												800
	Ala	Leu	Asp	Cys	Leu	Lys	Asn	Ala	Lys	Thr	Asp	Lys	Glu	Arg	Lys	Lys	
					805												815
	Cys	Leu	Lys	Asp	Leu	Pro	Lys	Asp	Leu	Gln	Lys	Lys	Val	Leu	Ala	Lys	
					820												830
	Glu	Ser	Val	Lys	Ala	Tyr	Leu	Asp	Cys	Val	Ser	Gln	Ala	Lys	Thr	Glu	
					835												845
	Ala	Glu	Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Arg	Lys	
					850												860
	Leu	Leu	Glu	Glu	Ala	Lys	Lys	Ser	Val	Lys	Ala	Xaa	Leu	Asp	Cys	Val	
					865												880
	Ser	Gln	Ala	Lys	Thr	Glu	Ala	Glu	Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	
					885												895
	Thr	Pro	Glu	Ala	Arg	Lys	Leu	Leu	Glu	Glu	Ala	Lys	Glu	Ser	Val	Lys	
					900												910
	Ala	Tyr	Lys	Asp	Cys	Val	Ser	Lys	Ala	Arg	Asn	Glu	Lys	Glu	Lys	Lys	
					915												925
	Glu	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Lys	Lys	Leu	Leu	Glu	Gln	
					930												940
	Gln	Val	Leu	Asp	Cys	Leu	Lys	Asn	Ala	Lys	Thr	Glu	Ala	Asp	Lys	Lys	
					945												960
	Arg	Cys	Val	Lys	Asp	Leu	Pro	Lys	Asp	Leu	Gln	Lys	Lys	Val	Leu	Ala	
					965												975
	Lys	Glu	Ser	Val	Lys	Ala	Tyr	Leu	Asp	Cys	Val	Ser	Arg	Ala	Arg	Asn	
					980												990
	Glu	Lys	Glu	Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Lys	
					995												1005
	Lys	Leu	Leu	Glu	Glu	Ala	Lys	Glu	Ser	Leu	Lys	Ala	Tyr	Lys	Asp	Cys	
					1010												1020

Leu Ser Gln Ala Arg Asn Glu Glu Glu Arg Arg Ala Cys Glu Lys Leu
 1025 1030 1035 1040
 Leu Thr Pro Glu Ala Arg Lys Leu Leu Glu Gln Glu Val Lys Lys Ser
 1045 1050 1055
 Ile Lys Ala Tyr Leu Asp Cys Val Ser Arg Ala Arg Asn Glu Lys Glu
 1060 1065 1070
 Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala Arg Lys Phe Leu
 1075 1080 1085
 Ala Lys Gln Val Leu Asn Cys Leu Glu Lys Ala Gly Asn Glu Glu Glu
 1090 1095 1100
 Arg Lys Ala Cys Leu Lys Asn Leu Pro Lys Asp Leu Gln Glu Asn Ile
 1105 1110 1115 1120
 Leu Ala Lys Glu Ser Leu Lys Ala Tyr Lys Asp Cys Leu Ser Gln Ala
 1125 1130 1135
 Arg Asn Glu Glu Glu Arg Arg Ala Cys Glu Lys Leu Leu Thr Pro Glu
 1140 1145 1150
 Ala Arg Lys Leu Leu Glu Gln Glu Val Lys Lys Ser Val Lys Ala Tyr
 1155 1160 1165
 Leu Asp Cys Val Ser Arg Ala Arg Asn Glu Lys Glu Lys Lys Glu Cys
 1170 1175 1180
 Glu Lys Leu Leu Thr Pro Glu Ala Arg Lys Phe Leu Ala Lys Glu Leu
 1185 1190 1195 1200
 Gln Gln Lys Asp Lys Ala Ile Lys Asp Cys Leu Lys Asn Ala Asp Pro
 1205 1210 1215
 Asn Asp Arg Ala Ala Ile Met Lys Cys Leu Asp Gly Leu Ser Asp Glu
 1220 1225 1230
 Glu Lys Leu Lys Tyr Leu Gln Glu Ala Arg Glu Lys Ala Val Ala Asp
 1235 1240 1245
 Cys Leu Ala Met Ala Lys Thr Asp Glu Glu Lys Arg Lys Cys Gln Asn
 1250 1255 1260
 Leu Tyr Ser Asp Leu Ile Gln Glu Ile Gln Asn Lys Arg Thr Gln Asn
 1265 1270 1275 1280
 Lys Gln Asn Gln Leu Ser Lys Thr Glu Arg Leu His Gln Ala Ser Glu
 1285 1290 1295
 Cys Leu Asp Asn Leu Asp Asp Pro Thr Asp Gln Glu Ala Ile Glu Gln
 1300 1305 1310
 Cys Leu Glu Gly Leu Ser Asp Ser Glu Arg Ala Leu Ile Leu Gly Ile
 1315 1320 1325
 Lys Arg Gln Ala Asp Glu Val Asp Leu Ile Tyr Ser Asp Leu Arg Asn
 1330 1335 1340
 Arg Lys Thr Phe Asp Asn Met Ala Ala Lys Gly Tyr Pro Leu Leu Pro
 1345 1350 1355 1360
 Met Asp Phe Lys Asn Gly Gly Asp Ile Ala Thr Ile Asn Ala Thr Asn
 1365 1370 1375
 Val Asp Ala Asp Lys Ile Ala Ser Asp Asn Pro Ile Tyr Ala Ser Ile
 1380 1385 1390
 Glu Pro Asp Ile Ala Lys Gln Tyr Glu Thr Glu Lys Thr Ile Lys Asp
 1395 1400 1405
 Lys Asn Leu Glu Ala Lys Leu Ala Lys Ala Leu Gly Gly Asn Lys Lys
 1410 1415 1420
 Asp Asp Asp Lys Glu Lys Ser Lys Lys Ser Thr Ala Glu Ala Lys Ala
 1425 1430 1435 1440
 Glu Asn Asn Lys Ile Asp Lys Asp Val Ala Glu Thr Ala Lys Asn Ile
 1445 1450 1455
 Ser Glu Ile Ala Leu Lys Asn Lys Lys Glu Lys Ser Gly Glu Phe Val
 1460 1465 1470
 Asp Glu Asn Gly Asn Pro Ile Asp Asp Lys Lys Lys Ala Glu Lys Gln
 1475 1480 1485
 Asp Glu Thr Ser Pro Val Lys Gln Ala Phe Ile Gly Lys Ser Asp Pro

1490	1495	1500
Thr Phe Val Leu Ala Gln Tyr Thr Pro Ile Glu Ile Thr Leu Thr Ser		
1505	1510	1515
Lys Val Asp Ala Thr Leu Thr Gly Ile Val Ser Gly Val Val Ala Lys		1520
	1525	1530
Asp Val Trp Asn Met Asn Gly Thr Met Ile Leu Leu Asp Lys Gly Thr		1535
	1540	1545
Lys Val Tyr Gly Asn Tyr Gln Ser Val Lys Gly Gly Thr Pro Ile Met		1550
	1555	1560
Thr Arg Leu Met Ile Val Phe Thr Lys Ala Ile Thr Pro Asp Gly Val		1565
	1570	1575
Ile Ile Pro Leu Ala Asn Ala Gln Ala Ala Gly Met Leu Gly Glu Ala		1580
1585	1590	1595
Gly Val Asp Gly Tyr Val Asn Asn His Phe Met Lys Arg Ile Gly Phe		1600
	1605	1610
Ala Val Ile Ala Ser Val Val Asn Ser Phe Leu Gln Thr Ala Pro Ile		1615
	1620	1625
Ile Ala Leu Asp Lys Leu Ile Gly Leu Gly Lys Gly Arg Ser Glu Arg		1630
	1635	1640
Thr Pro Glu Phe Asn Tyr Ala Leu Gly Gln Ala Ile Asn Gly Ser Met		1645
	1650	1655
Gln Ser Ser Ala Gln Met Ser Asn Gln Ile Leu Gly Gln Leu Met Asn		1660
1665	1670	1675
Ile Pro Pro Ser Phe Tyr Lys Asn Glu Gly Asp Ser Ile Lys Ile Leu		1680
	1685	1690
Thr Met Asp Asp Ile Asp Phe Ser Gly Val Tyr Asp Val Lys Ile Thr		1695
	1700	1705
Asn Lys Ser Val Val Asp Glu Ile Ile Lys Gln Ser Thr Lys Thr Leu		1710
	1715	1720
Ser Arg Glu His Glu Glu Ile Thr Thr Ser Pro Lys Gly Gly Asn		1725
1730	1735	1740

<210> 625
 <211> 877
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (22)...(825)

<221> misc_feature
 <222> 806
 <223> n = A,T,C or G

<400> 625	
aacaaataaa ggagtattaa a atg aaa caa agt ttg cgc gaa caa aaa tta	51
Met Lys Gln Ser Leu Arg Glu Gln Lys Leu	
1 5 10	
ttg aaa att tta gaa aat gat gtc ttg acg att ttg gat agt ttt tci	99
Leu Lys Ile Leu Glu Asn Asp Val Leu Thr Ile Leu Asp Ser Phe Ser	
15 20 25	
aat tat ctt ttt gaa ctg aga gaa gac ttg gac ttc ata gaa gaa gaa	147
Asn Tyr Leu Phe Glu Leu Arg Glu Glu Leu Asp Phe Ile Glu Glu Glu	
30 35 40	

atg gaa ggt gaa atc acc gaa caa aac ctt acc gct ctt tat gat ttt	195
Met Glu Gly Glu Ile Thr Glu Gln Asn Leu Thr Ala Leu Tyr Asp Phe	
45 50 55	
tct aat ttc tta gaa gac cat gtc aat gta ttt tat gag aat gtt ttg	243
Ser Asn Phe Leu Glu Asp His Val Asn Val Phe Tyr Glu Asn Val Leu	
60 65 70	
aat ata gat gat gtc aaa aca gaa cac ctt tat tca ggt ctc ata gat	291
Asn Ile Asp Asp Val Lys Thr Glu His Leu Tyr Ser Gly Leu Ile Asp	
75 80 85 90	
agt ctt aac gct aat ctt cac ttt gtc aag tca ttt ctc agt aat cag	339
Ser Leu Asn Ala Asn Leu His Phe Val Lys Ser Phe Leu Ser Asn Gln	
95 100 105	
gat tta gac ttc cgc ttt ttt aag gaa ata aac gat ggg caa gat ccc	387
Asp Leu Asp Phe Arg Phe Phe Lys Glu Ile Asn Asp Gly Gln Asp Pro	
110 115 120	
caa aaa aca tta tca aga tta att cct ctt caa agt ggg aaa aat gat	435
Gln Lys Thr Leu Ser Arg Leu Ile Pro Leu Gln Ser Gly Lys Asn Asp	
125 130 135	
gca agc tcg ttt aaa gcc aat aat tct ttt gtt tca tta gtt tat gtt	483
Ala Ser Ser Phe Lys Ala Asn Asn Ser Phe Val Ser Leu Val Tyr Val	
140 145 150	
tat gtt tac ttc atg cta gaa act atc atg cag tcg tat agg att ctc	531
Tyr Val Tyr Phe Met Leu Glu Thr Ile Met Gln Ser Tyr Arg Ile Leu	
155 160 165 170	
aga ttg cta gaa aaa cct atc aat aac aac ata agc gag gac atg cag	579
Arg Leu Leu Glu Lys Pro Ile Asn Asn Asn Ile Ser Glu Asp Met Gln	
175 180 185	
aac gat ata gag aat ttt ttt gtt caa gcg aat ttt tta gaa tac tat	627
Asn Asp Ile Glu Asn Phe Phe Val Gln Ala Asn Phe Leu Glu Tyr Tyr	
190 195 200	
gtt cag aac aaa ata tac cca acc aat cat gcc tat gac ttc acg cat	675
Val Gln Asn Lys Ile Tyr Pro Thr Asn His Ala Tyr Asp Phe Thr His	
205 210 215	
ttg atc atg gac tcc att att cct aat tgg att caa act gat atg agc	723
Leu Ile Met Asp Ser Ile Ile Pro Asn Trp Ile Gln Thr Asp Met Ser	
220 225 230	
gtt gaa gct aaa aag aaa gag ctt ttt gaa aaa tat ttt caa aac att	771
Val Glu Ala Lys Lys Lys Glu Leu Phe Glu Lys Tyr Phe Gln Asn Ile	
235 240 245 250	
gat gaa gta aca aac aaa atg ctc gat caa aaa ant caa aac aaa agt	819
Asp Glu Val Thr Asn Lys Met Leu Asp Gln Lys Xaa Gln Asn Lys Ser	
255 260 265	
aac gat tgagtggcgt taatgcgcta gaatagtgc taaaaataaga ataaaggagt	875
Asn Asp	

Ca

877

<210> 626
 <211> 268
 <212> PRT
 <213> Helicobacter pylori

<220>
 <221> VARIANT
 <222> 262
 <223> Xaa = Any Amino Acid

<400> 626
 Met Lys Gln Ser Leu Arg Glu Gln Lys Leu Leu Lys Ile Leu Glu Asn
 1 5 10 15
 Asp Val Leu Thr Ile Leu Asp Ser Phe Ser Asn Tyr Leu Phe Glu Leu
 20 25 30
 Arg Glu Glu Leu Asp Phe Ile Glu Glu Glu Met Glu Gly Glu Ile Thr
 35 40 45
 Glu Gln Asn Leu Thr Ala Leu Tyr Asp Phe Ser Asn Phe Leu Glu Asp
 50 55 60
 His Val Asn Val Phe Tyr Glu Asn Val Leu Asn Ile Asp Asp Val Lys
 65 70 75 80
 Thr Glu His Leu Tyr Ser Gly Leu Ile Asp Ser Leu Asn Ala Asn Leu
 85 90 95
 His Phe Val Lys Ser Phe Leu Ser Asn Gln Asp Leu Asp Phe Arg Phe
 100 105 110
 Phe Lys Glu Ile Asn Asp Gly Gln Asp Pro Gln Lys Thr Leu Ser Arg
 115 120 125
 Leu Ile Pro Leu Gln Ser Gly Lys Asn Asp Ala Ser Ser Phe Lys Ala
 130 135 140
 Asn Asn Ser Phe Val Ser Leu Val Tyr Val Tyr Val Tyr Phe Met Leu
 145 150 155 160
 Glu Thr Ile Met Gln Ser Tyr Arg Ile Leu Arg Leu Leu Glu Lys Pro
 165 170 175
 Ile Asn Asn Asn Ile Ser Glu Asp Met Gln Asn Asp Ile Glu Asn Phe
 180 185 190
 Phe Val Gln Ala Asn Phe Leu Glu Tyr Tyr Val Gln Asn Lys Ile Tyr
 195 200 205
 Pro Thr Asn His Ala Tyr Asp Phe Thr His Leu Ile Met Asp Ser Ile
 210 215 220
 Ile Pro Asn Trp Ile Gln Thr Asp Met Ser Val Glu Ala Lys Lys Lys
 225 230 235 240
 Glu Leu Phe Glu Lys Tyr Phe Gln Asn Ile Asp Glu Val Thr Asn Lys
 245 250 255
 Met Leu Asp Gln Lys Xaa Gln Asn Lys Ser Asn Asp
 260 265

<210> 627
 <211> 736
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (26)...(706)

<400> 627

aaaaaatcaa taaaaggggt ttagc	atg	caa	gca	gta	att	tat	ggc	aag	caa	52
	Met	Gln	Ala	Val	Ile	Tyr	Gly	Lys	Gln	
	1				5					
gtg att atg cac ctt cta aac tct cat	caa	gaa	aaa	ttg	caa	gaa	atc	100		
Val Ile Met His Leu Leu Asn Ser His	Gln	Glu	Lys	Leu	Gln	Glu	Ile			
10		20		25						
tat ctt tct aaa gaa ata gac aag aaa	ctt	ttt	ttc	gcg	ctc	aaa	aaa	148		
Tyr Leu Ser Lys Glu Ile Asp Lys Lys	Leu	Phe	Phe	Ala	Leu	Lys	Lys			
	30	35			40					
gca tgc cct aat atc atc aaa gtg gat	aat	aaa	aaa	gcg	caa	agc	ttg	196		
Ala Cys Pro Asn Ile Ile Lys Val Asp	Asn	Lys	Lys	Ala	Gln	Ser	Leu			
	45	50		55						
gct aag ggg ggg aat cat caa ggg gtt	ttg	gct	aag	gtg	gaa	ctg	ccc	244		
Ala Lys Gly Gly Asn His Gln Gly Val	Leu	Ala	Lys	Val	Glu	Leu	Pro			
	60	65		70						
tta gcg gtt tct tta aaa gag gtt aaa	aaa	gct	caa	aaa	ctt	ttg	gtc	292		
Leu Ala Val Ser Leu Lys Glu Val Lys	Lys	Ala	Gln	Lys	Leu	Leu	Val			
	75	80		85						
ctt tgc ggg att acg gat gtg ggg aat	att	gga	ggt	att	ttt	agg	agc	340		
Leu Cys Gly Ile Thr Asp Val Gly Asn	Ile	Gly	Gly	Ile	Phe	Arg	Ser			
	90	95		100		105				
gcg tat tgc tta gga atg ggt ggc gtt	att	tta	gat	ttt	gct	aaa	gaa	388		
Ala Tyr Cys Leu Gly Met Gly Gly Val	Ile	Leu	Asp	Phe	Ala	Lys	Glu			
	110	115		120						
ttg gct tat gag ggg att gtg cga tcc	agc	ttg	ggc	ctt	atg	tat	gat	436		
Leu Ala Tyr Glu Gly Ile Val Arg Ser	Ser	Leu	Gly	Leu	Met	Tyr	Asp			
	125	130		135						
ttg cct ttt agc gtt atg cct aac acg	ctg	gat	tta	atc	aat	gaa	ttg	484		
Leu Pro Phe Ser Val Met Pro Asn Thr	Leu	Asp	Leu	Ile	Asn	Glu	Leu			
	140	145		150						
aaa acg agc ggg ttt tta tgt ttg ggc	gcg	agc	atg	caa	ggc	tct	agt	532		
Lys Thr Ser Gly Phe Leu Cys Leu Gly	Ala	Ser	Met	Gln	Gly	Ser	Ser			
	155	160		165						
caa ata gaa aat cta tcc tta aaa aaa	tgc	gct	ctt	ttt	ttg	ggg	agc	580		
Gln Ile Glu Asn Leu Ser Leu Lys Lys	Cys	Ala	Leu	Phe	Leu	Gly	Ser			
	170	175		180		185				
gag cat gag ggg ttg tct aaa aaa atc	ctt	gct	aaa	atg	gat	act	ata	628		
Glu His Glu Gly Leu Ser Lys Lys Ile	Leu	Ala	Lys	Met	Asp	Thr	Ile			
	190	195		200						
ttg agc gta aaa atg cga aga gat ttt	gat	tgc	ctc	aat	gtg	agc	gtc	676		
Leu Ser Val Lys Met Arg Arg Asp Phe	Asp	Ser	Leu	Asn	Val	Ser	Val			
	205	210		215						
gca gca ggg atc tta atg gat aaa atc	aac	taggtggtca	attgaatgga	726						
Ala Ala Gly Ile Leu Met Asp Lys Ile	Asn									

220

225

acagaataaa

736

<210> 628

<211> 227

<212> PRT

<213> Helicobacter pylori

<400> 628

```

Met Gln Ala Val Ile Tyr Gly Lys Gln Val Ile Met His Leu Leu Asn
 1           5           10           15
Ser His Gln Glu Lys Leu Gln Glu Ile Tyr Leu Ser Lys Glu Ile Asp
          20           25           30
Lys Lys Leu Phe Phe Ala Leu Lys Lys Ala Cys Pro Asn Ile Ile Lys
          35           40           45
Val Asp Asn Lys Lys Ala Gln Ser Leu Ala Lys Gly Gly Asn His Gln
          50           55           60
Gly Val Leu Ala Lys Val Glu Leu Pro Leu Ala Val Ser Leu Lys Glu
65          70          75          80
Val Lys Lys Ala Gln Lys Leu Leu Val Leu Cys Gly Ile Thr Asp Val
          85           90           95
Gly Asn Ile Gly Gly Ile Phe Arg Ser Ala Tyr Cys Leu Gly Met Gly
          100          105          110
Gly Val Ile Leu Asp Phe Ala Lys Glu Leu Ala Tyr Glu Gly Ile Val
          115          120          125
Arg Ser Ser Leu Gly Leu Met Tyr Asp Leu Pro Phe Ser Val Met Pro
          130          135          140
Asn Thr Leu Asp Leu Ile Asn Glu Leu Lys Thr Ser Gly Phe Leu Cys
          145          150          155          160
Leu Gly Ala Ser Met Gln Gly Ser Ser Gln Ile Glu Asn Leu Ser Leu
          165          170          175
Lys Lys Cys Ala Leu Phe Leu Gly Ser Glu His Glu Gly Leu Ser Lys
          180          185          190
Lys Ile Leu Ala Lys Met Asp Thr Ile Leu Ser Val Lys Met Arg Arg
          195          200          205
Asp Phe Asp Ser Leu Asn Val Ser Val Ala Ala Gly Ile Leu Met Asp
          210          215          220
Lys Ile Asn
225

```

<210> 629

<211> 344

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (30)...(290)

<400> 629

```

aaccatgcct ttcatcgtc tctatcaaa atg tta ggg tct aaa aca tat tcc    53
                               Met Leu Gly Ser Lys Thr Tyr Ser
                               1           5

gtt tta aga tcg tat gaa aaa aca ttc tcg cct gaa gag ctt tgc att    101
Val Leu Arg Ser Tyr Glu Lys Thr Phe Ser Pro Glu Glu Leu Cys Ile
          10           15           20

```

tta atg ggc aaa aca tac gaa tac ccc atc atg ctt aaa gaa tta ttg 149
 Leu Met Gly Lys Thr Tyr Glu Tyr Pro Ile Met Leu Lys Glu Leu Leu
 25 30 35 40

atg ctt ttg gca aac gct agg gga ttg ctt gaa gcc ttg aaa gtg att 197
 Met Leu Leu Ala Asn Ala Arg Gly Leu Leu Glu Ala Leu Lys Val Ile
 45 50 55

ttc aac atg ctt ggc ttg tca aaa tta aaa gac aaa agc ccg ttt tct 245
 Phe Asn Met Leu Gly Leu Ser Lys Leu Lys Asp Lys Ser Pro Phe Ser
 60 65 70

ttg aga gtg ttg agc agt ttc aag gaa tcc aaa cgc ccc att aca 290
 Leu Arg Val Leu Ser Ser Phe Lys Glu Ser Lys Arg Pro Ile Thr
 75 80 85

tagaaagcct tacgattttt aaacaaacgc tctaaaaaaa gcttggtcgt atga 344

<210> 630
 <211> 87
 <212> PRT
 <213> Helicobacter pylori

<400> 630
 Met Leu Gly Ser Lys Thr Tyr Ser Val Leu Arg Ser Tyr Glu Lys Thr
 1 5 10 15
 Phe Ser Pro Glu Glu Leu Cys Ile Leu Met Gly Lys Thr Tyr Glu Tyr
 20 25 30
 Pro Ile Met Leu Lys Glu Leu Leu Met Leu Leu Ala Asn Ala Arg Gly
 35 40 45
 Leu Leu Glu Ala Leu Lys Val Ile Phe Asn Met Leu Gly Leu Ser Lys
 50 55 60
 Leu Lys Asp Lys Ser Pro Phe Ser Leu Arg Val Leu Ser Ser Phe Lys
 65 70 75 80
 Glu Ser Lys Arg Pro Ile Thr
 85

<210> 631
 <211> 31
 <212> DNA
 <213> Helicobacter pylori

<400> 631 31
 ctgaattcga atgaaaagaa ttttagtctc t

<210> 632
 <211> 29
 <212> DNA
 <213> Helicobacter pylori

<400> 632 29
 ccgctcagat taaaactcat aattcaaat

<210> 633
 <211> 29
 <212> DNA
 <213> Helicobacter pylori

<400> 633
cgcgatccg aagacatgtg caaccgatg

29

<210> 634
<211> 30
<212> DNA
<213> Helicobacter pylori

<400> 634
ccgctcgagc taaaagtttt gcaaaatcac

30

<210> 635
<211> 32
<212> DNA
<213> Helicobacter pylori

<400> 635
cgcgatccg attttacttg aaaaatttaa ac

32

<210> 636
<211> 31
<212> DNA
<213> Helicobacter pylori

<400> 636
ccgctcgagt tagaaagtgt agttcaaata c

31

<210> 637
<211> 24
<212> DNA
<213> Helicobacter pylori

<400> 637
gcggatcctt ttcttcaatg ttg

24

<210> 638
<211> 29
<212> DNA
<213> Helicobacter pylori

<400> 638
ccgctcgagt caaagtttta aacaaattc

29

BEST AVAILABLE COPY